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From: Marvich, Maria
Sent: Wednesday, April 06, 2005 10:28 AM
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Subject: 10/087167

*Please search SEQ ID NO:s nucleotides 1-1524 of 120 , 121 (508 amino acids),
nucleotides 2007-3668 of 104 and 105 (553 amino acid)*

:Thank you

Maria Bonovich Marvich, PhD
United States Patent and Trademark Office
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Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 09:56:57 ; Search time 6626.48 Seconds
(without alignment)
11144.035 Million cell updates/sec

Title: US-10-087-167-120_COPY_1_1524
Perfect score: 1524
Sequence: 1 atgcagcagctatctgtgga.....tggaggagatctggagcgtg 1524

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.cm.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sv.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1524	100.0	1767	6	AX555368 Sequence
2	1414.2	92.8	1782	6	AX555372 Sequence
3	1332	87.4	1848	6	AX555382 Sequence
4	1332	87.4	1863	6	AX555384 Sequence
5	1332	87.4	3972	6	AX555352 Sequence
6	1328.8	87.2	1767	6	AX555370 Sequence
7	1311.2	86.0	1776	6	AX555366 Sequence
8	1222.2	80.2	1800	6	AX555374 Sequence
9	1209	79.3	1428	6	AX555376 Sequence
10	1208.2	79.3	1809	6	AX555390 Sequence
11	1073	70.4	1800	6	AX555395 Sequence
12	955.6	62.7	1500	6	AX555315 Sequence
13	848.8	55.7	1515	6	AX555323 Sequence
14	836	54.9	2126	6	BD224646 Novel ecd
15	836	54.9	2126	6	AX274109 Sequence
16	763.6	50.1	1518	6	AX555341 Sequence
17	763.6	50.1	2840	3	MSU19812 Manduca sex
18	763.6	50.1	2840	6	AX555249 Sequence
19	760.4	49.9	1500	6	AX555317 Sequence

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38	623.2	40.9	2745	6	AS9203	Sequence 4
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ALIGNMENTS

RESULT 1
AX555368
LOCUS AX555368 1767 bp DNA
DEFINITION Sequence 120 from Patent WO02061102.
ACCESSION AX555368
VERSION AX555368.1 GI:25898887

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.
TITLE Control of gene expression in plants
JOURNAL Patent: WO 02061102-A 120 08-AUG-2002;
SYNOPSIS Syngenta Participations AG (CH)

FEATURES
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ORIGIN

Query Match

100.0%; Score 1524; DB 6; Length 1767.

Best Local Similarity 100.0%; Pred. No. 0;		Matches 1524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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RESULT 2

AX555372

LOCUS

DEFINITION

SEQUENCE

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

AX555372

Sequence 124 from Patent WO02061102.

AX555372

AX555372.1 GI:25898891

synthetic construct

synthetic construct

other sequences; artificial sequences.

1

Pascal, E.J., Valentine, S.A., Brown, J.A., Cockrell, A.S. and Johnson, B.D.

Control of gene expression in plants

Patent: WO 02061102-A 124 08-AUG-2002;

Syngenta

Location/Qualifiers

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Best Local Similarity		95.6%; Pred. No. 0;	
Matches 1471; Conservative		0; Mismatches 53; Indels 15; Gaps 1;	
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Db	241	TACTCTCCAAACCAAAAGTCTCGCTGACTAGGCAATCTGACAGAAAGTGAATCA	300
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Qy	361	ATTTTGAAGTGGATTTCTTACAGGATATAAAGCAATTTTAAACAGGATTTTCTGACAA	420
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RESULT 3	AX555382	1848 bp	DNA	linear	PAT 27-NOV-2002
LOCUS	Sequence 134 from Patent WO02061102.				
DEFINITION	AX555382				
ACCESSION	AX555382.1	GI:25898901			
VERSION					
KEYWORDS	synthetic construct				
SOURCE	other sequences; artificial sequences.				
ORGANISM	1				
REFERENCE	Pascal, E.J., Valentine, S.A., Brown, J.A., Cockrell, A.S. and Johnson, B.D.				
AUTHORS	Control of gene expression in plants				
TITLE	Patent: WO 02061102-A 134 08-AUG-2002;				
JOURNAL	Syngenta Participations AG (CH)				
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CDS					
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ORIGIN		Query Match	87.4%	Score 1332	DB 6	Length 1848	
		Best Local Similarity	92.1%	Pred. No. 0			
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Db	1	ATGCAGCAGCTATATGTGGATTTTTTTAGCCCTGCTTTATTTTATTTTGTGTTGG	60				
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Qy	421	GATATGTGTAATAAGATGCGCTCACAGATAGATGGCTTCAGTGGAGACTGATGCTT	480				
Db	421	GATATGTGTAATAAGATGCGCTCACAGATAGATGGCTTCAGTGGAGACTGATGCTT	480				
Qy	481	CTAACATTGACAGCAGCATAGATAAGTGCAGACATCATCGAAGAGAGTAGTAAACAA	540				
Db	481	CTAACATTGACAGCAGCATAGATAAGTGCAGACATCATCGAAGAGAGTAGTAAACAA	540				
Qy	541	GGTCAAGACAGTTGACTGTATCGACGGTATAGGCCCGAGTGGTGTGCTCCAGAGTCC	600				
Db	541	GGTCAAGACAGTTGACTGTATCGACGGTATAGGCCCGAGTGGTGTGCTCCAGAGTCC	600				
Qy	601	ACGTGCAAGAACAAAGAGAGAAAGGAAGCAGACAGAGAGAAAGACAACTGCCAGTC	660				
Db	601	ACGTGCAAGAACAAAGAGAGAAAGGAAGCAGACAGAGAGAAAGACAACTGCCAGTC	660				
Qy	661	AGTACGACGACAGTGGAGCATATGCTGCCATAATGCAATGTGACCCCTCCGCCCCCA	720				
Db	661	AGTACGACGACAGTGGAGCATATGCTGCCATAATGCAATGTGACCCCTCCGCCCCCA	720				
Qy	721	GAGCGGCAAGGATTCAGAAAGTGGTCCGAGGTTCTTAACGAGAGAGCTTAATGGAGAG	780				
Db	721	GAGCGGCAAGGATTCAGAAAGTGGTCCGAGGTTCTTAACGAGAGAGCTTAATGGAGAG	780				
Qy	781	AACAGACTGAAGATGTGACCCGCTGTGCGGCAACAGAGTCCCTGATCGGAGGCTC	840				
Db	781	AACAGACTGAAGATGTGACCCGCTGTGCGGCAACAGAGTCCCTGATCGGAGGCTC	840				
Qy	841	GTGTGGTACCCAGGACGGATACGACAGCTTTCCGAGAGAGATCTCAAAAGGGTGACGAG	900				
Db	841	GTGTGGTACCCAGGAGGGGTACGACAGCCGTCGAGGAGGAGATCTCAAGAGAGTTTACACAG	900				
Qy	901	ACTTGGCAATCAGAGATGAAGAGACGAAGCTCAGACATGCCATTTCCGCCAGATCACA	960				
Db	901	ACTTGGCAATCAGAGATGAAGAGACGAAGCTCAGACATGCCATTTCCGCCAGATCACA	960				

Db	901	ACATGGCAGTTAGAAAGAAAGAGAGAGAAACTGACATGCCCTTCCGTGATCACA	960
Qy	961	GAATGACCATCTTCACAGTACAGCTAATAGTCAGTTTGCCTTCCAAAGGCTTACCTGTTT	1020
Db	961	GAGATGACCATCTTTAAACAGTGCAGCTTATTGTAGAAATTCGAAAGGGACTACCGGATTC	1020
Qy	1021	TCAAAGATCTCACAACTGACACATCATATTATTAAGGATGCTCAAGCGAAGTGTATG	1080
Db	1021	TCCAAGATATCTAGTCGATCAAAATTTACATTTAAGGGCTCATCAGCGAAGTGTATG	1080
Qy	1081	ATGCTGCGAGTACGAGCGGTACGACGCGGTGTGCGATAGCGTTCTGTTCGCCAACAAC	1140
Db	1081	ATGCTGCGAGTACGAGCGGTACGACGCGGTGTGCGATAGCGTTCTGTTCGCCAACAAC	1140
Qy	1141	CAGCGGTACACTCGCGAACAACCTACCGCAAGCGGGCATGGCTACGTTCATCGAAGACCTG	1200
Db	1141	CAGCGGTACACTCGCGAACAACCTACCGCAAGCGGGCATGGCTACGTTCATCGAAGACCTG	1200
Qy	1201	CTGCACTTCTGCGCTGCATGTACTCGATGTGCAATGCAACGTCGATTAACGCTCTC	1260
Db	1201	CTGCACTTCTGCGCTGCATGTACTCGATGTGCAATGCAACGTCGATTAACGCTCTC	1260
Qy	1261	ACTGCCATCGTTATTTCTCGATTCGCGCGGCTAGACAGCACAAGTAGTAGAAGAG	1320
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Qy	1321	ATCCAGCGGTATTTACCTGAAACAGCTCGGGTGTACATCATGAACAGCAGCGCGCTG	1380
Db	1321	ATCCAGAGATACTACTTTGAAGAGCGCTCGGGTTTACATTTTAAATCAGCAGCGCGCTG	1380
Qy	1381	CCGCGTTGCGCGCTCATCTACCGAAGATTTCTGCGGTGTTCGCGAGTTGCGGACGCTG	1440
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Qy	1441	GGCATGCAAGATTCGAACATGTGCATCTCGCTGAAGCTCAAGAACAGAAAGCTCCGCCG	1500
Db	1441	GGCAGCGAGAACTCCAAACATGTGCATCTCGCTGAAGCTGAAGAACAGAAACTTCCGCCA	1500
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RESULT 4
AX555384
LOCUS AX555384 1863 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 136 from Patent WO02061102.
ACCESSION AX555384
VERSION AX555384.1 GI:25898903
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Pascal, E.J., Valentine, S.A., Brown, J.A., Cockrell, A.S. and Johnson, B.D.
TITLE Control of gene expression in plants
JOURNAL Patent: WO 02061102-A 136 08-AUG-2002;
SYNGENTA Participations AG (CH)
FEATURES
Location/Qualifiers
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QY
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Db	2664	AA	CAGACTGAAGAA	TGTGACGCGCTGT	CGCGGAAC	CGAAGTCCCTGAT	TCGAGGCTC	2723				
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Db	2724	GTG	TGGTAC	CCGAGGGGTAC	CGAGCAGCGCT	CGGAGGAAGAT	CTCAAGAGATTAC	CAG	2783			
Qy	901	ACT	TGGCAAT	CAGCAGATGA	AGAAGA	CGAAGACTC	CAGACATG	CCATTC	CGCCAGATCACA	960		
Db	2784	CA	TGCGAGT	TAGAAGAG	AGAGAGGAGGA	AACTGACATG	CCCTTC	CGTCAGATCACA	2843			
Qy	961	GAA	ATGACCAT	CCTC	CAGTAC	AGCTAA	TAGTCGAGTT	TCG	CCAAAGSCCTAC	CTGGTTTT	1020	
Db	2844	GAG	ATGACGAT	CTTAA	CAGTG	CGAGCTTAT	TGTAGAA	TTCC	CAAAGGAC	TACCGGATTC	2903	
Qy	1021	TCA	AGATCTCA	CAACCT	GAC	CAGATCACA	TATTA	AAAGGCATG	CTCAAGCGAAGT	GATG	1080	
Db	2904	TCC	AGATATCT	CAGTCCGAT	CAAA	TTTACAT	TATTA	AGGCGTCAT	CA	GGGAAGT	GATG	2963
Qy	1081	ATG	CTCGGAGT	ACGAGGCGGT	ACGACGCGGT	GTCCGAT	AGCGTTCT	GTT	TCGCCAA	CAAC	1140	
Db	2964	ATG	CTCGAGT	GCGCGGTAC	AGCGGTAC	AGCGCGGAC	CGGACG	CGGTGCT	GTT	TCGGAA	CAAC	3023
Qy	1141	CAG	CGGTAC	ACTCGCGAC	AACTAC	CGGCAAGCGGGG	CGATGCGCT	ACGT	CA	TCAAGAC	CTG	1200
Db	3024	CAG	CGGTAC	ACGCGGAC	AACTAC	CGGCAAGCGGGG	CGATGCT	CA	TCAAGAC	CTG	3083	
Qy	1201	CTG	CAC	TTCTGCGCT	GCATGTACT	CGATG	CGACGAC	CAACGTGCAT	TAC	CGCGCT	CTCT	1266
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Qy	1321	ATC	ACGCGGT	ATTACTCT	GAAACA	CGCTCGCGGT	GTACATCAT	GAAC	CAGCAG	CGCGTCG	1380	
Db	3204	ATC	CAGAGAT	TACTTTGA	AGACGCTCGCGGT	TTTACATTTT	AAATC	AGCAG	ACGCGCGTCG	3263		
Qy	1381	CCG	GTTGCCCGT	CATCTAC	CGGMAAGATTTCT	GTCGCGT	GTCTACCG	GAGTTCCG	GACG	CGTG	1444	
Db	3264	CCT	CGTGC	CGCGTGTCT	TCGCGAAGAT	CTCTCGGCGT	GTCTGAC	GGA	ACTCGG	CAGCGT	3322	
Qy	1441	GGC	ATG	CAGAA	TGTGCATCT	CGCTGA	AGCTTCA	AGAA	CAGGA	AGCTG	CCCGG	1501
Db	3324	GGC	ACG	CAGAA	CTTCCA	CACTGTGCATCT	CGCTGA	AGCTG	GA	AGAA	CAGGA	3381
Qy	1501	TT	CCTGG	AGAGATCT	CGGACGTG	1524						
Db	3384	TT	CCTCG	AGGAGATCT	CGGACGTG	3407						

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RESULT 6
AX555370          AX555370          1767 bp      DNA
LOCUS              Sequence 122 from Patent WO02061102.
DEFINITION
AX555370
ACCESSION
AX555370.1      GI:25898889
VERSION
KEYWORDS
SOURCE
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1      Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and
      Johnson,B.D.
      Control of gene expression in plants
      Patent: WO 02061102-A 122 08-AUG-2002;
      Syngenta Participations AG (CH)
      Location/Qualifiers
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	LTLRQHRISATSSSESNKQORQLTVSTRMPCVPESTCKNKRREKAQREKDL	Qy	961	GAATGACCATCTCTCAGAGTACAGTAACTAGTCCAGTTTGCCTCAAGGCTTACCTGGTTT	1020
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ORIGIN		Qy	1141	CAGGCGTACACTCGCGCAACATACCGCAAGGGGCGCATGCTCATCGAAGACCTG	1200
	Query Match 87.2%; Score 1328.8; DB 6; Length 1767;	Db	1141	CAGGCGTACACTCGCGCAACATACCGCAAGGGGCGCATGCTCATCGAAGACCTG	1200
	Best Local Similarity 92.0%; Pred: No. 2.4e-313;	Qy	1201	CTGCACCTTCTGCGGTGATGTACTGCGATGCGATGGAGCAACGTCATTTACCGCTCTC	1260
	Matches 1402; Conservative 0; Mismatches 122; Indels 0; Gaps 0;	Db	1201	CTGCACCTTCTGCGGTGATGTACTGCGATGCGATGGAGCAACGTCATTTACCGCTCTC	1260
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Qy	121 ACCATGAAGCTACTGCTTCTATCGAAACGAAGTACGATATTGCGCATTTAAAAGCTC	180			
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Qy	181 AGTGTCTTCCAAAGAAAACCGAAGTGGCCAGTGTCTGAAGAACAACTGGAGTGTCCG	240			
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Db	421 GATAATGTGAATAAAGATGCGCTCACAGATAGATTTGCTTCACTGGAGACTGATATGCTT	480			
Qy	481 CTAACATTGAGACAGCATAGAAATAGTGCACATCATCATCGAAGAGAGTAGTAACAAA	540			
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RESULT 7
AX555366 LOCUS 1776 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 118 from Patent WO02061102.
ACCESSION AX555366
VERSION AX555366.1 GI:25898885
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Pascal, E.J., Valentine, S.A., Brown, J.A., Cockrell, A.S. and Johnson, B.D.
TITLE Control of gene expression in plants
JOURNAL Patent: WO 02061102-A 118 08-AUG-2002;
Syngenta Participations AG (CH)
FEATURES Location/Qualifiers

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TITLE	Control of gene expression in plants
JOURNAL	Patent: WO 0206102-A 126 08-2002;
FEATURES	Syngenta Participations AG (CH)
source	Location/Qualifiers
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	Best Local Similarity 87.8%; Pred. No. 3.1e-287;
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DB	
QY	61 TACTGTTTTCTTTGTCGATGCTACCTGTGTTTGGTGTGTACTCTTCGAGGATCCGCC 120
DB	
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QY	481 CTAAACATTGAGACAGCATAGATAAGTGGACATCATCATCGGAAGAGAGTAGTAGTAAACAA 540
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other sequences; artificial sequences.		
1	Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.	
TITLE	Control of gene expression in plants	
JOURNAL	Patent: WO 02061102-A 128 08-AUG-2002; Syngenta Participations AG (CH)	
FEATURES	Location/Qualifiers	
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ORIGIN		
Query Match	79.3%; Score 1209; DB 6; Length 1428;	
Best Local Similarity	91.4%; Pred. No. 5.1e-284;	
Matches 1281; Conservative	0; Mismatches 120; Indels 0; Gaps 0;	
QY	124	ATGAGCTACTGCTCTTATCGAACCAAGCATCGGATATTTCGCGACTTTAAAGAGCTCAAG 183
DB	1	ATGAGCTACTGCTCTTATCGAACCAAGCATCGGATATTTCGCGACTTTAAAGAGCTCAAG 60
QY	184	TGCTCCAAAGAAAACCGAAGTGCAGTGTCTGGAAGAAACAATCGGAGTGTGCTGATC 243
DB	61	TGCTCCAAAGAAAACCGAAGTGCAGTGTCTGGAAGAAACAATCGGAGTGTGCTGATC 120
QY	244	TTCTCCAAACCAAAGGTCTCGCTGACTAGGCACATCTCACAGAGTGGAAATCAAGG 303
DB	121	TTCTCCAAACCAAAGGTCTCGCTGACTAGGCACATCTCACAGAGTGGAAATCAAGG 180
QY	304	CTAGAAAGACTGGAACAGCTATTCTCTGATTTTCTCTGAGAGACCTTGACATGATT 363
DB	181	CTAGAAAGACTGGAACAGCTATTCTCTGATTTTCTCTGAGAGACCTTGACATGATT 240
QY	364	TTGAAAATGGATTCTTTACAGATATAAAGCATTTGTTAAACAGGATTTTGTACAAGAT 423
DB	241	TTGAAAATGGATTCTTTACAGATATAAAGCATTTGTTAAACAGGATTTTGTACAAGAT 300
QY	424	AATGTGAATTAAGATCCCGTACAGATAGATTGGCTTCAGTGGAGACTGATGCTCTTA 483
DB	301	AATGTGAATTAAGATCCCGTACAGATAGATTGGCTTCAGTGGAGACTGATGCTCTTA 360
QY	484	ACATTGAGACAGCATAGAATAAGTGGACATCATCATCGGAAGAGAGTAGTAACAAGGT 543
DB	361	ACATTGAGACAGCATAGAATAAGTGGACATCATCATCGGAAGAGAGTAGTAACAAGGT 420
QY	544	CAAAAGACAGTTGATGTATGACGCGTATGAGCCCGAGTGGCTGCTCCAGAGTCCACG 603
DB	421	CAAAAGACAGTTGATGTATGACGCGTATGAGCCCGAGTGGCTGCTCCAGAGTCCACG 480
QY	604	TGCAGAACAAAAGAGAGAAAAGGAGACACAGAGAGAAAACACAACTGCGCAGTCACT 663
DB	481	TGCAGAACAAAAGAGAGAAAAGGAGACACAGAGAGAAAACACAACTGCGCAGTCACT 540
QY	664	ACGACGACAGTGGACGATCATATGCTTGCCTGACATTAATGCAATGTGACCTCGGCCCCAGAG 723

Db	541	ACGACGACAGTGGACGATCATATGCTGCCATAATGTAATGTGACCTCCGCCCCCCAGAG 600
QY	724	GCGGCAAGGATTCAAGAGTGTCCGAGGTTCTTAACGGAGAGCTAATGAGGAGAAC 783
Db	601	GCGGCAAGGATTCAAGAGTGTCCGAGGTTCTTAACGGAGAGCTAATGAGGAGAAC 660
QY	784	AGACTCAAGAATGTGACGCGCTGTGCGGCAACCAAGAACTCCCTGATCGCGAGGCTCGTG 843
Db	661	AGACTCAAGAATGTGACGCGCTGTGCGGCAACCAAGAACTCCCTGATCGCGAGGCTCGTG 720
QY	844	TGTTACCAAGACGATACGAGAGCTTCGGAAGAGGATCTCAAAGGGTGACGAGACT 903
Db	721	TGTTACCAAGAGGGGTACGAGAGCTTCGGAAGAGGATCTCAAAGAGGTTACACAGACA 780
QY	904	TGCAATACGAGATCAAGAAGACGAGAGCTCAGACATGCCATTCCGCGACAGATCACAGAA 963
Db	781	TGCAATACGAGATCAAGAAGACGAGAGCTCAGACATGCCATTCCGCGACAGATCACAGAG 840
QY	964	ATGACCATCTCAAGTACAGCTAATAGTCGAGTTTTCGCAAGAGGCTTACTGCTGTTTTTCA 1023
Db	841	ATGACCATCTTAACAGTGCAGCTTATTGTAGAAATTCGAAAGGACTACCGGATTTCTCC 900
QY	1024	AGATCTCAACCTGACGAGATCAATATTAAAGGCATGCTCAAGCGAAGTGATGATG 1083
Db	901	AGATATCTCAGTCCGATCAATATTAAAGGCGTCATCAAGCGAAGTGATGATG 960
QY	1084	CTCGAGTAGCGAGGCGGTACGACGCGTGTCCGATAGCGTTCTGTTGCGCAACAACACAG 1143
Db	961	CTCGAGTAGCGGCGAGCGTACGACGCGGCGACGACGAGCGTGTGTTCCGGAACAACACAG 1020
QY	1144	GCCTACACTCGCGACAACTACCCAAAGGCGGCGATGCGCTTACGTCATCGAAGACCTGCTG 1203
Db	1021	GCCTACACTCGCGACAACTACCCAAAGGCGGCGATGCTTACGTCATCGAAGACCTGCTG 1080
QY	1204	CATTCTGCGCTGCATGCTGATCGATCGATCGACAACTGATACGCGCTCTCTCACT 1263
Db	1081	CATTCTGCGCTGCATGCTGATCGATCGATCGACAACTGATACGCGCTCTCTCACT 1140
QY	1264	GCCATCGTTATTTCTCGGATCGCGCGGCTTAGAGCAGCCACAGCTAGTAGAAGATC 1323
Db	1141	GCCATCGTTATTTCTCGGATCGCGCGGCTTAGAGCAGCCACACCTTTTAGTGGAGAAATC 1200
QY	1324	CAGCGGTATTACCTGAAACAGCTGCGGCTGATCATCATGAACGACGACGCGGCTGCGCG 1383
Db	1201	CAGAGATACTACTTGAAGACGCTGCGGCTTTTACATTTTAAATCAGCAGCGCGCTCGCT 1260
QY	1384	CGTTGCGCGCTACTACTACGCGAAGATTCTGTCGCTGCTTACCGAGTTTCGCGACGCTGGGC 1443
Db	1261	CGTTGCGCGCTGCTGTTTCGCGAAGATCTCTCGGCTGCTGACGGAACCTGCGCACGCTCGGC 1320
QY	1444	ATGCAAGATTGCAACATGTGCATCTCGTGAAGCTCAAGAAACAGGAAGCTGCCCGCTTC 1503
Db	1321	ACGCAAGATTGCAACATGTGCATCTCGTGAAGCTCAAGAAACAGGAAGCTGCCCGCTTC 1380
QY	1504	CTGAGAGAGATCTGGGAGCTG 1524
Db	1381	CTGAGAGAGATCTGGGAGCTG 1401

RESULT 10		
AX555390	1809 bp	DNA
LOCUS	Sequence 142 from Patent WO02061102.	linear
DEFINITION		
ACCESSION	AX555390	
VERSION	AX555390.1	GI:25898909
KEYWORDS		
SOURCE		synthetic construct
ORGANISM		synthetic construct
REFERENCE		other sequences; artificial sequences.
AUTHORS		1 Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.
TITLE		Control of gene expression in plants

JOURNAL	Patent: WO 02061102-A 142 08-AUG-2002;	
FEATURES	Syngenta Participations AG (CH)	
source	Location/Qualifiers	
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ORIGIN		
	79.3%; Score 1208.2; DB 6; Length 1809;	
	Query Match	
	Best Local Similarity 90.9%; Pred. No. 8.3e-284;	
	Matches 1285; Conservative 0; Mismatches 128; Indels 0; Gaps 0;	
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Db		
Qy	172 AAAAAGCTCAAGTGCTCCAAAGAAAAACCGAAGTGGCCCAAGTGTCTGAAGAACAACTGG 231	
Db		
Qy	430 AAAAAGCTCAAGTGCTCCAAAGAAAAACCGAAGTGGCCCAAGTGTCTGAAGAACAACTGG 489	
Db		
Qy	232 GAGTGTGGTACTCTCCAAAAACAAAGGTCTCCGTGACTAGGGGACATCTGACAGAA 291	
Db		
Qy	490 GAGTGTGGTACTCTCCAAAAACAAAGGTCTCCGTGACTAGGGGACATCTGACAGAA 549	
Db		
Qy	292 GTGAATCAAGGCTAGAAAGCTGGAACAGCTATTTCTACTGATTTTCTCCAGAGAC 351	
Db		
Qy	550 GTGAATCAAGGCTAGAAAGCTGGAACAGCTATTTCTACTGATTTTCTCCAGAGAC 609	
Db		
Qy	352 CTTGACATGATTTGAAATGGATTCTTTACAGATATAAAGCATTTGTTAAAGGATTA 411	
Db		
Qy	610 CTTGACATGATTTGAAATGGATTCTTTACAGATATAAAGCATTTGTTAAAGGATTA 669	
Db		
Qy	412 TTTGTACAAGATAATGTGAATAAGATGCCGTACAGATAGATGGCTTCAGTGGAGACT 471	
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Qy	670 TTTGTACAAGATAATGTGAATAAGATGCCGTACAGATAGATGGCTTCAGTGGAGACT 729	
Db		
Qy	472 GATATGCTCTTAACATTGACACAGCATAGATAAGTCCGACATCATCTCGAAGAGAGT 531	
Db		
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Db		
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Qy	652 CTGCCAGTCAAGACAGCATGATCATATGCTGGCATTAATGCAATGTGACCT 711	
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Qy	712 CCGCCCCCAGAGGGCGAAGATTACGAAAGTGTCCCGAGTGTCTTAACCGAGAAAGCTA 771	
Db		

Db	970	CCGCCCCCAGAGGGCGCAAGGATTCAAGAGTGTGCCGAGGTTCTTAACGAGAGAGCTA	1029
Qy	772	ATGGAGCAGAAACAGACTGAAGAATGTGACGCCGTGTGCGGGAACCAAGAGTCCCTGATC	831
Db	1030	ATGGAGCAGAAACAGACTGAAGAATGTGACGCCGTGTGCGGGAACCAAGAGTCCCTGATC	1089
Qy	832	CGAGGCTGTGTGTGTACAGGACGGATA CGAGACAGCTTTCGGAAGAGATCTCAAAAGG	891
Db	1090	CGAGGCTGTGTGTGTACAGGACGGGTACGAGCAGCGCGTTCGGAAGAGATCTCAAGAGA	1149
Qy	892	GTGACGACAGCTTGGCAATCAGCAGTGAAGAGCAAGAGACTCAGACATGCAATTCGCG	951
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Qy	952	CAGATCACAGAAATGACCATCTCACAGTACAGCTTAATAGTCGAGTTCGCCAAAGCCCTA	1011
Db	1210	CAGATCACAGAGATGACGATCTTAACAGTGCAGCTTATTTAGATTTTCGAAAGGACTA	1269
Qy	1012	CCTGGTTCCTCAAGATCTCAACCTGACAGATCAATATTATTAAGGCATGCTCAAGC	1071
Db	1270	CGGCGATTCTCCAGATATCTCAGTCCGATCAAAATTTACATTTATTAAGCGCTCATCAGC	1329
Qy	1072	GAGTGTGATGCTCGGAGTAGCAGGCGGTACGACGCGGTGTCGAGTAGCGTCTGTTC	1131
Db	1330	GAGTGTGATGCTCGGAGTAGCAGGCGGTACGACGCGGTGTCGAGTAGCGTCTGTTC	1389
Qy	1132	GCCAAACACGCGGTACACTCGCAGCAAACTACCCGAGCGGCGATGCGCTACGTCATC	1191
Db	1390	GCGAAACACGCGGTACACTCGCAGCAAACTACCCGAGCGGCGATGCGCTACGTCATC	1449
Qy	1192	GAGACCTGCTGACATTTGCGCGTGCATGTACTCGATGTCGATGTCGATGCAACAGTCGAT	1251
Db	1450	GAGGACCTGCTGACATTTGCGCGTGCATGTACTCGATGTCGATGTCGATGCAACAGTCG	1509
Qy	1252	GCGCTCTCAGTCCATGCTTATTTATTCGATGTCGCGCGGCGCTAGAGCAGCCACAGCTA	1311
Db	1510	GCGCTCTCAGTCCATGCTTATTTATTCGATGTCGCGCGGCGCTAGAGCAGCCACAGCTA	1569
Qy	1312	GTAGAAGAGATCCAGCGGTATTACCTGAACAGCTGCGGGTGTACATCATGAACACAGCAC	1371
Db	1570	GTGAGAGAAATCCAGAGATCTACTTGAAGAGCTGCGGGTTTACATTTTAAATCAGCAC	1629
Qy	1372	AGCGGCTGCGCGGTTGCGCGCTCATCTACGCAAGATTTCTGCGGTGCTTACCGAGTTG	1431
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Qy	1432	CGGACGCTGGGATGTCAGAAATTCGAAACATGTCATCTCGCTGAGCTCAAGTCAAGACAG	1491
Db	1690	CGCAGCTGCGGACGCGAAGCTCCAAACATGTCATCTCGCTGAGCTGAAGTGAAGAACAG	1749
Qy	1492	CTGCGCGGTTCTCTGAGGAGATCTGGGACGTG 1524	
Db	1750	CTTCCGCCATTCTCGAGGAGATCTGGGACGTG 1782	
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LOCUS	AX555395		linear
DEFINITION	AX555395		
ACCESSION	AX555395.1		
VERSION	GI:25898914		
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	other sequences; artificial sequences.		
REFERENCE	1		
AUTHORS	Pascal, E.J., Valentine, S.A., Brown, J.A., Cockrell, A.S. and Johnson, B.D.		
TITLE	Control of gene expression in plants		
JOURNAL	Patent: WO 02061102-A 147 08-AUG-2002;		
FEATURES	Syngenta Participations AG (CH)		
source	Location/Qualifiers		
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ORIGIN

Query Match	70.4%;	Score 1073;	DB 6;	Length 1800;
Best Local Similarity	79.2%;	Pred. No. 8.5e-251;		
Matches 1404;	Conservative 0;	Mismatches 120;	Indels 249;	Gaps 1;
QY	1	ATGCAGCAGCTATATGTGGATTTTTTTTAGCCCTCGCTTATACGCTATTTATTTGCTTGG	60	
DB	1	ATGCAGCAGCTATATGTGGATTTTTTTTAGCCCTCGCTTATACGCTATTTATTTGCTTGG	60	
QY	61	TACTGTTTTCTTTTGTGATGCTCACCCCTGTTGTTGGTGTACTTCTCGCAGGATCCGCC	120	
DB	61	TACTGTTTTCTTTTGTGATGCTCACCCCTGTTGTTGGTGTACTTCTCGCAGGATCCGCC	120	
QY	121	ACCATGAAGCTACTGTCTTCTATCGAAACAAGCATGCGGATATTTGCCGACTTTAAAAAGCTC	180	
DB	121	ACCATGAAGCTACTGTCTTCTATCGAAACAAGCATGCGGATATTTGCCGACTTTAAAAAGCTC	180	
QY	181	AAGTGCTCCAAAGAAAAACCGAAGTGCGCCAAGTGTCTGAAGAACNACTGGAGTGTGCG	240	
DB	181	AAGTGCTCCAAAGAAAAACCGAAGTGCGCCAAGTGTCTGAAGAACNACTGGAGTGTGCG	240	
QY	241	TACTCTCCAAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAAAGTGAATCA	300	
DB	241	TACTCTCCAAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAAAGTGAATCA	300	
QY	301	AGGCTAGAAAGACTGGAAACAGCTATTCTCTACTGATTTTTCTCGAAGAGACCTTGACATG	360	
DB	301	AGGCTAGAAAGACTGGAAACAGCTATTCTCTACTGATTTTTCTCGAAGAGACCTTGACATG	360	
QY	361	ATTTTGAANAATGGATTCTTTTACAGGATATAAAGCATTGTTAAACAGGATTTATTTGTACAA	420	
DB	361	ATTTTGAANAATGGATTCTTTTACAGGATATAAAGCATTGTTAAACAGGATTTATTTGTACAA	420	
QY	421	GATAATGTGAATAAAGATGCCGTCTACAGATAGTTGGCTTCAGTGGAGACTGATAGCTT	480	
DB	421	GATAATGTGAATAAAGATGCCGTCTACAGATAGTTGGCTTCAGTGGAGACTGATAGCTT	480	
QY	481	CTAACATTGAGACACATAGATAAGTGCACATCATCATCGGAAGAGAGTAGTAACAAA	540	
DB	481	CTAACATTGAGACACATAGATAAGTGCACATCATCATCGGAAGAGAGTAGTAACAAA	540	
QY	541	GGTCAAAAGACAGTTGACTGTATCGACCGGTATGAGCCCGAGTGGTTCGTCCAGAGTC-	599	
DB	541	GGTCAAAAGACAGTTGACTGTATCGACCGGTATGAGCCCGAGTGGTTCGTCCAGAGTCC	600	
QY	600	-----	599	
DB	601	AGGTGCAAGCTTGCCTCCCGCCGACCGATGTACGCTGGGGAGCGAGCTCCACTTAGACGCG	660	
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Qy	983	AGCTAATAGTCGAGTTTGC	1500 bp	DNA	linear	PAT 27-NOV-2002
Db	716	AGCTAATAGTCGAGTTTGC	Sequence 67 from Patent WO02061102.			
Qy	1043	AGATCACAATTATTAAGG	AX555315			
Db	776	AGATCACAATTATTAAGG	Sequence 67 from Patent WO02061102.			
Qy	1103	ACGACGCGGTCTCGGATAG	AX555315.1	GI:25898834		
Db	836	ACGACGCGGTCTCGGATAG	synthetic construct			
Qy	1163	ACCGCAAGCGCGGATGGCT	other sequences; artificial sequences.			
Db	955	ACCGCAAGCGCGGATGGCT	1			
Qy	1223	ACTCGATGTCGATGGACAA	Pascal,B.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and			
Db	956	ACTCGATGTCGATGGACAA	Johnson,B.D.			
Qy	1283	ATCGSCCGGGCTTAGAGCAG	Control of gene expression in plants			
Db	1016	ATCGSCCGGGCTTAGAGCAG	Patent: WO 02061102-A 67 08-AUG-2002;			
Qy	1343	CGCTGCGGGTGTACATCAT	Syngenta Participations AG (CH)			
Db	1076	CGCTGCGGGTGTACATCAT	Location/Qualifiers			
Qy	1403	CGAAGATTCTGTCGGTGCT	1..1500			
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Qy	1463	GCATCTCGCTGAAGCTCA	/mol_type="unassigned DNA"			
Db	1196	GCATCTCGCTGAAGCTCA	/db_xref="taxon:32630"			
Qy	1523	TG 1524	1..1500			
Db	1256	TG 1257	/note="unnamed protein product; Ecdysone Receptor chimera"			
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LOCUS	AX555323	Sequence 75 from Patent WO02061102.				
DEFINITION	AX555323	1515 bp				
ACCESSION	AX555323	DNA				
VERSION	AX555323.1	linear				
KEYWORDS	GI:25898842					
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
source						
CDS						

Qy	563	CGACGCGTATGAGCCCGAGT	62.7%; Score 955.6; DB 6; Length 1500;			
Db	296	CGGTGGGATGAGCCCGAGT	Best Local Similarity 99.6%; Pred. No. 3.9e-222;			
Qy	623	AAAGGAGCAGACAGAGAA	Matches 958; Conservative 0; Mismatches 4; Indels 0; Gaps 0;			
Db	356	AAAGGAGCAGACAGAGAA				
Qy	683	ATATGCTGCGCAATATGCA				
Db	416	ATATGCTGCGCAATATGCA				
Qy	743	TGTTCCCGAGGTTCTTAAC				
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Qy	803	CGCTGTCCGGAACACGAA				
Db	536	CGCTGTCCGGAACACGAA				
Qy	863	AGCAGCTTCGGAAGAGAT				
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Qy	923	AAGACGAAGACTCAGACAT				
Db	656	AAGACGAAGACTCAGACAT				

ORIGIN

Query Match	62.7%; Score 955.6; DB 6; Length 1500;
Best Local Similarity	99.6%; Pred. No. 3.9e-222;
Matches	958; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy	563 CGACGCGTATGAGCCCGAGTGGTGGTCCGAGATCCAGTCCGCAAGAACAAAGAGAG 622
Db	296 CGGTGGGATGAGCCCGAGTGGTGGTCCGAGATCCAGTCCGCAAGAACAAAGAGAG 355
Qy	623 AAAGGAGCAGACAGAGAAAGACAACTGCCAGTCACTAGCAGCAGAGTGAGGATC 682
Db	356 AAAGGAGCAGACAGAGAAAGACAACTGCCAGTCACTAGCAGCAGAGTGAGGATC 415
Qy	683 ATATGCTGCGCAATATGCAATGTGACCTCCGCCCCAGAGCGGCGGAGGATTCACGAG 742
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Qy	743 TGTTCCCGAGGTTCTTAACCGAGAGCTAATGAGCAGAACACAGCTGAAGAAATGTGACGC 802
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Db	536 CGCTGTCCGGAACACGAAAGTCCCTGATCCGAGGCTCGTGTGTTACCGAGGATGATG 595
Qy	863 AGCAGCTTCGGAAGAGATCTCAAGGGGTGACGAGACTTGGCAATCAGCAGATGAAG 922
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1161 GTCTGGTCTTACCGAGTTCGGGACGCTGGGCATGCAGAAATTCGAAATGTGCATCTCGCT 1220
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1221 GAAGCTCAAGAACAGAGAACTGCGCCGCTTCTGGAGGAGATCTGGACGTG 1272

RESULT 14
BD224646
LOCUS
DEFINITION Novel ecdysone receptors and methods for their use. PAT 17-JUL-2003
ACCESSION BD224646
VERSION BD224646.1 GI:33034416
KEYWORDS JP 2002525053-A/1
SOURCE Ostrinia nubilalis (European corn borer)
ORGANISM Ostrinia nubilalis

REFERENCE
AUTHORS Albertsen, M.C., Brooke, C.D., Garnaat, C.W. and Roth, B.A.
TITLE Novel ecdysone receptors and methods for their use
JOURNAL Patent: JP 2002525053-A 1 13-AUG-2002;
PIONEER HI BRED INTERNATIONAL INC
COMMENT OS Ostrinia nubilalis
PN JP 2002525053-A/1
PD 13-AUG-2002
PF 10-SEP-1999 JP 2000570318
PR 10-SEP-1998 US 60/099793
PI MARC C ALBERTSEN, CATHERINE D BROOKE, CARL W GARNAA, BRADLEY PI
ALLEN ROTH

PC C12N15/09, A01H5/00, C07K14/705, C12N5/10, C12P21/02//C07K19/00,
PC C12N15/00,
PC C12N5/00,
CC Nucleotide sequence and deduced amino acid sequence of CC
Ecdysone receptor
FH Key Location/Qualifiers
FT CDS (368)..(2005).
Location/Qualifiers
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/db_xref="taxon:29057"

FEATURES
source
Query Match 54.9%; Score 836; DB 6; Length 2126;
Best Local Similarity 90.1%; Pred. No. 6 4e-193;
Matches 912; Conservative 0; Mismatches 85; Indels 15; Gaps 1;
QY 528 GAGTAGTAACAAGAGTCAAGACAGTTGACTGTATCGACGGTATGAGCCCGAGTGGCT 587
DB 940 GAATGTCAAGATGCGGTTGAAGAGTGTAGCGTGGCATGAGCCCGAGTGGCT 999
QY 588 CGTCCAGAGTCCACGTGCAAGAACAAAGAGAGAAAGAGACAGACAGAGAGAAAGA 647
DB 1000 GGTGCCAAGACGAGTGTGCGCAAAAAGAGAAAGAGAGAGAGAGAGAGAGAGAG 1059
QY 648 CAATCTCGAGTACGACAGACAGTGGACGATCATATGCTGCCATTAATGCAATGTGA 707
DB 1060 CAATCTCGAGTACGACAGACAGTGGACGATCATATGCTGCCATTAATGCAATGTGA 1119
QY 708 CCCTCCGCCCCCAGAGCGGCAAGGATTT-----CACGAGTGGTCCCGAG 752
DB 1120 TCCGCCACCCCGGAGGCGAGGATTTCTGGAATGTTTGCAGCATGAAGTGGTCCCGCG 1179
QY 753 GTTCTCAAGAGAGAGTAAATGAGAGACAGACTGAAGATGTGACCGCGTGTCCGC 812
DB 1180 GTTCTCTCGAGAGAGTGTATGAGAGAGAGTGTGTTGAAGAACATACCCCTCCACGCG 1239
QY 813 GAACAGAGAGTCCCTGTGATCGGAGGCTCGTGTGGTACGAGACGATACGAGAGCCTTC 872
DB 1240 CAACAGCAGTTCCTGATCGGAGGCTGTGTGTACCGAGCGATACGAGAGCCTTC 1299

QSDAEDBDSMPFRQITMTILVQLIVFAKGLPGFSKISQPDQITLLKACSEVM
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LLTAIVTFSDRPGLEQPOLVEIQRYYLINTLRVYIMHQHSAPRCVIAKILSVLITE
LRTIGMONSNMCI SLKLNKRLPPLEIEIWDVLAAPTDSVLGDELHLDGEDVAMAH
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ORIGIN
Query Match 55.7%; Score 848.8; DB 6; Length 1515;
Best Local Similarity 90.9%; Pred. No. 4.6e-196;
Matches 920; Conservative 0; Mismatches 77; Indels 15; Gaps 1;
QY 528 GAGTAGTAACAAGTCAAGACAGTTGACTGTATCGACGGTATGAGCCCGAGTGGCT 587
DB 261 GAAATGTCAAGATGCGCGTTGAAGAGTGTAGCGGTGGCATGAGCCCGAGTGGCT 320
QY 588 CGTCCAGAGTCCACGTCAAGAACAAAGAGAGAGAAAGAGACAGACAGAGAGAAAGA 647
DB 321 GGTGCCAAGACCGAGTGTGCGCAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 380
QY 648 CAATCTCGAGTACGACAGACAGTGGACGATCATATGCTGCCATTAATGCAATGTGA 707
DB 381 CAATCTCGAGTACGACAGACAGTGGACGATCATATGCTGCCATTAATGCAATGTGA 440
QY 708 CCCTCCGCCCCCAGAGCGGCAAGGATTT-----CACGAGTGGTCCCGAG 752
DB 441 TCCACCCCGCGGAGGCGAGGATTTCTGGAATGTTTGCAGCATGAAGTGGTCCCGCG 500
QY 753 GTTCTCAAGAGAGAGTAAATGAGACAGAAACAGACTGAAGATGTGACCGCGCTGTCCGC 812
DB 501 GTTCTCTCGAGAGAGTGTGAGACAGAGTGGACAGATCGGCTGAAGAACATACCCCTCCACGCG 560
QY 813 GAACAGAGTCCCTGTATCGGAGGCTCGTGTGGTACGAGACGATACGAGAGCCTTC 872
DB 561 CAACAGCAGTTCCTGATCGGAGGCTGTGTGTGTACGAGCGGATACGAGAGCCTTC 620
QY 873 GGAAGAGGATCTCAAGAGGTTGACGAGTGGCAATCAGCAGATGAAGAGAGAGAGAG 932
DB 621 GGAAGAGGATCTCAAGAGGTTGACGAGTGGCAATCAGCAGATGAAGAGAGAGAGAG 680
QY 933 CTCAGACATGCCATTCGCGCAGATCACAGAAATGACCATCTCTCAAGTACAGTAAATAGT 992
DB 681 CTCAGACATGCCATTCGCGCAGATCACAGAAATGACCATCTCTCAAGTACAGTAAATAGT 740
QY 993 CGAGTTTGCAGAGGCTACCTGGTTTTCAGAGATCTCAGAACCTGACAGATCACATT 1052
DB 741 CGAGTTTGCAGAGGCTACCTGGTTTTCAGAGATCTCAGAACCTGACAGATCACATT 800
QY 1053 ATTAAGGATGCTCAAGGAAATGATGATGCTGCGAGTAGCGAGCGGTACGACGCGT 1112
DB 801 ATTAAGGATGCTCAAGGAAATGATGATGCTGCGAGTAGCGAGCGGTACGACGCGT 860
QY 1113 GTCGATAGCGTTCTGTTCCGCAACAAACAGCGGTACACTCGCGAACATACCGCAAGGC 1172
DB 861 GTCGATAGCGTTCTGTTCCGCAACAAACAGCGGTACACTCGCGAACATACCGCAAGGC 920
QY 1173 GGGCATGGCTAGTATCGAAGACTGCTGACATCTGCGCGTGTGATGCTGCTGATGTC 1232
DB 921 GGGCATGGCTAGTATCGAAGACTGCTGACATCTGCGCGTGTGATGCTGCTGATGTC 980
QY 1233 GATGGAACAAGTGCATTTAGCGCTCTCTCACTGCGATCGTTATATTTCTCGGATCGCGCGG 1292
DB 981 GATGGAACAAGTGCATTTAGCGCTCTCTCACTGCGATCGTTATATTTCTCGGATCGCGCGG 1040
QY 1293 CTTAGAGACCCACAGTATGAGAGATCCAGCGGTATTACCTGAACACGCTCGGGT 1352
DB 1041 CTTAGAGACCCACAGTATGAGAGATCCAGCGGTATTACCTGAACACGCTCGGGT 1100
QY 1353 GTACATCATGACACAGACGCGCTGCGCGGTGCTGCGCGTCTCATCTAGCGAAGATTCT 1412
DB 1101 GTACATCATGACACAGACGCGCTGCGCGGTGCTGCGCGTCTCATCTAGCGAAGATTCT 1160
QY 1413 GTCGCTGCTTACCGAGTTCGCGAGCTGGGCGATGCAGAAATCGAAATGTGATCTCGCT 1472

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 08:10:36 ; Search time 839.013 Seconds
(without alignments)
10752.734 Million cell updates/sec

Title: US-10-087-167-120_COPY_1_1524
Perfect score: 1524
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseqn1990s:
3: Geneseqn2000s:
4: Geneseqn2001as:
5: Geneseqn2001bs:
6: Geneseqn2002as:
7: Geneseqn2002bs:
8: Geneseqn2003as:
9: Geneseqn2003bs:
10: Geneseqn2003cs:
11: Geneseqn2003ds:
12: Geneseqn2004as:
13: Geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1524	100.0	1767	6	ABT07367 Chimeric
2	1524	100.0	1767	10	ADF49192 Ecdysone
3	1414.2	92.8	1782	6	ABT07369 Chimeric
4	1414.2	92.8	1782	10	ADF49196 Ecdysone
5	1332	87.4	1848	6	ABT07376 Chimeric
6	1332	87.4	1848	10	ADF49206 Ecdysone
7	1332	87.4	1863	6	ABT07377 Chimeric
8	1332	87.4	1863	10	ADF49208 Ecdysone
9	1332	87.4	3972	6	ABT07353 Ecdysone
10	1332	87.4	3972	10	ADF49176 Ecdysone
11	1328.8	87.2	1767	6	ABT07368 Chimeric
12	1328.8	87.2	1767	10	ADF49194 Ecdysone
13	1311.2	86.0	1776	6	ABT07365 Chimeric
14	1311.2	86.0	1776	10	ADF49190 Ecdysone
15	1222.2	80.2	1800	6	ABT07370 Chimeric
16	1222.2	80.2	1800	10	ADF49198 Ecdysone
17	1209	79.3	1428	6	ABT07371 Chimeric
18	1209	79.3	1428	10	ADF49200 Ecdysone
19	1208.2	79.3	1809	6	ABT07382 Chimeric
20	1208.2	79.3	1809	10	ADF49214 Ecdysone

21	1073	70.4	1800	6	ABT07386 Chimeric
22	1073	70.4	1800	10	ADF49219 Ecdysone
23	955.6	62.7	1500	6	ABT07331 Chimeric
24	955.6	62.7	1500	10	ADF49139 Ecdysone
25	848.8	55.7	1515	6	ABT07335 Chimeric
26	848.8	55.7	1515	10	ADF49147 Ecdysone
27	836	54.9	2126	3	AAA10312 European
28	763.6	50.1	1518	6	ABT07344 Chimeric
29	763.6	50.1	1518	10	ADF49165 Ecdysone
30	763.6	50.1	2840	6	ABT07274 Manduca s
31	763.6	50.1	2840	10	ADF49073 Manduca s
32	763.6	50.1	2840	12	ADI33132 Tobacco h
33	760.4	49.9	1500	6	ABT07332 Chimeric
34	760.4	49.9	1500	10	ADF49141 Ecdysone
35	742.8	48.7	1509	6	ABT07330 Chimeric
36	742.8	48.7	1509	10	ADF49137 Ecdysone
37	719.4	47.2	763	6	ABT07276 Ostrinia
38	719.4	47.2	763	10	ADF49077 Pall army
39	656.8	43.1	1533	6	ABT07337 Chimeric
40	656.8	43.1	1533	10	ADF49151 Ecdysone
41	638.6	41.9	838	6	ABT07277 Spodopter
42	638.6	41.9	838	10	ADF49079 Pall army
43	638	41.9	3054	13	ADR48569 DNA seque
44	636	41.7	1524	6	ABT07336 Chimeric
45	636	41.7	1524	10	ADF49149 Ecdysone

ALIGNMENTS

RESULT 1
ABT07367
ID ABT07367 standard; DNA; 1767 BP.
XX
AC ABT07367;
XX
DT 29-AUG-2003 (revised)
DT 07-NOV-2002 (first entry)
XX
DE Chimeric ecdysone receptor coding sequence SEQ ID NO: 120.
XX
KW Plant; gene expression control; insect; hormone receptor; fertility;
KW ecdysone receptor; gene; ds.
XX
OS Manduca sexta.
OS Ostrinia nubilalis.
OS Chimeric.
XX
PN WO200261102-A2.
XX
PD 08-AUG-2002.
XX
PF 24-OCT-2001; 2001WO-US051417.
XX
PR 24-OCT-2000; 2000US-0242969P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
DR WPI; 2002-619259/66.
XX
DR P-PSDB; ABJ05373.
XX
PT New receptor cassette encoding a chimeric receptor polypeptide, useful in
XX
PT regulating expression of target polypeptides in plants in the presence of
XX
PT appropriate ligands that may be used in controlling plant fertility.
XX
PS Claim 13; Page 270-272; 319pp; English.
XX
CC The present invention relates to a receptor cassette encoding a chimeric
XX
CC receptor polypeptide comprising at least one DNA binding domain, a hinge
XX
CC domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
XX
CC domain of an insect Ecr, where the ligand binding domain is heterologous

CC with respect to the hinge domain and an activation domain. The chimeric insect hormone receptors and receptor cassettes are useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility. The method is useful for decreasing or increasing plant gene expression. The present sequence is a coding sequence described in the exemplification of the invention. (Updated on 29-AUG-2003 to standardise OS field)			
XX	Sequence 1767 BP; 474 A; 438 C; 473 G; 382 T; 0 U; 0 Other;		
Query Match 100.0%; Score 1524; DB 6; Length 1767;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 ATGCAGCAGCTATATGTGGATTTTATAGCCCTGCCTTCATACGCTATTTATTTGCTTGG 60	Qy	901 ACTTGCAATCAGCAGATGAAGACGAGACTCAGACATGCCATTCCGCCAGATCACA 960
Db	1 ATGCAGCAGCTATATGTGGATTTTATAGCCCTGCCTTCATACGCTATTTATTTGCTTGG 60	Db	901 ACTTGCAATCAGCAGATGAAGACGAGACTCAGACATGCCATTCCGCCAGATCACA 960
Qy	61 TACTGTTTCTTTGTCGATGCTCACCCTGTTGTTGGTGTACTTCTCGAGGATCCGCC 120	Qy	961 GAAATGACCATCTCTCAGCTACAGCTAATAGTCGAGTTTTCGCCAAGGCTTACCTGGTTTT 1020
Db	61 TACTGTTTCTTTGTCGATGCTCACCCTGTTGTTGGTGTACTTCTCGAGGATCCGCC 120	Db	961 GAAATGACCATCTCTCAGCTACAGCTAATAGTCGAGTTTTCGCCAAGGCTTACCTGGTTTT 1020
Qy	121 ACCATGAAGCTACTGCTTCTTATCGAACAAAGCATGCGATATTGCGGACTTTAAAAAGCTC 180	Qy	1021 TCAAAGATCTCACAACCTGACCAGATCATTATTTAAAGGCATGCTCAAAGCGAAGTGATG 1080
Db	121 ACCATGAAGCTACTGCTTCTTATCGAACAAAGCATGCGATATTGCGGACTTTAAAAAGCTC 180	Db	1021 TCAAAGATCTCACAACCTGACCAGATCATTATTTAAAGGCATGCTCAAAGCGAAGTGATG 1080
Qy	181 AAGTGCTCCAAAGAAAACCGAAGTGCGCCAAAGTGTCTGAAGAACAACTGGGAGTGTGCG 240	Qy	1081 ATGCTCGAGTAGCGAGGCGGTACGACGCGGTGTCCGATAGCGTTCTGTTTCGCCAACAAAC 1140
Db	181 AAGTGCTCCAAAGAAAACCGAAGTGCGCCAAAGTGTCTGAAGAACAACTGGGAGTGTGCG 240	Db	1081 ATGCTCGAGTAGCGAGGCGGTACGACGCGGTGTCCGATAGCGTTCTGTTTCGCCAACAAAC 1140
Qy	241 TACTCTCCAAACCAAGAGTCTCCGCTAGTGGCAGCATCTCAGAGAAAGTGAATCA 300	Qy	1141 CAGGCGGTACATCTCGGACAACTACCGCAAGGCGGCGATGCGCTTACGTCAGAGACCTG 1200
Db	241 TACTCTCCAAACCAAGAGTCTCCGCTAGTGGCAGCATCTCAGAGAAAGTGAATCA 300	Db	1141 CAGGCGGTACATCTCGGACAACTACCGCAAGGCGGCGATGCGCTTACGTCAGAGACCTG 1200
Qy	301 AGGCTAGAAAGACTGCGAAGCTATTTCTACTGATTTTCTCTCGAAGAACCTTGACATG 360	Qy	1201 CTGCACTTCTGCGCGTGCATGTACTCGATGCGGCGGCTTACGTCAGTACGCGCTCCTC 1260
Db	301 AGGCTAGAAAGACTGCGAAGCTATTTCTACTGATTTTCTCTCGAAGAACCTTGACATG 360	Db	1201 CTGCACTTCTGCGCGTGCATGTACTCGATGCGGCGGCTTACGTCAGTACGCGCTCCTC 1260
Qy	361 ATTTTGAAGTGGATTTTACAGATATAAAGCATTTGTTAAAGGATTTATTTGTACAA 420	Qy	1261 ACTGCCATCGTTATATTCTCGGATCGGCGGCGCTTAGAGCAGCCACAGCTAGTAGAAGAG 1320
Db	361 ATTTTGAAGTGGATTTTACAGATATAAAGCATTTGTTAAAGGATTTATTTGTACAA 420	Db	1261 ACTGCCATCGTTATATTCTCGGATCGGCGGCGCTTAGAGCAGCCACAGCTAGTAGAAGAG 1320
Qy	421 GATATGTGAATAAAGATCCGTCAGATAGATTGGCTTCAGTGGAGACTGATATGCT 480	Qy	1321 ATCAGCGGTATTAACCTGAACACGCTGCGGCTGTACATCATGAACGACAGCGGCTCG 1380
Db	421 GATATGTGAATAAAGATCCGTCAGATAGATTGGCTTCAGTGGAGACTGATATGCT 480	Db	1321 ATCAGCGGTATTAACCTGAACACGCTGCGGCTGTACATCATGAACGACAGCGGCTCG 1380
Qy	481 CTAACATTGAGACAGCATAGAATAAGTGCAGATCATCATATCGGAAGAGTAGTAACAAA 540	Qy	1381 CCGGTTGCGCGCTCATCTACGCAAGATTCTGTCGGTGTCTTACCGAGTTGCGGACGCTG 1440
Db	481 CTAACATTGAGACAGCATAGAATAAGTGCAGATCATCATATCGGAAGAGTAGTAACAAA 540	Db	1381 CCGGTTGCGCGCTCATCTACGCAAGATTCTGTCGGTGTCTTACCGAGTTGCGGACGCTG 1440
Qy	541 GGTCAAAGACAGTTGACTGTATCGACGCGTATGAGCCCGAGTGGTCTCCAGAGTCC 600	Qy	1441 GGATGACAGAAATTCGAAACATGTGCTATCGCTGAAGCTCAAGAACAGAGAGTCCGCCCG 1500
Db	541 GGTCAAAGACAGTTGACTGTATCGACGCGTATGAGCCCGAGTGGTCTCCAGAGTCC 600	Db	1441 GGATGACAGAAATTCGAAACATGTGCTATCGCTGAAGCTCAAGAACAGAGAGTCCGCCCG 1500
Qy	601 ACCTGCAAGAACAAAAGAGAGAAAAGGACACAGAGAGAAAACAACTGCCAGTTC 660	Qy	1501 TTCTCGAGGAGATCTGGGACGCTG 1524
Db	601 ACCTGCAAGAACAAAAGAGAGAAAAGGACACAGAGAGAAAACAACTGCCAGTTC 660	Db	1501 TTCTCGAGGAGATCTGGGACGCTG 1524
Qy	661 AGTACGACGACGTGACGATCATATGCTTGCATTAATGCAATGTGACCCCTCGGCCCA 720	Qy	1501 TTCTCGAGGAGATCTGGGACGCTG 1524
Db	661 AGTACGACGACGTGACGATCATATGCTTGCATTAATGCAATGTGACCCCTCGGCCCA 720	Qy	1501 TTCTCGAGGAGATCTGGGACGCTG 1524
Qy	721 GAGCGCGCAGGATTCACGAAGTGTCCGAGGTTCTTAACGAGAGAGTAAATGGAGCAG 780	Qy	1501 TTCTCGAGGAGATCTGGGACGCTG 1524
Db	721 GAGCGCGCAGGATTCACGAAGTGTCCGAGGTTCTTAACGAGAGAGTAAATGGAGCAG 780	Qy	1501 TTCTCGAGGAGATCTGGGACGCTG 1524
Qy	781 AACAGACTGAAGATGTGACGCGCTGTCCGCGAACCAAGAGTCCCTGATTCGCGAGGCTC 840	Qy	1501 TTCTCGAGGAGATCTGGGACGCTG 1524
Db	781 AACAGACTGAAGATGTGACGCGCTGTCCGCGAACCAAGAGTCCCTGATTCGCGAGGCTC 840	Qy	1501 TTCTCGAGGAGATCTGGGACGCTG 1524
Qy	841 GTGTGGTACAGAGCGGATCAGAGCGCTTCGGAAGAGGATCTCAAAAGGGGTGACGAG 900	Qy	1501 TTCTCGAGGAGATCTGGGACGCTG 1524
Db	841 GTGTGGTACCAGGCGGATCAGAGCGCTTCGGAAGAGGATCTCAAAAGGGGTGACGAG 900	Qy	1501 TTCTCGAGGAGATCTGGGACGCTG 1524

RESULT 2
ADP49192
ID ADP49192 standard; DNA; 1767 BP.
XX
AC ADP49192;
XX
DT 12-FEB-2004 (first entry)
XX
DE Ecdysone receptor/VP16 transactivation domain DNA seq id 120.
XX
KW receptor cassette; chimeric receptor polypeptide; DNA binding domain;
KW hinge domain; ecdysone receptor; Ecr; ligand binding domain;
KW activation domain; transgenic seed; transgenic plant; plant line;
KW herbicide; pesticide; chimeric ecdysone receptor; Ecr;
KW yeast GAL4 DNA binding domain; VP16 transactivation domain; ds; gene.
XX
OS Synthetic.
OS Manduca sexta.
OS Ascomycota.
OS Ostrinia nubilalis.
OS Herpes simplex virus unknown type.
XX
PN US2003154509-A1.
XX
PD 14-AUG-2003.
XX
PF 24-OCT-2001; 2001US-00087167.

XX 24-OCT-2001; 2001US-00087167.
 XX (PASC/) PASCAL E J.
 XX (VALE/) VALENTINE S A.
 XX (BROW/) BROWN J A.
 XX (COCK/) COCKRELL A S.
 XX (JOHN/) JOHNSON B D.
 XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 XX WPI; 2003-897756/82.
 XX P-PSDB; ADF49193.
 XX New receptor cassette encoding a chimeric receptor polypeptide, useful
 XX PT for regulating the expression of target polypeptides in plants in the
 XX PT presence of appropriate chemical ligands.
 XX PS Example 23; SEQ ID NO 120; 186pp; English.
 XX The invention describes a receptor cassette encoding a chimeric receptor
 XX CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
 XX CC (D) domain of an ecdysone receptor (ECR) of an insect, a ligand binding
 XX CC (E) domain that is heterologous with respect to the D domain, and an
 XX CC activation domain. The receptor cassette and method are useful in
 XX CC regulating the expression of target polypeptides in plants in the
 XX CC presence of appropriate chemical ligands. The transgenic seeds and plants
 XX CC can be used for the breeding of improved plant lines that, for e.g.
 XX CC increase the effectiveness of conventional methods such as herbicide or
 XX CC pesticide treatment. This sequence encodes an ecdysone receptor-Vp16
 XX CC transactivation domain fusion protein.
 XX SQ Sequence 1767 BP; 474 A; 438 C; 473 G; 382 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1524; DB 10; Length 1767;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCAGCAGCTATATGAGATTTTATAGCCCTGCTTATAGCTATTTATTTGCTTGG 60
 DB 1 ATGCAGCAGCTATATGAGATTTTATAGCCCTGCTTATAGCTATTTATTTGCTTGG 60
 QY 61 TACTGTTCTTTTGTGCGATGCTCACCCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 120
 DB 61 TACTGTTCTTTTGTGCGATGCTCACCCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 120
 QY 121 ACCATGAAGCTACTGTTCTTATCGAACAAGCATGCGATATTTGCGGACTTAAAAAGCTC 180
 DB 121 ACCATGAAGCTACTGTTCTTATCGAACAAGCATGCGATATTTGCGGACTTAAAAAGCTC 180
 QY 181 AAGTGTCTCCAAAGAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTGCG 240
 DB 181 AAGTGTCTCCAAAGAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTGCG 240
 QY 241 TACTCTCCCAACCAACCAAGGTCTCCGCTGACTAGGGCAGCATCTGACAGAAAGTGAATCA 300
 DB 241 TACTCTCCCAACCAACCAAGGTCTCCGCTGACTAGGGCAGCATCTGACAGAAAGTGAATCA 300
 QY 301 AGGCTAGAAAGACTGGAAAGCTATTTCTACTGATTTTCTCCGAGAAAGCTTTGACATG 360
 DB 301 AGGCTAGAAAGACTGGAAAGCTATTTCTACTGATTTTCTCCGAGAAAGCTTTGACATG 360
 QY 361 ATTTTGAAGATGATTTCTTACAGGATATTAAGGATTTTAAAGGATTTTGTATACAA 420
 DB 361 ATTTTGAAGATGATTTCTTACAGGATATTAAGGATTTTAAAGGATTTTGTATACAA 420
 QY 421 GATTAATGTAATAAGATGCGGTACAGATAGATTTGGCTTCAGTGGAGACTGATATGCTT 480
 DB 421 GATTAATGTAATAAGATGCGGTACAGATAGATTTGGCTTCAGTGGAGACTGATATGCTT 480
 QY 481 CTAACATTGAGACAGCATAGATTAAGTGGACATCATCATCGGAAGAGAGTAGTAACAAA 540
 DB 481 CTAACATTGAGACAGCATAGATTAAGTGGACATCATCATCGGAAGAGAGTAGTAACAAA 540

QY 541 GGTCAAAGACAGTTGACTGTATCGACGGTATAGGCCCGAGTGGTGGTCCCGAGAGTCC 600
 DB 541 GGTCAAAGACAGTTGACTGTATCGACGGTATAGGCCCGAGTGGTGGTCCCGAGAGTCC 600
 QY 601 ACGTGCAAGAACAAAAGAAAGAAAGAACACACAGAGAGAGAAAGAAAGAAAGTCCAGTCC 660
 DB 601 ACGTGCAAGAACAAAAGAAAGAAAGAACACACAGAGAGAGAAAGAAAGAAAGTCCAGTCC 660
 QY 661 AGTACGACGACAGTGGACGATCATATGCTTCCCAATTAATGCAATGTGACCTCCGCCCA 720
 DB 661 AGTACGACGACAGTGGACGATCATATGCTTCCCAATTAATGCAATGTGACCTCCGCCCA 720
 QY 721 GAGCGGCAAGGATTCACGAAGTGGTCCCGAGGTTCTTAACGGAAGAACTAATGAGCAG 780
 DB 721 GAGCGGCAAGGATTCACGAAGTGGTCCCGAGGTTCTTAACGGAAGAACTAATGAGCAG 780
 QY 781 AACAGACTGAAGAAATGTGACCGCTGTGCGGGAACACGAAAGTCCCTGATCGCGAGGCTC 840
 DB 781 AACAGACTGAAGAAATGTGACCGCTGTGCGGGAACACGAAAGTCCCTGATCGCGAGGCTC 840
 QY 841 GTGTGTTACCAAGGACGATACGAGCAGCTTCGGAAGAGGATCTCAAAGGGGTGACGAG 900
 DB 841 GTGTGTTACCAAGGACGATACGAGCAGCTTCGGAAGAGGATCTCAAAGGGGTGACGAG 900
 QY 901 ACTTGCCCAATCAGCAGATGAAGAAAGACGAAAGACTCAGACATGCCATTCCGCCAGATCA 960
 DB 901 ACTTGCCCAATCAGCAGATGAAGAAAGACGAAAGACTCAGACATGCCATTCCGCCAGATCA 960
 QY 961 GAAATGACCATCTCTCAGAGTACAGTAATAGTGTGAGTTTGCAGAGGCTTACCTGGTTT 1020
 DB 961 GAAATGACCATCTCTCAGAGTACAGTAATAGTGTGAGTTTGCAGAGGCTTACCTGGTTT 1020
 QY 1021 TCAGAGATCTCACACCTGACAGATCACATTTATTAAGGAGGATCTCAAGCGAAGTATG 1080
 DB 1021 TCAGAGATCTCACACCTGACAGATCACATTTATTAAGGAGGATCTCAAGCGAAGTATG 1080
 QY 1081 ATGTGCGGAGTAGCGAGCGGTACGACGCGGTGTGCGATAGCGTTCTGTTCGCCAACAA 1140
 DB 1081 ATGTGCGGAGTAGCGAGCGGTACGACGCGGTGTGCGATAGCGTTCTGTTCGCCAACAA 1140
 QY 1141 CAGGCGTACACTCGCGCAAACTACCGCAAGCGGCGCATGGCCCTACGTCATCGAAGACCTG 1200
 DB 1141 CAGGCGTACACTCGCGCAAACTACCGCAAGCGGCGCATGGCCCTACGTCATCGAAGACCTG 1200
 QY 1201 CTGCACTTCTGCGGCTGCAATGTCTGATGTCGATGTCGATGTCGATGTCGATGTCGATG 1260
 DB 1201 CTGCACTTCTGCGGCTGCAATGTCTGATGTCGATGTCGATGTCGATGTCGATGTCGATG 1260
 QY 1261 ACTGCGCATCTGTTATTTCTCGGATCGCGCGGCTTAGAGCAGCCACAGCTAGTAGAAGAG 1320
 DB 1261 ACTGCGCATCTGTTATTTCTCGGATCGCGCGGCTTAGAGCAGCCACAGCTAGTAGAAGAG 1320
 QY 1321 ATTCAGCGGTATTTACCTGAACACGTCGCGGTGTACATCATGAAACAGACACGCGGTG 1380
 DB 1321 ATTCAGCGGTATTTACCTGAACACGTCGCGGTGTACATCATGAAACAGACACGCGGTG 1380
 QY 1381 CCGCGTTGCGCGCTCATCTACCGGAGATTTCTGCGTCTTACCGAGTTGGGAGCGCTG 1440
 DB 1381 CCGCGTTGCGCGCTCATCTACCGGAGATTTCTGCGTCTTACCGAGTTGGGAGCGCTG 1440
 QY 1441 GGCATGCAAGATTCGAAACATGTGCAATCTCGCTGAAGCTCAAGAACAGGAGTGGCGCG 1500
 DB 1441 GGCATGCAAGATTCGAAACATGTGCAATCTCGCTGAAGCTCAAGAACAGGAGTGGCGCG 1500
 QY 1501 TTCTCGGAGGAGATCTGGGACGTTG 1524
 DB 1501 TTCTCGGAGGAGATCTGGGACGTTG 1524

RESULT 3
 ABT07369
 ID ABT07369 standard; DNA; 1782 BP.

QY 1366 CAGCACAGCGCTCGCCGGTTGGCCGTCATCTACGCGAAGATCTGTGCGTGCTTACC 1425
DB |||||
QY 1381 CAGCACAGCGCTCGCCGGTTGGCCGTCATCTACGCGAAGATCTGTGCGTGCTTACC 1440
DB |||||
QY 1426 GAGTTGGCGACCGCTGGCATGCGAATTCGAACATGTGCATCTCGCTGAAGCTCAAGAAC 1485
DB |||||
QY 1441 GAGTTGGCGACCGCTGGCATGCGAATTCGAACATGTGCATCTCGCTGAAGCTCAAGAAC 1500
DB |||||
QY 1486 AGGAAGCTGCCCGCTTCCTGAGGAGATCTGGGACGTG 1524
DB |||||
QY 1501 AGGAAGCTGCCCGCTTCCTGAGGAGATCTGGGACGTG 1539
DB |||||

RESULT 4

ADF49196

ID ADF49196 standard; DNA; 1782 BP.

XX AC

XX ADF49196;

XX DT

XX 12-FEB-2004 (first entry)

XX DE

XX Ecdysone receptor/VP16 transactivation domain DNA seq id 124.

XX KW

KW receptor cassette; chimeric receptor polypeptide; DNA binding domain;

KW KW

KW hinge domain; ecdysone receptor; EcR; ligand binding domain;

KW KW

KW activation domain; transgenic seed; transgenic plant; plant line;

KW KW

KW herbicide; pesticide; chimeric ecdysone receptor; EcR;

KW KW

KW yeast GAL4 DNA binding domain; VP16 transactivation domain; ds; gene.

XX OS

OS Synthetic.

OS OS

OS Ostrinia nubilalis.

OS OS

OS Ascomycota.

OS OS

OS Herpes simplex virus unknown type.

XX PN

PN US2003154509-A1.

XX XX

XX PD

XX 14-AUG-2003.

XX XX

XX 24-OCT-2001; 2001US-00087167.

XX XX

XX 24-OCT-2001; 2001US-00087167.

XX PA

PA (PASC/) PASCAL E J.

XX PA

PA (VALE/) VALENTINE S A.

XX PA

PA (BROW/) BROWN J A.

XX PA

PA (COCK/) COCKRELL A S.

XX PA

PA (JOHN/) JOHNSON B D.

XX PI

PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

XX XX

XX WPI; 2003-897756/82.

XX DR

DR P-PSDB; ADF49197.

XX XX

XX New receptor cassette encoding a chimeric receptor polypeptide, useful

XX PT

PT for regulating the expression of target polypeptides in plants in the

XX PT

PT presence of appropriate chemical ligands.

XX XX

XX Example 23; SEQ ID NO 124; 186pp; English.

XX PS

PS The invention describes a receptor cassette encoding a chimeric receptor

XX CC

CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge

XX CC

CC (D) domain of an ecdysone receptor (EcR) of an insect, a ligand binding

XX CC

CC (E) domain that is heterologous with respect to the D domain, and an

XX CC

CC activation domain. The receptor cassette and method are useful in

XX CC

CC regulating the expression of target polypeptides in plants in the

XX CC

CC presence of appropriate chemical ligands. The transgenic seeds and plants

XX CC

CC can be used for the breeding of improved plant lines that, for e.g.,

XX CC

CC increase the effectiveness of conventional methods such as herbicide or

XX CC

CC pesticide treatment. This sequence encodes an ecdysone receptor-VP16

XX CC

CC transactivation domain fusion protein.

XX XX

XX Sequence 1782 BP; 475 A; 445 C; 475 G; 387 T; 0 U; 0 Other;

XX SQ

Query Match 92.8%; Score 1414.2; DB 10; Length 1782;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1471; Conservative 0; Mismatches 53; Indels 15; Gaps 1;
QY 1 ATGACGACGCTATATGTGGATTTTTTTAGCCCTGCTTCATACGCTATTTATTTCTGG 60
DB |||||
QY 61 TACTGTTTCTTTTGTGCGATGTCACCCCTGTTGTTGGTGTACTTCTCGAGGATCCGCC 120
DB |||||
QY 61 TACTGTTTCTTTTGTGCGATGTCACCCCTGTTGTTGGTGTACTTCTCGAGGATCCGCC 120
DB |||||
QY 121 ACCATGAAGCTACTGTTCTTATCGAACCAAGCATCGGATATTTGCGGACTTAAAAAGCTC 180
DB |||||
QY 121 ACCATGAAGCTACTGTTCTTATCGAACCAAGCATCGGATATTTGCGGACTTAAAAAGCTC 180
DB |||||
QY 181 AAGTGCTCCAAAGAAAAAACCAGAAAGTGGCCCAAGTGTCTGAGAACCAACTGGGAGTGTCCG 240
DB |||||
QY 181 AAGTGCTCCAAAGAAAAAACCAGAAAGTGGCCCAAGTGTCTGAGAACCAACTGGGAGTGTCCG 240
DB |||||
QY 241 TACTCTCCCAAAACCAAAAGGTCCTCGCTGACTAGGCGACATCTGACAGAAGTGAATCA 300
DB |||||
QY 241 TACTCTCCCAAAACCAAAAGGTCCTCGCTGACTAGGCGACATCTGACAGAAGTGAATCA 300
DB |||||
QY 301 AGGCTAGAAAAGACTGGAAACAGCTATTTTCTACTGATTTTTCCTCGAGAAGACCTTGACATG 360
DB |||||
QY 301 AGGCTAGAAAAGACTGGAAACAGCTATTTTCTACTGATTTTTCCTCGAGAAGACCTTGACATG 360
DB |||||
QY 361 ATTTTGAAGTGGATTTTACAGGATATATAAAGCATTTGTTAACAGGATTTTGTACAA 420
DB |||||
QY 361 ATTTTGAAGTGGATTTTACAGGATATATAAAGCATTTGTTAACAGGATTTTGTACAA 420
DB |||||
QY 421 GATATGTTGAATAAAGATGCGCTGACAGATAGATTGGCTTCAGTGGAGACTGATATGCTT 480
DB |||||
QY 421 GATATGTTGAATAAAGATGCGCTGACAGATAGATTGGCTTCAGTGGAGACTGATATGCTT 480
DB |||||
QY 481 CTAACATTGAGACAGCATAGATAAAGTGCACATCATCATCGAAGAGAGTAGTAGTACAAA 540
DB |||||
QY 481 CTAACATTGAGACAGCATAGATAAAGTGCACATCATCATCGAAGAGAGTAGTAGTACAAA 540
DB |||||
QY 541 GGTCAAAGACAGTTGACTGTATCGAGCGGTATGAGCCCGAGTGTGTCGAGAGTCC 600
DB |||||
QY 541 GGTCAAAGACAGTTGACTGTATCGAGCGGTATGAGCCCGAGTGTGTCGAGAGTCC 600
DB |||||
QY 601 ACCTGCAAGCAACAAGAGAGAGAAAGGACACAGAGAGAAAGACAACTGCCAGTCC 660
DB |||||
QY 601 CAGTGTGCGCAAAAGAGAGAGAAAGGACACAGAGAGAGAAAGACAACTGCCAGTCC 660
DB |||||
QY 661 AGTACGACGACAGTGGACGATCATATGCTGCGCATATGCAATGTCACCTCCGCCCCCA 720
DB |||||
QY 661 AGTACGACGACAGTGGACGATCATATGCTGCGCATATGCAATGTCACCTCCGCCCCCA 720
DB |||||
QY 721 GAGGCGGCAAGGATT-----CAGGAAGTGTCCCGAGGTTCTTAAAGGAG 765
DB |||||
QY 721 GAGGCGGCAAGGATTCTGGAATGTTTGCAGCATGAAAGTGTCCCGGTTCTTCTCGGAG 780
DB |||||
QY 766 AGCTTAATCGAGCAGACAGACTGGAAGATGTGACCCGCTGTGCGGCAAGACCAAGAGTCC 825
DB |||||
QY 781 AAGCTGATGGAGCAGAAATCGGCTGAAAGAACATACCCCTCCACCCCAACAGCAGTTC 840
DB |||||
QY 826 CTGATCCGAGGCTCGTGTGGTACACGAGCGGATACGAGCAGCTTTCGGAAGAGGATCTC 885
DB |||||
QY 841 CTGATCCGAGGCTCGTGTGGTACACGAGCGGATACGAGCAGCTTTCGGAAGAGGATCTC 900
DB |||||
QY 886 AAAAGGGTGCAGACTTTGGCAATCAGCGATGAAAGAGACCAAGACTCAGACATGCCA 945
DB |||||
QY 901 AAAAGGGTGCAGACTTTGGCAATCAGCGATGAAAGAGACCAAGACTCAGACATGCCA 960
DB |||||
QY 946 TTCCGCCAGATCACGAATGACCTCCTCACAGTACAGCTAATAGTTCGAGTTTGCACAA 1005
DB |||||
QY 961 TTCCGCCAGATCACGAATGACCTCCTCACAGTACAGCTAATAGTTCGAGTTTGCACAA 1020
DB |||||
QY 1006 GGCCTACCTGGTTTTTCAAAAGATCTCACAACTGACGACATCACAATTATTAAGGCGATGC 1065
DB |||||

Db 1021 GGCCTACCTGGTTTTCAAAAGATCTCAACCTGACAGATCAATTATTAAGCGCATGC 1080
 Qy 1066 TCAAGCGAAGTATGATCTCGAGTACGAGGCGGTACGAGCGGTGTCGATAGCGTT 1125
 Db 1081 TCAAGCGAAGTATGATCTCGAGTACGAGGCGGTACGAGCGGTGTCGATAGCGTT 1140
 Qy 1126 CTGTTCCGCAACACAGCGGTACACTCGCGACAACTACCGCAAGCGGGCATGCGCTAC 1185
 Db 1141 CTGTTCCGCAACACAGCGGTACACTCGCGACAACTACCGCAAGCGGGCATGCGCTAC 1200
 Qy 1186 GTCATCGAAGACCTGCTGCTCACTTCTGCGCGTGCATGTACTCGATGTCGATGGCAACGTTG 1245
 Db 1201 GTCATCGAAGACCTGCTGCTCACTTCTGCGCGTGCATGTACTCGATGTCGATGGCAACGTTG 1260
 Qy 1246 CATTACGCGCTCTCACTGCGCATGTTATTTCTCGATTCGCGCGGCTAGACAGCGCA 1305
 Db 1261 CATTACGCGCTCTCACTGCGCATGTTATTTCTCGATTCGCGCGGCTAGACAGCGCA 1320
 Qy 1306 CAGCTAGTAGAGATCCAGCGGTATTTACCTGAAACAGCTGCGGGTGTACATGAAC 1365
 Db 1321 CAGCTAGTAGAGATCCAGCGGTATTTACCTGAAACAGCTGCGGGTGTACATGAAC 1380
 Qy 1366 CAGCACAGCGCTCGCGCGTTCGCGCGTTCATCTACGCGAAGATTCTCTCGGTGCTTACC 1425
 Db 1381 CAGCACAGCGCTCGCGCGTTCGCGCGTTCATCTACGCGAAGATTCTCTCGGTGCTTACC 1440
 Qy 1426 GAGTTGCGGACGCTGGGATGCGAATTCGAAACATGTCATCTCGCTGAAGCTCAAGAAC 1485
 Db 1441 GAGTTGCGGACGCTGGGATGCGAATTCGAAACATGTCATCTCGCTGAAGCTCAAGAAC 1500
 Qy 1486 AGGAGAGTCCCGCGCTTCCTGGAGGAGATCTGGGACGTG 1524
 Db 1501 AGGAGAGTCCCGCGCTTCCTGGAGGAGATCTGGGACGTG 1539

RESULT 5
 ABT07376
 ID ABT07376 standard; DNA; 1848 BP.
 XX
 AC ABT07376;
 XX
 DT 29-AUG-2003 (revised)
 DT 07-NOV-2002 (first entry)
 XX
 DE Chimeric ecdysone receptor coding sequence SEQ ID NO: 134.
 XX
 KW Plant; gene expression control; insect; hormone receptor; fertility;
 KW ecdysone receptor; gene; ds.
 XX
 OS Manduca sexta.
 OS Chimeric.
 XX
 PN WO200261102-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 24-OCT-2001; 2001WO-US051417.
 XX
 PR 24-OCT-2000; 2000US-0242969P.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 XX
 DR WPI; 2002-619259/66.
 XX
 DR P-PSDB; ABJ05378.
 XX
 XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
 PT regulating expression of target polypeptides in plants in the presence of
 PT appropriate ligands that may be used in controlling plant fertility.
 XX

PS Example 25; Page 296-298; 319pp; English.
 XX
 CC The present invention relates to a receptor cassette encoding a chimeric
 CC receptor polypeptide comprising at least one DNA binding domain, a hinge
 CC domain of an ecdysone receptor (ECR) of an insect, a ligand binding
 CC domain of an insect ECR, where the ligand binding domain is heterologous
 CC with respect to the hinge domain and an activation domain. The chimeric
 CC insect hormone receptors and receptor cassettes are useful in regulating
 CC expression of target polypeptides in plants in the presence of
 CC appropriate ligands that may be used in controlling plant fertility. The
 CC method is useful for decreasing or increasing plant gene expression. The
 CC present sequence is a coding sequence described in the exemplification of
 CC the invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 1848 BP; 488 A; 456 C; 523 G; 381 T; 0 U; 0 Other;
 Query Match 87.4%; Score 1332; DB 6; Length 1848;
 Best Local Similarity 92.1%; Pred. No. 0;
 Matches 1404; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
 Qy 1 ATGCAGCAGCTATATGTGGATTTTTTTAGCCCTGCCCTTCATACGCTATTTATTTGCTTGG 60
 Db 1 ATGCAGCAGCTATATGTGGATTTTTTTAGCCCTGCCCTTCATACGCTATTTATTTGCTTGG 60
 Qy 61 TACTGTTTCTTTTGTGATGCTCACCTGTGTTGTTGTTGTTTACTTCTGCGGGATCGCC 120
 Db 61 TACTGTTTCTTTTGTGATGCTCACCTGTGTTGTTGTTTACTTCTGCGGGATCGCC 120
 Qy 121 ACCATGAAGTACTGTTCTTCTATCGAACAGCAGCAGCTATTTTCCGACCTTAAAGAGCTC 180
 Db 121 ACCATGAAGTACTGTTCTTCTATCGAACAGCAGCAGCTATTTTCCGACCTTAAAGAGCTC 180
 Qy 181 AAGTGCTCCAAAGAAAAACCGAAGTGCGCCAAGTGTCTGAAGAAACAATGCGAGTGC 240
 Db 181 AAGTGCTCCAAAGAAAAACCGAAGTGCGCCAAGTGTCTGAAGAAACAATGCGAGTGC 240
 Qy 241 TACTTCTCCAAACCAAAAGGTCTCCGCTGACTAGGGGCACATCTGACAGAGTGGATCA 300
 Db 241 TACTTCTCCAAACCAAAAGGTCTCCGCTGACTAGGGGCACATCTGACAGAGTGGATCA 300
 Qy 301 AGGCTAGAAAGACTGGAACAGCTATTTCTACTGATTTTTTCTCCGAGAGACCTTGACATG 360
 Db 301 AGGCTAGAAAGACTGGAACAGCTATTTCTACTGATTTTTTCTCCGAGAGACCTTGACATG 360
 Qy 361 ATTTTGAAGATGGATTCTTTACAGGATATAAAAGCATTTGTTAACAGGATTTTGTACAA 420
 Db 361 ATTTTGAAGATGGATTCTTTACAGGATATAAAAGCATTTGTTAACAGGATTTTGTACAA 420
 Qy 421 GATAATGTGAATAAAGATGCGCTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCT 480
 Db 421 GATAATGTGAATAAAGATGCGCTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCT 480
 Qy 481 CTAACATTGAGACAGCATAGAAATAGTCCGACATCATCTCGAAGAGAGTAGTAACAAA 540
 Db 481 CTAACATTGAGACAGCATAGAAATAGTCCGACATCATCTCGAAGAGAGTAGTAACAAA 540
 Qy 541 GGTCAAAAGACAGTTGACTGTATCGACGCGTATGAGGCCGAGTGCCTCCAGAGTCC 600
 Db 541 GGTCAAAAGACAGTTGACTGTATCGACGCGTATGAGGCCGAGTGCCTCCAGAGTCC 600
 Qy 601 ACCTGCAAGAACAAAAGAGAAAGAAAGAACACAGAGAGAAAGAAAGAAAGAAAGAAAG 660
 Db 601 ACCTGCAAGAACAAAAGAGAAAGAAAGAAAGAACACAGAGAGAAAGAAAGAAAGAAAG 660
 Qy 661 AGTACGACGACAGTGGAGCATCATATGCTGCCATAATGCAATGTGACCTCCGCCCCCA 720
 Db 661 AGTACGACGACAGTGGAGCATCATATGCTGCCATAATGCAATGTGACCTCCGCCCCCA 720
 Qy 721 GAGGCGGCAAGGATTCAGAAAGTGGTCCGAGGTTCTTAAACGAGAAAGCTAATGAGGAG 780
 Db 721 GAGGCGGCAAGGATTCAGAAAGTGGTCCGAGGTTCTTAAACGAGAAAGCTAATGAGGAG 780
 Qy 781 AACAGACTGAAGAATGTGACGCCCTGTCTCGGCGAACAGAGTCCCTGATCGCGAGGCTC 840

Db 781 AACGACTGAAGATGTAGCGCGTGTGCGGACCAAGAGTCCCTGATCGGAGGCTC 840
 QY 841 GTGTGGTACCGAGCGGATACAGAGCGCTTCGGAAGAGATCTCAAAAGGGTACGAG 900
 Db 841 GTGTGGTACCGAGCGGATACAGAGCGCTTCGGAAGAGATCTCAAGAGAGTTACACAG 900
 QY 901 ACTTGGCAATCAGCAGATGAGAACGAGCACTCAGACATGCCATTCGGCCAGATCACA 960
 Db 901 ACATGCGAGTTAGAGAGAGAACGAGGAGAACTGACATGCCCTTCGTCAGATCACA 960
 QY 961 GAAATGACCATCTCACAGTACAGCTAATAGTCGAGTTTGCACAAAGGCTACCTGTTTT 1020
 Db 961 GAGATGACGATCTTAACAGTCAGCTTATGTAGATTCGCAAGGGACTACCGGATTC 1020
 QY 1021 TCAAGATCTCAACCTGACAGATCACAATTAATAAGGCAATGCTCAAGCGAAGTGATG 1080
 Db 1021 TCCAAGATATCTCAGTCGATCAAAATTAATTAAGGCGTCATCAAGCGAAGTGATG 1080
 QY 1081 ATGCTGCGAGTAGCGAGCGGTACGACGGGTGTCGATAGGTTCTGTTCCCAACAC 1140
 Db 1081 ATGCTGCGAGTAGCGCGGTACGACGGGTGTCGATAGGTTCTGTTCCCAACAC 1140
 QY 1141 CAGGCGTACACTCGGACAACTACCGCAAGCGGCGATGCCCTAGCTCATCGAAGACCTG 1200
 Db 1141 CAGGCGTACCGCGGACAACTACCGCAAGCGGCGATGCCCTAGCTCATCGAAGACCTG 1200
 QY 1201 CTGCACTTCTGCGCTGCACTGATCTGATGTCGATGGACAACTGATTAACGCTCTCTC 1260
 Db 1201 CTGCACTTCTGCGCTGATGATCTGATGTCGATGGACAACTGATTAACGCTCTCTC 1260
 QY 1261 ACTGCCATGTTATATCTCGATCGGCGGCGCTAGACGCCACAGCTAGTAGAGAG 1320
 Db 1261 ACGGCCATGTTATATCTCAGACCGCGCGGCGCTAGACGCCACCTTTTAGTGAGGAA 1320
 QY 1321 ATCCACGCTATTACCTGAACAGCTGCGGCTGTACATCATGAACGACAGCGCGTCTG 1380
 Db 1321 ATCCAGAGATATCTTGAAGACCTGCGGCTGTACATTTAATCAGCAGCGCGTCTG 1380
 QY 1381 CCGCGTTGGCGCTCATCTACGCAAGATCTGCTGCTTACCGAGTTGGGACGCTG 1440
 Db 1381 CCTCGTGGCGCTGCTGTTGGCAAGATCCTCGGCGTGTGACGGAACCTGGCGACGCTC 1440
 QY 1441 GGATCGAGAAATTCGAAATGTCATCTGCTGAAGCTCAAGACAGGAGCTGCGCGCG 1500
 Db 1441 GGCACGAGAACTCCAAACATGTCATCTGCTGAAGCTGAAGAACAGGAAATTCGCGCA 1500
 QY 1501 TTCCTGGAGAGATCTGGGACGCTG 1524
 Db 1501 TTCCTGGAGAGATCTGGGACGCTG 1524

RESULT 6

ADFA9206
 ID ADFA9206 standard; DNA; 1848 BP.

XX AC ADFA9206;
 XX

DT 12-FEB-2004 (first entry)
 XX

DE Ecdysone receptor/C1 transactivation domain DNA seq id 134.

XX receptor cassette; chimeric receptor polypeptide; DNA binding domain;
 KW hinge domain; ecdysone receptor; ECR; ligand binding domain;
 KW activation domain; transgenic seed; transgenic plant; plant line;
 KW herbicide; pesticide; chimeric ecdysone receptor; ECR;
 KW yeast GAL4 DNA binding domain; C1 transactivation domain; ds; gene.

XX Synthetic.
 OS Manduca sexta.
 OS Ascomycota.
 OS Zea mays.

XX

US2003154509-A1.

XX XX
 PD 14-AUG-2003.

XX 24-OCT-2001; 2001US-00087167.
 PF

XX 24-OCT-2001; 2001US-00087167.
 PR

XX (PASC/) PASCAL E J.
 PA (VALE/) VALENTINE S A.
 PA (BROW/) BROWN J A. S.
 PA (COCK/) COCKRELL A. S.
 PA (JOHN/) JOHNSON B D.

XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 PI

XX WPI; 2003-897756/82.
 DR

XX New receptor cassette encoding a chimeric receptor polypeptide, useful
 PT for regulating the expression of target polypeptides in plants in the
 PT presence of appropriate chemical ligands.
 XX

PS Example 25; SEQ ID NO 134; 186pp; English.

XX The invention describes a receptor cassette encoding a chimeric receptor
 CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
 CC (D) domain of an ecdysone receptor (ECR) of an insect, a ligand binding
 CC (E) domain that is heterologous with respect to the D domain, and an
 CC activation domain. The receptor cassette and method are useful in
 CC regulating the expression of target polypeptides in plants in the
 CC presence of appropriate chemical ligands. The transgenic seeds and plants
 CC can be used for the breeding of improved plant lines that, for e.g.
 CC increase the effectiveness of conventional methods such as herbicide or
 CC pesticide treatment. This sequence encodes an ecdysone receptor-C1
 CC transactivation domain fusion protein.

XX SQ Sequence 1848 BP; 488 A; 456 C; 523 G; 381 T; 0 U; 0 Other;

Query Match 87.4%; Score 1332; DB 10; Length 1848;
 Best Local Similarity 92.1%; Pred. No. 0;
 Matches 1404; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 1 ATGCGACGCTATATGTGGATTTTATAGCCCTGCTTCATACGCTATTTATTTGCTTGG 60
 Db 1 ATGCGACGCTATATGTGGATTTTATAGCCCTGCTTCATACGCTATTTATTTGCTTGG 60

QY 61 TACTGTTCTTTTGTGATGCTCACCTGTTGTTGGTGTACTTCTCGAGGATCCGCC 120
 Db 61 TACTGTTCTTTTGTGATGCTCACCTGTTGTTGGTGTACTTCTCGAGGATCCGCC 120

QY 121 ACCATGAGCTACTGTCTTCTATCGAACAGCATGCGATATTTGCCGACTTAAAAAGCTC 180
 Db 121 ACCATGAGCTACTGTCTTCTATCGAACAGCATGCGATATTTGCCGACTTAAAAAGCTC 180

QY 181 AAGTGTCTCCAAAGAAAAACCGAAGTGCAGGCTGCGCAAGTGTCTGAAGAACAACTGGGAGTGTCCG 240
 Db 181 AAGTGTCTCCAAAGAAAAACCGAAGTGCAGGCTGCGCAAGTGTCTGAAGAACAACTGGGAGTGTCCG 240

QY 241 TACTCTCCAAACCCAAAAGGTCTCGCTGACTAGGGCAGCATCTGCAGAGTGGGAATCA 300
 Db 241 TACTCTCCAAACCCAAAAGGTCTCGCTGACTAGGGCAGCATCTGCAGAGTGGGAATCA 300

QY 301 AGGCTAGAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAGAAGACCTTTGACATG 360
 Db 301 AGGCTAGAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAGAAGACCTTTGACATG 360

QY 361 ATTTTGAAGTGGATTTCTTTACAGGATATAAAGCAATTTGTAAACAGATTTATTTGACAA 420
 Db 361 ATTTTGAAGTGGATTTCTTTACAGGATATAAAGCAATTTGTAAACAGATTTATTTGACAA 420

QY 421 GATAATGTGAATAAAGATGCCGTACAGATAGATTGCTTCAGTGGAGACTGATATGCGCT 480
 Db 421 GATAATGTGAATAAAGATGCCGTACAGATAGATTGCTTCAGTGGAGACTGATATGCGCT 480

QY 481 CTAACATTGACACAGCATAGATTAAGTGGCGATCATCATCGAAGAGAGTAGTAACAAA 540
DB |||||
QY 481 CTAACATTGACACAGCATAGATTAAGTGGCGATCATCATCGAAGAGAGTAGTAACAAA 540
DB |||||
QY 541 GGTCAAAAGACAGTTGACTGTATCGACCGGTATGAGGCCGAGTGGTCCGAGAGTCC 600
DB |||||
QY 541 GGTCAAAAGACAGTTGACTGTATCGACCGGTATGAGGCCGAGTGGTCCGAGAGTCC 600
DB |||||
QY 601 ACGTCAAGAACAAAAGAGAAAGAAAGAACAGACAGAGAGAAAGAAAGAAAGAAAGTCCAGTC 660
DB |||||
QY 601 ACGTCAAGAACAAAAGAGAAAGAAAGAACAGACAGAGAGAAAGAAAGAAAGAAAGTCCAGTC 660
DB |||||
QY 661 AGTACGACAGAGTGGACGATCATATGCTGCCATTAATGCAATGTGACCCCTCCGCCCCCA 720
DB |||||
QY 661 AGTACGACAGAGTGGACGATCATATGCTGCCATTAATGCAATGTGACCCCTCCGCCCCCA 720
DB |||||
QY 721 GAGCGGCAAGGATTCAAGAGTGTCCGAGGTTCTTAACGGAGAGCTTAATGGAGCAG 780
DB |||||
QY 721 GAGCGGCAAGGATTCAAGAGTGTCCGAGGTTCTTAACGGAGAGCTTAATGGAGCAG 780
DB |||||
QY 781 AACAGACTGAAGATGTGACCGCGTCTCGGCAACAGAAAGTCCCTGATCGCAGGCTC 840
DB |||||
QY 781 AACAGACTGAAGATGTGACCGCGTCTCGGCAACAGAAAGTCCCTGATCGCAGGCTC 840
DB |||||
QY 841 GTGTGGTACCGAGCGGATACGAGCAGCTTTCGGAAGAGGATCTCAAAAGGGTGACGCGAG 900
DB |||||
QY 841 GTGTGGTACCGAGCGGATACGAGCAGCTTTCGGAAGAGGATCTCAAAAGGGTGACGCGAG 900
DB |||||
QY 901 ACTTGGCAATCAGCAGATGAAGAACAGAGACTCAGACATGCCATTCGCCAGCATACA 960
DB |||||
QY 901 ACTTGGCAATCAGCAGATGAAGAACAGAGACTCAGACATGCCATTCGCCAGCATACA 960
DB |||||
QY 961 GAAATGACCATCTCACAGTACAGCTAATAGTTCGAGTTTGCACAAAGGCTACCTGGTTTT 1020
DB |||||
QY 961 GAAATGACCATCTCACAGTACAGCTAATAGTTCGAGTTTGCACAAAGGCTACCTGGTTTT 1020
DB |||||
QY 1021 TCAAGATCTCAACACCTGACAGATACATTAATTAAGGCGATGCTCAAGCGAAGTATG 1080
DB |||||
QY 1021 TCAAGATCTCAACACCTGACAGATACATTAATTAAGGCGATGCTCAAGCGAAGTATG 1080
DB |||||
QY 1081 ATGCTCGAGTACGAGGCGGTACGACGCGGTTCGGATAGGTTCTGTTCGCCAACAAAC 1140
DB |||||
QY 1081 ATGCTCGAGTACGAGGCGGTACGACGCGGTTCGGATAGGTTCTGTTCGCCAACAAAC 1140
DB |||||
QY 1141 CAGCGGTACACTCGCAGCAACTACCGCAAGCGGGGATGCTTACGTCATCGAAGACCTG 1200
DB |||||
QY 1141 CAGCGGTACACTCGCAGCAACTACCGCAAGCGGGGATGCTTACGTCATCGAAGACCTG 1200
DB |||||
QY 1201 CTGCACTTCTGCGGTGATGTTACTCCATGAGCATGGCAATGTGCACTACCGGTGCTC 1260
DB |||||
QY 1201 CTGCACTTCTGCGGTGATGTTACTCCATGAGCATGGCAATGTGCACTACCGGTGCTC 1260
DB |||||
QY 1261 ACTGCCATCTGTTATATTCGAGTACGCGCGGCTAGAGCAGCAGCAGCTAGTAGAAGAG 1320
DB |||||
QY 1261 ACTGCCATCTGTTATATTCGAGTACGCGCGGCTAGAGCAGCAGCAGCTAGTAGAAGAG 1320
DB |||||
QY 1321 ATCCAGCGGATTAACCTGAACAACGCTGCGGTGTACATCATGAAACGACAGCGCGTGC 1380
DB |||||
QY 1321 ATCCAGCGGATTAACCTGAACAACGCTGCGGTGTACATCATGAAACGACAGCGCGTGC 1380
DB |||||
QY 1381 CCGGTTGCGCGCTCATCTACGGAAGATTTCTGTCGGTGTCTTACCGAGTTGGCGAGCTG 1440
DB |||||
QY 1381 CCGGTTGCGCGCTCATCTACGGAAGATTTCTGTCGGTGTCTTACCGAGTTGGCGAGCTG 1440
DB |||||
QY 1441 GGCATGAGAAATTCGAACATGTGCATCTCGTGAAGCTCAAGAACAGGAGTGCGCCCG 1500
DB |||||
QY 1441 GGCATGAGAAATTCGAACATGTGCATCTCGTGAAGCTCAAGAACAGGAGTGCGCCCG 1500
DB |||||
QY 1501 TTCTTGAGAGATCTGGGACGTG 1524
DB |||||
QY 1501 TTCTTGAGAGATCTGGGACGTG 1524
DB |||||

RESULT 7
ID ABT07377
XX ABT07377 standard; DNA; 1863 BP.
AC
XX ABT07377;
DT 29-AUG-2003 (revised)
DT 07-NOV-2002 (first entry)
XX
XX Chimeric ecdysone receptor coding sequence SEQ ID NO: 136.
XX Plant; gene expression control; insect; hormone receptor; fertility;
XX ecdysone receptor; gene; ds.
XX Manduca sexta.
OS Manduca sexta.
OS Chimeric.
XX WO200261102-A2.
XX
XX 08-AUG-2002.
XX
XX 24-OCT-2001; 2001WO-US051417.
XX
XX 24-OCT-2000; 2000US-0242969P.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Pascal EU, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
XX MPI: 2002-619259/66.
XX P-PSDB; ABJ05379.
XX
XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
XX regulating expression of target polypeptides in plants in the presence of
XX appropriate ligands that may be used in controlling plant fertility.
XX
XX Example 25; Page 301-304; 319pp; English.
XX
XX The present invention relates to a receptor cassette encoding a chimeric
XX receptor polypeptide comprising at least one DNA binding domain, a hinge
XX domain of an ecdysone receptor (EcR) of an insect, a ligand binding
XX domain of an insect EcR, where the ligand binding domain is heterologous
XX with respect to the hinge domain and an activation domain. The chimeric
XX insect hormone receptors and receptor cassettes are useful in regulating
XX expression of target polypeptides in plants in the presence of
XX appropriate ligands that may be used in controlling plant fertility. The
XX method is useful for decreasing or increasing plant gene expression. The
XX present sequence is a coding sequence described in the exemplification of
XX the invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 1863 BP; 487 A; 489 C; 510 G; 377 T; 0 U; 0 Other;

Query Match 87.4%; Score 1332; DB 6; Length 1863;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 1404; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
QY 1 ATGCAGACGCTATATGTGGATTTTATAGCCCTCCCTTCATACGCTATTTATTTGCTTGG 60
DB 1 ATGCAGACGCTATATGTGGATTTTATAGCCCTCCCTTCATACGCTATTTATTTGCTTGG 60
QY 61 TACTGTTTCTTTTTCGATGCTCACCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 120
DB 61 TACTGTTTCTTTTTCGATGCTCACCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 120
QY 121 ACCATGAGCTACTGTTCTTCTATCGAACAGCATGCGATATTTGCCGACTTTAAAAAGTCT 180
DB 121 ACCATGAGCTACTGTTCTTCTATCGAACAGCATGCGATATTTGCCGACTTTAAAAAGTCT 180
QY 181 AAGTCTCCAAAGAAAAACCGAAGTGCAGGAGTGTCTGAAAGAACAACTGGAGTGTGCGC 240
DB 181 AAGTCTCCAAAGAAAAACCGAAGTGCAGGAGTGTCTGAAAGAACAACTGGAGTGTGCGC 240

XX	Sequence 1863 BP; 487 A; 489 C; 510 G; 377 T; 0 U; 0 Other;	
XX	Query Match 87.4%; Score 1332; DB 10; Length 1863;	
XX	Best Local Similarity 92.1%; Pred. No. 0;	
XX	Matches 1404; Conservative 0; Mismatches 120; Indels 0; Gaps 0;	
QY	1 ATGCAGCAGCTATATGTGGATTTTATAGCCCTCCCTTCATACGCTATTTATTTGCTTGG 60	961 GAGATGACGATCTTAACAGTGCAGCTTATTGTAGAAATTCGCAAGGGAGCTACCGGGATTC 1020
DB	1 ATGCAGCAGCTATATGTGGATTTTATAGCCCTCCCTTCATACGCTATTTATTTGCTTGG 60	1021 TCAAGATCTCAACACCTGACAGATCACTATTATAAGGCATGCTCAAGCGAAGTGATG 1080
QY	61 TACTGTTCTTTTGTGCGATGCTCACCCCTGTTGTTGGTGTACTCTTGCAGGGATCCGCC 120	1021 TCAAGATATCTCAGTCCGATCAAAATTTAATTTAAAGGCGTCTATCAAGCGAAGTGATG 1080
DB	61 TACTGTTCTTTTGTGCGATGCTCACCCCTGTTGTTGGTGTACTCTTGCAGGGATCCGCC 120	1081 ATGCTCGAGTAGTCAGAGGCGGTACGACGCGGTGTGCGATAGCGTTCCTGTCGCCAACAAC 1140
QY	121 ACCATGAAGCTACTGCTCTTCTATCGAACCAAGCATGCGATATTTGCCGACTTTAAAGAGCTC 180	1081 ATGCTCGAGTAGTCAGAGGCGGTACGACGCGGTGTGCGATAGCGTTCCTGTCGCCAACAAC 1140
DB	121 ACCATGAAGCTACTGCTCTTCTATCGAACCAAGCATGCGATATTTGCCGACTTTAAAGAGCTC 180	1141 CAGGCGTACATCGCGCAAACTACCGCAAGGCGGGCATGCGCTACGTCATCGAAGACCTG 1200
QY	181 AAGTGCTCCAAAGAAAAACCGAAGTGCAGAGTGTCTGAAGAACAACTGGAGTGTGCG 240	1141 CAGGCGTACATCGCGCAAACTACCGCAAGGCGGGCATGCGCTACGTCATCGAAGACCTG 1200
DB	181 AAGTGCTCCAAAGAAAAACCGAAGTGCAGAGTGTCTGAAGAACAACTGGAGTGTGCG 240	1201 CTGCACTTCTGCGCGTGCATGCTACTCGATGTCAGACAACTGTCATTTACGCGCTCCTC 1260
QY	241 TACTCTCCAAACCAAAAGCTCCGCTGACTAGGCGACATCTGACAGAAAGTGGAAATCA 300	1201 CTGCACTTCTGCGCGTGCATGCTACTCGATGTCAGACAACTGTCATTTACGCGCTCCTC 1260
DB	241 TACTCTCCAAACCAAAAGCTCCGCTGACTAGGCGACATCTGACAGAAAGTGGAAATCA 300	1261 ACTGCCATCGTTATATTCTCGGATCGCGCGGCTAGAGAGCCACAGCTAGTAGAAGAG 1320
QY	301 AGGCTAGAAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAAGAGACCTTGACATG 360	1261 ACCGCCATCGTTATATTCTCAGACCGCGCCAGGCTCGAGCAACCCCTTTTAGTGGAGAA 1320
DB	301 AGGCTAGAAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAAGAGACCTTGACATG 360	1321 ATCCAGGGTATTAACCTGAACAGCTGCGGGTGTACATCATGAACAGCACACGCGTGC 1380
QY	361 ATTTTGAAGTGGATTTCTTACAGATATAAAGCAATTTTAAACAGGATTTATTTGTACAA 420	1321 ATCCAGGGTATTAACCTGAACAGCTGCGGGTGTACATCATGAACAGCACACGCGTGC 1380
DB	361 ATTTTGAAGTGGATTTCTTACAGATATAAAGCAATTTTAAACAGGATTTATTTGTACAA 420	1381 CCGGTTGCGCGCTCATCTACGGAAGATTTCTGCGTGTCTTACCGAGTTTGGGACGCTG 1440
QY	421 GATATGTCAATAAAGATCCGCTACAGATAGATTGGCTTCACTGGAGACTGATATGCT 480	1381 CCGGTTGCGCGCTCATCTACGGAAGATTTCTGCGTGTCTTACCGAGTTTGGGACGCTG 1440
DB	421 GATATGTCAATAAAGATCCGCTACAGATAGATTGGCTTCACTGGAGACTGATATGCT 480	1441 GGATGCGAAGTTTGAACATGTGTCATCTGCTGAAGTCTGAGTCAAGAACAGGAGCTGCCGCG 1500
QY	481 CTAACATTGAGACAGCATAGATAAAGTGCAGCATCATCATCGGAAGAGAGTAGTAACAAA 540	1441 GGATGCGAAGTTTGAACATGTGTCATCTGCTGAAGTCTGAGTCAAGAACAGGAGCTGCCGCG 1500
DB	481 CTAACATTGAGACAGCATAGATAAAGTGCAGCATCATCATCGGAAGAGAGTAGTAACAAA 540	1501 TTCTCGAGGAGATCTGGGACGCTG 1524
QY	541 GGTCAAGACAGTTGACTGTATCGACGCGTATGAGCGCGTGTGCTCCAGAGTCC 600	1501 TTCTCGAGGAGATCTGGGACGCTG 1524
DB	541 GGTCAAGACAGTTGACTGTATCGACGCGTATGAGCGCGTGTGCTCCAGAGTCC 600	
QY	601 ACCTGCAAGAACAAAAGAGAGAAAAGGAGCACAGAGAGAAAAGACAACTGCCAGTC 660	RESULT 9
DB	601 ACCTGCAAGAACAAAAGAGAGAAAAGGAGCACAGAGAGAAAAGACAACTGCCAGTC 660	ABT07353 standard; DNA; 3972 BP.
QY	661 AGTACGACAGCTGAGCATCATATGCTTGCATTAATGCAATGTGACCTCCGCCCA 720	XX ABT07353;
DB	661 AGTACGACAGCTGAGCATCATATGCTTGCATTAATGCAATGTGACCTCCGCCCA 720	XX 07-NOV-2002 (first entry)
QY	721 GAGCGCGCAGGATTCACGAAGTGTCCGAGGTTCTTAACGAGAGAGCTAATGGAGCAG 780	XX Ecdysone receptor containing vector pCGS202 DNA SEQ ID NO: 104.
DB	721 GAGCGCGCAGGATTCACGAAGTGTCCGAGGTTCTTAACGAGAGAGCTAATGGAGCAG 780	XX Plant; gene expression control; insect; hormone receptor; fertility;
QY	781 AACAGACTGAAGAAATGTGACGCGCTGTGCGGGAACCAAGTCCCTGATCGCGAGGCTC 840	XX ecdysone receptor; gene; ds.
DB	781 AACAGACTGAAGAAATGTGACGCGCTGTGCGGGAACCAAGTCCCTGATCGCGAGGCTC 840	XX Synthetic.
QY	841 GTGTGTTACAGACCGATACGAGCGCTTCGGAAGAGATCTCAAGAGGTGAGCGAG 900	XX WO200261102-A2.
DB	841 GTGTGTTACAGACCGATACGAGCGCTTCGGAAGAGATCTCAAGAGGTGAGCGAG 900	XX 08-AUG-2002.
QY	901 ACTTGGCAATCAGCAGATGAAGAGACGAAGATCTCAGACATGCTTCCGCCAGATCA 960	XX 24-OCT-2001; 2001WO-US051417.
DB	901 ACTTGGCAATCAGCAGATGAAGAGACGAAGATCTCAGACATGCTTCCGCCAGATCA 960	XX 24-OCT-2000; 2000US-0242969P.
QY	961 GAAATGACCATCTTCACAGTACAGCTTAATAGTCGAGTTTGCCTGAGGCTTCTGTTT 1020	XX (SYGN) SYNGENTA PARTICIPATIONS AG.
DB		XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
		XX WPI; 2002-619259/66.
		XX P-P5DB; ABU05371.
		XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
		XX regulating expression of target polypeptides in plants in the presence of
		XX appropriate ligands that may be used in controlling plant fertility.

PS Claim 28; Page 255-258; 319pp; English.

XX The present invention relates to a receptor cassette encoding a chimeric
CC receptor polypeptide comprising at least one DNA binding domain, a hinge
CC domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
CC domain of an insect Ecr, where the ligand binding domain is heterologous
CC with respect to the hinge domain and an activation domain. The chimeric
CC insect hormone receptors and receptor cassettes are useful in regulating
CC expression of target polypeptides in plants in the presence of
CC appropriate ligands that may be used in controlling plant fertility. The
CC method is useful for decreasing or increasing plant gene expression. The
CC present sequence is a coding sequence described in the exemplification of
CC the invention

SQ Sequence 3972 BP; 1027 A; 895 C; 929 G; 1121 T; 0 U; 0 Other;

Query Match 87.4%; Score 1332; DB 6; Length 3972;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 1404; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY	1	ATGCGACGCTATATGCTGATTTTATGCTTACCTGCTTACATACGCTATTTATTTGCTGG	60
DB	1884	ATGCGACGCTATATGCTGATTTTATGCTTACCTGCTTACATACGCTATTTATTTGCTGG	1943
QY	61	TACTGTTCTTTGTCGATGCTCACCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	120
DB	1944	TACTGTTCTTTGTCGATGCTCACCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	2003
QY	121	ACCATGAAGCTACTGTTCTTATCGAACAAGCATGCGATTTTGGCGACTTAAAGCTC	180
DB	2004	ACCATGAAGCTACTGTTCTTATCGAACAAGCATGCGATTTTGGCGACTTAAAGCTC	2063
QY	181	AGTGTCTCAAGAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTCC	240
DB	2064	AGTGTCTCAAGAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTCC	2123
QY	241	TACTCTCCAAACCAAGGCTCGCTGCTAGTGGGCATCTGACAGAGTGGGAATCA	300
DB	2124	TACTCTCCAAACCAAGGCTCGCTGCTAGTGGGCATCTGACAGAGTGGGAATCA	2183
QY	301	AGGCTAGAAAGCTGGAACAGCTATTTCTACTGATTTTCTCGAAGAACCTTGACATG	360
DB	2184	AGGCTAGAAAGCTGGAACAGCTATTTCTACTGATTTTCTCGAAGAACCTTGACATG	2243
QY	361	ATTTTGAAATGATTTCTTTACAGGATATAAAGCAATTTGTTAAACAGATTTTGTACAA	420
DB	2244	ATTTTGAAATGATTTCTTTACAGGATATAAAGCAATTTGTTAAACAGATTTTGTACAA	2303
QY	421	GATAATGTGATTAAGATGCGCTCACAGATAGATTGCTTCACTGGAGACTGATATGCCT	480
DB	2304	GATAATGTGATTAAGATGCGCTCACAGATAGATTGCTTCACTGGAGACTGATATGCCT	2363
QY	481	CTAACATTGAGACAGATAGATAAAGTGGCAGCATCATCATCGGAAGAGAGTAGTAACAA	540
DB	2364	CTAACATTGAGACAGATAGATAAAGTGGCAGCATCATCATCGGAAGAGAGTAGTAACAA	2423
QY	541	GGTCAAAAGACAGTTGACTGATCGACCGTATGAGGCCCGAGTGGTCCCGAGAGTCC	600
DB	2424	GGTCAAAAGACAGTTGACTGATCGACCGTATGAGGCCCGAGTGGTCCCGAGAGTCC	2483
QY	601	ACGTGCAAGAACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	660
DB	2484	ACGTGCAAGAACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2543
QY	661	AGTACGACGACAGTGGAGCATCATATGCTTGGCCATATGCAATGTGACCTCCGCCCCCA	720
DB	2544	AGTACGACGACAGTGGAGCATCATATGCTTGGCCATATGCAATGTGACCTCCGCCCCCA	2603
QY	721	GAGCGCGCAAGGATTCACGAAGTGGTCCGAGGTTTCTTAAACGGAAGAGCTAATGGAGCAG	780
DB	2604	GAGCGCGCAAGGATTCACGAAGTGGTCCGAGGTTTCTTAAACGGAAGAGCTAATGGAGCAG	2663
QY	781	AACAGACTGAAGATGTGACGCCCTGCTCGCGCAACCAAGAGTCCCTGATCGCGAGGCTC	840

DB	2664	AACAGACTGAAGAAATGTGACGCCCTGTGCGCGAACCAAGAGTCCCTGATCGCGAGGCTC	2723
QY	841	GTGTGGTACCAAGGACGGATACGACGCTTTCGGAAGAGGATCTCAAAAGGCTGACGCAG	900
DB	2724	GTGTGGTACCAAGGAGGGGTACGACGCGCTTCGGAAGAGGATCTCAAGAGGTTACACAG	2783
QY	901	ACTTGGCAATCAGCAGATGAAGAAGCAAGACTCAGACATGCCATTCGCCAGATACACA	960
DB	2784	ACATGGCAGTTTAGAAGAAGAGAGAGGAGAACTGACATGCCCTTCGTCAGATACACA	2843
QY	961	GAAATGACCATCTTCACAGTACAGTAAATAGTCAGTTTTCGCAAGGCTTACCTGTTT	1020
DB	2844	GAGATGACGATCTTTAAACAGTGCAGCTTATTGTAGAAATTCGAAAGGGGACTACCGGATTC	2903
QY	1021	TCAAAGATCTCACAACTGACAGATCACATTTATTAAGAGGATGCTCAAGCGAAGTGTATG	1080
DB	2904	TCCAAGATATCTCAGTCCGATCAAAATTAATTTAAGAGGCTCATCAAGCGAAGTGTATG	2963
QY	1081	ATGCTGCGAGTAGCGAGGCGGTACGACGCGGTGTCGGATAGCGTTTCTGTTCGCCAACAA	1140
DB	2964	ATGCTGCGAGTGGCGCGACGCTTACGACGCGGCGACGCGACGCGTGTCTGTCGGAACAA	3023
QY	1141	CAGGCGTACACTCGCGCAAACTACCGCAAGCGCGGCATGGCTTCTGTCGAGACCTG	1200
DB	3024	CAGGCGTACACGCGCGCAAACTACCGCAAGCGCGGCATGGCTTCTGTCGAGACCTG	3083
QY	1201	CTGCACTTCTGCGCGTGTACTGATGCGATGCGTGGCAACGCTGATTTACGCGCTCTC	1260
DB	3084	CTGCACTTCTGCGCGTGTACTGATGCGATGCGTGGCAACGCTGATTTACGCGCTCTC	3143
QY	1261	ACTGCGCATCTTATATTTCTCGGATCGCGCGGCTTAGAGCAGCCACAGCTAGTAGAAGAG	1320
DB	3144	ACCGCATCTTATATTTCTCAGACCGCGCGGCTTAGAGCAGCCACCTTTTGTGGAGGAA	3203
QY	1321	ATTCAGCGGTATTAATCTGAAACAGCTGCGGGGTACATCATGAACAGCAGACGCGCTG	1380
DB	3204	ATTCAGAGATATTAATCTGAAACAGCTGCGGGGTACATCATTTTAAATCAGCAGCAGCTG	3263
QY	1381	CGCGGTGGCGGCTCATCTACGCGAAGATCTGCGGTCTTACCGAGTTGCGGAGCGCTG	1440
DB	3264	CGCGGTGGCGGCTCATCTACGCGAAGATCTGCGGTCTTACCGAGTTGCGGAGCGCTG	3323
QY	1441	GCGATGCGAATTCGAACATGTCATCTGCTGAAGCTCAAGAACAGAGGAGCTGCGCGCG	1500
DB	3324	GCGATGCGAATTCGAACATGTCATCTGCTGAAGCTCAAGAACAGAGGAGGAACTTCCGCCA	3383
QY	1501	TTCTTGGAGGAGATCTGGGACCTG 1524	
DB	3384	TTCTTGGAGGAGATCTGGGACCTG 3407	

RESULT 10

ADP49176
ID ADP49176 standard; DNA; 3972 BP.

XX

AC ADP49176;

XX

DT 12-FEB-2004 (first entry)

XX

Ecdysone receptor/VP16 transactivation domain DNA seq id 104.

DE

XX receptor cassette; chimeric receptor polypeptide; DNA binding domain;

KW hinge domain; ecdysone receptor; Ecr; ligand binding domain;

KW activation domain; transgenic seed; transgenic plant; plant line;

KW herbicide; pesticide; chimeric ecdysone receptor; Ecr;

XX yeast GAL4 DNA binding domain; VP16 transactivation domain; db; gene.

OS Synthetic.

OS Manduca sexta.

OS Ascomycota.

OS Herpes simplex virus unknown type.

XX

PN	US2003154509-A1.
PP	
PD	XX
PB	14-AUG-2003.
PF	XX
PI	24-OCT-2001; 2001US-00087167.
PR	XX
PS	24-OCT-2001; 2001US-00087167.
PT	XX
PA	(PASC/) PASCAL E J.
PA	(VALE/) VALENTINE S A.
PA	(BROW/) BROWN J A.
PA	(COCK/) COCKRELL A S.
PA	(JOHN/) JOHNSON B D.
XX	
PI	Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX	
DR	WPI; 2003-897756/82.
XX	
PT	New receptor cassette encoding a chimeric receptor polypeptide, useful
PT	for regulating the expression of target polypeptides in plants in the
PT	presence of appropriate chemical ligands.
XX	
PS	Example 11; SEQ ID NO 104; 186pp; English.
XX	
CC	The invention describes a receptor cassette encoding a chimeric receptor
CC	polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
CC	(D) domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
CC	(E) domain that is heterologous with respect to the D domain, and an
CC	activation domain. The receptor cassette and method are useful in
CC	regulating the expression of target polypeptides in plants in the
CC	presence of appropriate chemical ligands. The transgenic seeds and plants
CC	can be used for the breeding of improved plant lines that, for e.g.
CC	increase the effectiveness of conventional methods such as herbicide or
CC	pesticide treatment. This sequence encodes an ecdysone receptor-Vp16
CC	c-transactivation domain fusion protein.
XX	
SQ	Sequence 3972 BP; 1027 A; 895 C; 929 G; 1121 T; 0 U; 0 Other;
	Query Match 87.4%; Score 1332; DB 10; Length 3972;
	Best Local Similarity 92.1%; Pred. No. 0;
	Matches 1404; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
Oy	1 ATGCAGCAGCTATATGTGGATTTTTTTTAGCCCTGCCCTTCACGCTATTATTGTCTTGG 60
Db	1884 ATGCAGCAGCTATATGTGGATTTTTTTTAGCCCTGCCCTTCACGCTATTATTGTCTTGG 1943
Oy	61 TACTGTCTTCTTGTCGATGCTCACCCCTGTTGTTGGTGTTACTCTCGAGGATCGGCC 120
Db	1944 TACTGTCTTCTTGTCGATGCTCACCCCTGTTGTTGGTGTTACTCTCGAGGATCGGCC 2003
Oy	121 ACCATGAAGCTACTGTCTTCTATCGAAACAAGCATGCGATATTTGCCGACTTAAAAAGCTC 180
Db	2004 ACCATGAAGCTACTGTCTTCTATCGAAACAAGCATGCGATATTTGCCGACTTAAAAAGCTC 2063
Oy	181 AAGTGCTCCAAAGAANAACCGAAGTCGCCCAAGTGCTCGAAGACRACTCGGAGTGTCGC 240
Db	2064 AAGTGCTCCAAAGAANAACCGAAGTCGCCCAAGTGCTCGAAGACRACTCGGAGTGTCGC 2123
Oy	241 TACTCTCCAAAACCAAAGGCTCCCGCTGACTAGGGCACATCTGACAGAAGTGGAAATCA 300
Db	2124 TACTCTCCAAAACCAAAGGCTCCCGCTGACTAGGGCACATCTGACAGAAGTGGAAATCA 2183
Oy	301 AGGCTAGAAAGACTGGAAACAGCTATTTCCTACTGATATTTTCTCTGAGAAGACCTTGACATG 360
Db	2184 AGGCTAGAAAGACTGGAAACAGCTATTTCCTACTGATATTTTCTCTGAGAAGACCTTGACATG 2243
Oy	361 ATTTTGAAANTGGATTCTTTTACAGSATATAAAGCATTTGTTAACAGGATATTATTGTACAA 420
Db	2244 ATTTTGAANATGGATTCTTTTACAGSATATAAAGCATTTGTTAACAGGATATTATTGTACAA 2303
Oy	421 GATAATGTGAATAAGACTGCCGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCCT 480
Db	2304 GATAATGTGAATAAGACTGCCGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCCT 2363

[illegible]

QY 361 ATTTTGAATGATGATTTCTTTTACAGGATATAAAAGCAATTTGTTAAACAGGATTTATTTGTACAA 420
 DB |||||||
 QY 361 ATTTTGAATGATGATTTCTTTTACAGGATATAAAAGCAATTTGTTAAACAGGATTTATTTGTACAA 420
 DB |||||||
 QY 421 GATAATGTGAATAAAGATGCCGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCCT 480
 DB |||||||
 QY 421 GATAATGTGAATAAAGATGCCGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCCT 480
 DB |||||||
 QY 481 CTAACATTTGAGACAGCATAGATAAGTGGACATCATATCGGAAGAGAGTAGTAACAAA 540
 DB |||||||
 QY 481 CTAACATTTGAGACAGCATAGATAAGTGGACATCATATCGGAAGAGAGTAGTAACAAA 540
 DB |||||||
 QY 541 GGTCAAGACAGCTTCACTGTATCGACGCGTATGAGCCCGAGTGGCTGCTCCAGAGTCC 600
 DB |||||||
 QY 541 GGTCAAGACAGCTTCACTGTATCGACGCGTATGAGCCCGAGTGGCTGCTCCAGAGTCC 600
 DB |||||||
 QY 601 AGCTGCAAGAACAAAAGAGAGAAAAGGAGACACAGAGAGAAAAGACAAAATGCCAGTTC 660
 DB |||||||
 QY 601 AGCTGCAAGAACAAAAGAGAGAAAAGGAGACACAGAGAGAAAAGACAAAATGCCAGTTC 660
 DB |||||||
 QY 661 AGTACGACAGAGTGGACGATCATATGCTGCGCATATGCAATGTGACCTCGGCCCA 720
 DB |||||||
 QY 661 AGTACGACAGAGTGGACGATCATATGCTGCGCATATGCAATGTGACCTCGGCCCA 720
 DB |||||||
 QY 721 GAGCGGCAAGGATTCACGAAGTGGTCCGAGGTTCTTAACGAGAGAGCTAATGAGAGCAG 780
 DB |||||||
 QY 721 GAGCGGCAAGGATTCACGAAGTGGTCCGAGGTTCTTAACGAGAGAGCTAATGAGAGCAG 780
 DB |||||||
 QY 781 AACAGACTGAAGAATGTGACGCGCTGTGCGGGAACACAGAAGTCCCTGATCGCGAGGCTC 840
 DB |||||||
 QY 781 AACAGACTGAAGAATGTGACGCGCTGTGCGGGAACACAGAAGTCCCTGATCGCGAGGCTC 840
 DB |||||||
 QY 841 GTGTGTTACAGAACGATACAGAGAGCCTTCCGAAGAGAGATCTCAAAAGGTTGACGAG 900
 DB |||||||
 QY 841 GTGTGTTACAGAACGATACAGAGAGCCTTCCGAAGAGAGATCTCAAAAGGTTGACGAG 900
 DB |||||||
 QY 901 ACTTGGCAATCAGCAGATGAAGAGACGAAGACTCAGACATGCCATTCGCCAGATCACA 960
 DB |||||||
 QY 901 ACTTGGCAATCAGCAGATGAAGAGACGAAGACTCAGACATGCCATTCGCCAGATCACC 960
 DB |||||||
 QY 961 GAAATGACCATCTCACAGTACAGTAAATAGTCCAGTTTGGCCAAAGGCTTACTCTGTTT 1020
 DB |||||||
 QY 961 GAAATGACCATCTCACAGTACAGTAAATAGTCCAGTTTGGCCAAAGGCTTACTCTGTTT 1020
 DB |||||||
 QY 998 GAGATCAGCATCTGACAGTTTCACTCATCGTAGAATTCGCAAAAGGCTTCCGAGGCTTC 1017
 DB |||||||
 QY 1021 TCAAGATCTCAAACTGACAGATCACAATTAATTAAGGATGCTCAAGCGAAGTATG 1080
 DB |||||||
 QY 1018 GCCAAGATCTCGCAGTCGATCAATCAATCAGCTTAAAGGCGTGTTCAGTGAGGTGATG 1077
 DB |||||||
 QY 1081 ATCTCGGATAGCGAGGCGGTACGAGCGGTGTCGATAGCGTTCTGTTTCGCCAACAAAC 1140
 DB |||||||
 QY 1078 ATGCTCGAGTGGCCGCGGTACGAGCGCGGCACCGACGCGTACTGTTTCGCCAACAAAC 1137
 DB |||||||
 QY 1141 CAGCGGTACACTCGCAGCAACTACCGCAAGCGGCGATGCGCTACGTATCGAAGACCTG 1200
 DB |||||||
 QY 1138 CAGCGGTACTCCCGGACAACTACCGCAAGCGGCGATGCTTCTACGTATCGAAGATCTC 1197
 DB |||||||
 QY 1201 CTGCACTTCTGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
 DB |||||||
 QY 1198 TTGCACCTTCTGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1257
 DB |||||||
 QY 1261 ACTGCCATCTTATTTCTCGGATCGCGCGGCTTACAGCAGCCACACAGCTAGTAGAAGAG 1320
 DB |||||||
 QY 1258 ACGCCCATTTGTCATTTTCTCAGACCGGCTGCGGCTCGAGCAACCTTATTTGGTGAAGAA 1317
 DB |||||||
 QY 1321 ATCCAGCGGTATTAACCTGAACACCGCTCGGCTGTACATCATATGAACACAGCAGCGCTG 1380
 DB |||||||
 QY 1318 ATCCAGCGGTATTAACCTGAACACCGCTCGGCTGTACATCATATGAACACAGCAGCGCTG 1377
 DB |||||||
 QY 1381 CCGCGTTGCCCGCTGATCTTACGCGAAGATTTCTGCGGTGCTTACCGAGTTGCGGACGCTG 1440
 DB |||||||
 QY 1378 CCGCGCTGCCCGTGTGTTCTTCCGCAAGATCTTCCGCGGATTAATGACGAGCTGCGGACCTC 1437
 DB |||||||
 QY 1441 GGCATGCAAGATTCGACATGTGATCTCTCGTGAAGCTCAAGACAGGAGCTGCGCGCG 1500

DB 1438 GGCATGCAAGACTCCAACATGTGCATCTGTTGAAGCTGAAGAATAGGAAGCTGCCCGC 1497
 QY 1501 TTCTCTGGAGGAGATCTGGAGCTG 1524
 DB 1498 TTCTCTGGAGGAGATCTGGAGCTG 1521
 DB |||||||
 RESULT 15
 ID ABT07370 standard; DNA; 1800 BP.
 AC ABT07370;
 XX AC
 XX 29-AUG-2003 (revised)
 DT 07-NOV-2002 (first entry)
 XX
 XX Chimeric ecdysone receptor coding sequence SEQ ID NO: 126.
 XX Plant; gene expression control; insect; hormone receptor; fertility;
 XX ecdysone receptor; gene; ds.
 KW Ostrinia nubilalis.
 OS Manduca sexta.
 OS Chimeric.
 XX WO200261102-A2.
 XX
 XX 08-AUG-2002.
 XX
 XX 24-OCT-2001; 2001WO-US051417.
 XX
 XX 24-OCT-2000; 2000US-0242969P.
 PR
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA
 XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 XX
 XX WPI: 2002-619259/66.
 DR P-PSDB; ABJ05376.
 DR
 XX
 XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
 PT regulating expression of target polypeptides in plants in the presence of
 PT appropriate ligands that may be used in controlling plant fertility.
 XX
 XX Example 23; Page 286-288; 319pp; English.
 PS
 XX The present invention relates to a receptor cassette encoding a chimeric
 CC receptor polypeptide comprising at least one DNA binding domain, a hinge
 CC domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
 CC domain of an insect Ecr, where the ligand binding domain is heterologous
 CC with respect to the hinge domain and an activation domain. The chimeric
 CC insect hormone receptors and receptor cassettes are useful in regulating
 CC expression of target polypeptides in plants in the presence of
 CC appropriate ligands that may be used in controlling plant fertility. The
 CC method is useful for decreasing or increasing plant gene expression. The
 CC present sequence is a coding sequence described in the exemplification of
 CC the invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 XX Sequence 1800 BP; 482 A; 444 C; 485 G; 389 T; 0 U; 0 Other;
 SQ
 Query Match 80.2%; Score 1222.2; DB 6; Length 1800;
 Best Local Similarity 87.8%; Pred. No. 0;
 Matches 1351; Conservative 0; Mismatches 173; Indels 15; Gaps 1;
 QY 1 ATCCAGCAGCTATATGTGGATTTTTTTAGCCCTGCCCTTCATAGCTATTTATTTGCTTG 60
 DB |||||||
 QY 1 ATCCAGCAGCTATATGTGGATTTTTTTAGCCCTGCCCTTCATAGCTATTTATTTGCTTG 60
 DB |||||||
 QY 61 TACTGTTCTTTTGTGTCGATGCTCACCTGTTGTTGTTGTTTACTTCTGCGAGGATCGCC 120
 DB |||||||
 QY 61 TACTGTTCTTTTGTGTCGATGCTCACCTGTTGTTGTTGTTTACTTCTGCGAGGATCGCC 120
 DB |||||||

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 11:02:48 ; Search time 5198.63 Seconds
(without alignments)
11158.701 Million cell updates/sec

Title: US-10-087-167-120_COPY_1_1524
Perfect score: 1524
Sequence: 1 atcagcagctatgtgga.....tggaggagatctggagcgtg 1524

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	321.6	21.1	963	CNS0905M	BX067382 single re
2	242.8	15.9	851	CNS011ME	AL100448 Drosophil
3	226.2	14.8	728	BM650826	BM650826 170006873
4	214.6	14.1	470	AA538642	AA538642 LD18219.5
5	183.6	12.0	607	AA664510	AA664510 ESTFRg2-
6	161.1	10.6	1050	CNS016YX	AL107379 Drosophil
7	159.6	10.5	574	AI258616	AI258616 LP01848.5
8	140.0	9.2	1031	BQ584428	BQ584428 AGENCOURT
9	139.6	9.2	842	CNS06JRC	AL401698 T7 end of
10	138.4	9.1	651	CNS09352	CNS09352 170005999
11	138.4	9.1	667	CD673041	CD673041 fg19q05.Y
12	138.4	9.1	867	BQ222200	BQ222200 AGENCOURT
13	138.4	9.1	918	BQ214241	BQ214241 AGENCOURT
14	138.4	9.1	1685	CR614375	CR614375 full-leng
15	138.4	9.1	1763	CR610600	CR610600 full-leng
16	138.4	9.1	1828	CR617823	CR617823 full-leng
17	138.4	9.1	1922	CR604070	CR604070 full-leng
18	138.4	9.1	1924	CR609885	CR609885 full-leng
19	138.4	9.1	1965	CR598124	CR598124 full-leng
20	138.4	9.1	1978	CR598123	CR598123 full-leng
21	138.4	9.1	2041	BC033500	BC033500 Homo sapi
22	138.2	9.1	721	BE382387	BE382387 601298693
23	133	8.7	1088	BX463524	BX463524 BX463524
24	127.6	8.4	1082	BX367164	BX367164 BX367164

25	127.4	8.4	866	4	BG675073
26	126.4	8.3	957	5	BE878950
27	125.8	8.3	1003	5	BX344136
28	125.8	8.3	1026	5	BQ052341
29	124.4	8.2	986	5	BQ877581
30	123.8	8.1	622	5	BQ636916
31	123.8	8.1	1135	5	BX365740
32	123.6	8.1	2035	3	CR749648
33	123.2	8.1	965	1	AL582953
34	122.6	8.0	972	1	AL522399
35	119.2	7.8	920	1	AL522738
36	118.8	7.8	1085	5	BX406790
37	118.6	7.8	1132	4	BM553603
38	117.6	7.7	1114	5	BX444140
39	117.6	7.7	1138	5	BM912640
40	117.6	7.7	1158	4	BM554635
41	117	7.7	1963	3	AK077620
42	115.6	7.6	649	6	CD304821
43	114.6	7.5	618	6	CD309514
44	113.6	7.5	444	9	AG215235
45	112.4	7.4	1074	5	BX342843

ALIGNMENTS

RESULT 1
CNS0905M
LOCUS
DEFINITION
CNS0905M 963 bp mRNA linear HTC 08-JAN-2003
Single read from an extremity of a full-length cDNA clone made from Anopheles gambiae total adult females. 5-PRIME end of clone
FKOAC51AC03 of strain 6-9 of Anopheles gambiae (African malaria mosquito).
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

BX067382
BX067382.1 GI:27640663
HTC.
Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
1 (bases 1 to 963)
Genoscope.
Direct Submission
Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.Genoscope.cns.fr)
Location/Qualifiers
1..963
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="6-9"
/db_xref="taxon:7165"
/clone="FKOAC51AC03"
/plasmid="pME18S-EL"
/note="end : 5-PRIME"
ORIGIN
Query Match 21.1%; Score 321.6; DB 3; Length 963;
Best Local Similarity 75.0%; Pred. No. 1.8e-77;
Matches 441; Conservative 0; Mismatches 144; Indels 3; Gaps 3;
QY 937 GACATGCCATCCCGCAGATCACAGAAATGACCATCTCCACAGTACAGCTAATAGTCGAG 996
DB 9 GAATATCCACTTCCGGCACAATACGGAAATCACCATCTCCACAGTACAGCTAATCGTCGAG 68
QY 997 TTTCGCAAGGCCTACTCTGGTTTTCACAGATCTCACACCTGACAGATCATATTATTA 1056
DB 69 TTCGCGAGGGAGTCCGCAATTCACCAAGATCCCGC-AGAGATCAGATAACGTTACTTA 127
QY 1057 AAGGATGTCGAAGCGAAGTATGATGCTGCGAGTAGCAGCGGGTACACCGGGTGTGCG 1116
DB 128 AAGGCTCTCCAGTGAGGTATGATGTTTGCAGATGGCCCGCGGTACGACCGCGAACC 187

QY	1117	GATAGCGTCTGTTGGCCAAACACAGCGCGTACACCTCGCGACAACTACCGCAAGCGCGGC	1176	QY	1058	AGGCATGCTCAAGCGAAGTGTGCTGCGTAGCGAGCGGTACGACGCGGTGTGCGG	1117
Db	188	GACTCCATCTCTTTGGCAACACCGATCGTACACGCGCGACTCGTACAGATGGCGGC	247	Db	266	AGGCCTGCTGCTGAGGTGATGCTGCGTATGGCAGCAGCTATACCCACAGCTCGG	325
QY	1177	ATGCGCTACGTCATCGAAGACCTGCTGCACTTCTGCGCGTGCATGCTACTGATGTCGATG	1236	QY	1118	ATAGCGTTCGTGTTCCGCCAACCAACGCGGTACACTCGCGCAACACTACCGCAAGCGCGGCA	1177
Db	248	ATGCGGACACGATCGAGGACCTGCTGCACTTCTGCGCGGAGATGTACACGCTCACGGTG	307	Db	326	ACTCAATATTTCTCGGAATAATAGATCATATACGCGGGAATTTTACAAAATGGCGCGAA	385
QY	1237	GACAACTGCTATACGCGCTCTCACGCGCATGTTATATTTCTGGATCGCGCGCGCTA	1296	QY	1178	TGGCTAGCTCATCGAAGACCTGCTGCACTTCTGCGCGTGCATGCTACTGATGTCGATGG	1237
Db	308	GACAACTGCGAGTACGCGCTGCTGACCGCATGCTCATCTTCTCCGACGCGCGCGCTC	367	Db	386	TGGCTGATAACATTTGAAGACCTGCTGCACTTCTGCGCGCAAAATGTTCTCGATGAAGTGG	445
QY	1297	GAGCAGCCACAGCTAGTAGAAGATCCAGCGGTATTACCTGAACACGCTGCGGGGTAC	1356	QY	1238	ACAACTGCTATACGCGCTCTCACGCGCATGTTATATTTCTCGATCGCGCGCGCTAG	1297
Db	368	GAGAAGCGGAGCTGGTGAACAGATCCAGAGCTACTACATCGACACGCTGCGCGTAC	427	Db	446	ACAACTGCTATACGCGCTCTCACGCGCATGTTATATTTCTCGATCGCGCGCGCTAG	1297
QY	1357	ATCATGAACAGCAGCGGTGCGCGGTGCGCGTATCTACGCGAGATGCTGTGCG	1416	QY	1298	AGCAGCCACAGCTAGTAGAAGATCCAGCGGTATTACCTGAACACGCTGCGGGGTACA	1357
Db	428	ATCCTGAACCGGACCGGGCGAC-CCGAAGTGTAGCGTACGTTCCGGAA-CTGCTGTGCG	485	Db	506	AGAAGGCCCACTAGTTCGAAGCGATCCAGAGCTACTACATCGACACGCTACCGATTATA	565
QY	1417	GTGCTTACCGAGTTGCGGACGCTGGCATGCGAATTCGAACATGTGCATCTCGCTGAAG	1476	QY	1358	TGCTTACCGAGTTGCGGACGCTGGCGGTGCGCGTCACTACGCGAAGATTTCTGTGCG	1417
Db	486	ATCTGACCGAGCTGCGGACGCTCGGCAACAGACTCGGAGATGCTCTCGCTCAAG	545	Db	566	TACTCAACCGCACGCGGACTCAATG-AGCTGCTTCTACGCAAGCTGCTCTCGA	624
QY	1477	CTCAAGAACAGAACTGCGCGCGTCTGAGGAGATCTGGGACGTTG	1524	QY	1418	TGCTTACCGAGTTGCGGACGCTGGCGATGCAAAATTCGAACATGTGCATCTCGTGAAGC	1477
Db	546	CTGAAGAACCGTAAGCTGCGCGCTTCTGAGGAGATATGGGACGTTG	593	Db	625	TCTTACCGAGCTGCGTACGCTGGGCAACAGACGCGGAGATGTTGTTCTCCTACAAAGC	684
RESULT 2				QY	1478	TCAGAACAGGAGCTGCGCGCTTCTGAGGAGATCTGGGACGTT	1523
CNS011ME		851 bp	DNA	linear			
LOCUS							
DEFINITION							
ACCESSION							
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
COMMENT							
FEATURES							
source							
ORIGIN							

Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org).

ORIGIN

Query Match 14.8%; Score 226.2; DB 4; Length 728;
Best Local Similarity 61.7%; Pred. No. 4.6e-51;
Matches 404; Conservative 0; Mismatches 233; Indels 18; Gaps 2;

Qy 551 AGTTGACTGTATCGACGGCGTATGAGGCCGAGTGGTGTCTCCAGAGTCCACGTGCGAAGA 610
Db 79 AGAAGTGTCTCGCGTGTGCGTGTGCGCGAGTGGTGTCTCCAGAGTCCAGTGTGCGCA 138

Qy 611 ACAAGAAGAGAGAAAGAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 670
Db 139 TCAAGCGGAG 198

Qy 671 CAGTGGAGATCATATGCTGCTCCATATGCAATGTGACCTCCGCGCCCGAGAGCGGCA 730
Db 199 CCACCACCGTGTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 258

Qy 731 GGATTACGAGAGTGTCTCCGAG-----GTTCTTAACGAGAGAGTAAATGAGAGC 778
Db 259 TGAAGTGTGATCACCGCCCGCGAGTACCGCTACTGCGGAGAGAGTGTGTAACG 318

Qy 779 AGAAGAGTGAAGATGTGAGCGCGCTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 838
Db 319 AAAACGAG 378

Qy 839 TCGTGTGTGACGAG 898
Db 379 TGATCTGTGACGAG 438

Qy 899 AGACTTGGCAATCAGCAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 958
Db 439 TTA-----ACTCACCAGAGAGAGAGAGAGATCCCGAGAAATCCACTTCGCGGACATA 492

Qy 959 CAGAAATGACCATCTCAGTACAGTAAATGATGAGTTGCGGAGAGAGAGAGAGAGAGAG 1018
Db 493 CGGAAATCACCATCTCAGTACAGTAAATGATGAGTTGCGGAGAGAGAGAGAGAGAGAG 552

Qy 1019 TTTCAAGATCTCAGACCTGACAGATCAGACATTAATTAAGGAGAGAGAGAGAGAGAG 1078
Db 553 TTACCAAGATCTCCGAGAGAGATCAGATTAAGTTTAAAGGAGAGAGAGAGAGAGAGAG 612

Qy 1079 TGATGTGCGAGTGTGAGCGGCTGTGAGCGGCTGTGAGAGAGAGAGAGAGAGAGAGAG 1138
Db 613 TGATGTGCGAGTGTGAGCGGCTGTGAGCGGCTGTGAGAGAGAGAGAGAGAGAGAGAG 672

Qy 1139 ACCAGCGTACACTCGGAG 1193
Db 673 ACCGATCGTACAGCGGAG 727

RESULT 4
AA538642 470 bp mRNA linear EST 19-APR-2001
LOCUS LD18219.5prime LD Drosophila melanogaster embryo Bluescript
DEFINITION Drosophila melanogaster cDNA clone LD18219 5prime similar to M74078: Drosophila melanogaster ecdysone receptor (Ecr) mRNA, complete cds, mRNA sequence.

ACCESSION AA538642
VERSION AA538642.1 GI:2285158
KEYWORDS EST.

SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 470)
AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Teang, G., Lewis, S., and Rubin, G.M.
TITLE BDGP/HHMI Drosophila EST Project

Unpublished (2001)
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
Plate: 182 row: B column: 7
High quality sequence stop: 343.

FEATURES
source
1..470
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="BDGP EST:BDcin017358"
/db_xref="taxon:7227"
/clone="LD18219"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
/clone_lib="LD Drosophila melanogaster embryo Bluescript"
/note="Organ: embryo; Vector: Bluescript SK; Site 1:
EcoRI; Site 2: XhoI; Constructed using Stratagene ZAP-CDNA
Synthesis kit. Oligo dt-primed and directionally cloned at
EcoRI and XhoI in Bluescript SK(+/-)"

ORIGIN
Query Match 14.1%; Score 214.6; DB 1; Length 470;
Best Local Similarity 72.0%; Pred. No. 6.8e-48;
Matches 280; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

Qy 1135 AACACACGCGGTACATCGCGCAACATACCGCAAGCGCGGCGATCGCTCATCGAA 1194
Db 1 AATAATAGATCATATACGCGGATCTTACAAAATGCGCGAATGGCTGATAACATTGAA 60

Qy 1195 GACCTGTGCACTCTTCCGCTGCTACTGATGTCGATGTCGATGTCGATGTCGATGTCG 1254
Db 61 GACCTGTGCACTCTTCCGCGCAATGTTCTCGATGAAGGTGGACACGTCGATACGCG 120

Qy 1255 CTCTCACTGCATCGTTATATCTCGGATCGCGCGGCGCTAGACGACGACGCTAGTA 1314
Db 121 CTCTCACTGCATCGTTATATCTCGGATCGCGCGGCGCTAGACGACGCTAGTA 180

Qy 1315 GAAGAGATCCAGCGGTATTACCTGAACACGCTGCGGGTGTATCATGATGAACGACACAG 1374
Db 181 GAAGAGATCCAGCGGTATTACCTGAACACGCTGCGGGTGTATCATGATGAACGACACAG 240

Qy 1375 GCGTCCGCGGTGCGCGCTCATCTACGCGAGATTTCTGCTGCTTACCGAGTTGCGG 1434
Db 241 GCGCACTCAATGAGCTGCTCTTCTACGCAAGCTGCTCTCGATCTTACCGAGTGCCT 300

Qy 1435 AGCTGGGCGATCGAGAAATTCGAACATGTGCATCTCGCTGAAGCTCAAGAACAGAGCTG 1494
Db 301 AGCTGGGCGATCGAGAAATTCGAACATGTGCATCTCGCTGAAGCTCAAGAACAGAGCTG 360

Qy 1495 CGCGCGTCTCTGAGGAGATCTGGGACGT 1523
Db 361 CCCAAGTTCCTCGAGGAGATCTGGGACGT 389

RESULT 5
AA664510/c 607 bp mRNA linear EST 14-NOV-1997
LOCUS ESTFrg2- Human Brain, Clontech Homo sapiens cDNA clone pUC19-Frg2
DEFINITION 3', mRNA sequence.

ACCESSION AA664510
VERSION AA664510.1 GI:2619123
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 607)
AUTHORS Ming, H. and Huang, B.R.

TITLE
JOURNAL
COMMENT

Research on mechanism of p75NTR induced apoptosis
Unpublished (1997)
Other ESTs: ESTFrg2+
Contact: Ming Hong
National Laboratory of Medical Molecular Biology
Chinese Academic of Medical Sciences & PUMC
5 Dongdan Santiao, Beijing 100005, P.R.China
Tel: 86-10-65296406
Email: huangbrcdm.imicams.ac.cn
Seq primer: M13 Reverse
High quality sequence stop: 607.

FEATURES

source

Location/Qualifiers
1. .607
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="pUC19-Frg2"
/sex="male"
/tissue_type="brain"
/dev_stage="embryonic"
/lab_host="E.coli Y1090r-"
/clone_lib="Human Brain, Clontech"
/note="Organ: Brain; Vector: lambda gtl1; Site_1: EcoRI;
Site_2: EcoRI"

ORIGIN

Query Match 12.0%; Score 183.6; DB 1; Length 607;
Best Local Similarity 87.1%; Pred. No. 2.8e-39;
Matches 243; Conservative 0; Mismatches 31; Indels 5; Gaps 4;

QY 294 GGAATCAAGGCTAGAAAGACTGGAACAGCTATTCTACTGATTTTCTCGAGAAAGACCT 353
DB |||||
QY 566 GNGATCCAGGCTNGAAAGCCTGGAACGGCTTTTCNACGGATTNCCCGGAGGACCCCT 507
DB |||||
QY 354 TCACATGATTG--AAAATGATTCTTTACAGGATATAAAGCAAT-GTTAACAGGATT 410
DB |||||
QY 506 TGACNCGATTTTGGAAAAGGGATTCTTTACNGGATTTTAAACCACTTGGTTAAACAGGATT 447
QY 411 ATTTGTA-CAAGATAATGTAATAAGATGCGTCACAGATAGATTGGCTT-CAGTGGAG 468
DB |||||
QY 446 ATTTGTACCAAGATTAATGTAATAAGATGCGTCACAGATAGATTGGCTTCCAGTGGAG 387
QY 469 ACTGATATGCTCTTAACATTTAGACAGCATAGATAAGTGGACATCATCATCGGAAGAG 528
DB |||||
QY 386 ACTGATATGCTCTTAACATTTAGACAGCATAGATAAGTGGACATCATCATCGGAAGAG 327
QY 529 AGTACTACAAGGTCAAAGCAGTGTGACTGTATCGAGC 567
DB |||||
QY 326 AGTAGTAAACAAAGGTCAAAGCAGTGTGACTGTATCGCGC 288

RESULT 6

CNS016YX

LOCUS

DEFINITION
Drosophila melanogaster genome survey sequence Sp6 end of BAC
BACN17G18 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

1050 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephidroidae; Drosophilidae; Drosophila.
1 (bases 1 to 1050)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequence :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaut at CPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES

source

Location/Qualifiers
1. .1050
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN17G18"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : Sp6"

ORIGIN

Query Match 10.6%; Score 161; DB 9; Length 1050;
Best Local Similarity 55.0%; Pred. No. 5.9e-33;
Matches 254; Conservative 1; Mismatches 203; Indels 4; Gaps 2;

QY 1058 AGGCATCTCAAGCGAAGTGATGCTGCGAGTAGCGAGCGGTACGACGCGGTGTCGG 1117
DB |||||
QY 388 AGGCTGCTCGTCGAGGTGNTGCTGCGTGTGGCAGCGCTATGCCACAGCTCGG 447
DB |||||
QY 1118 ATAGCGTTCTGTCGCCCAACAAACAGCGGTACACTCGCGACAACTACCGCAAGCGGGCA 1177
DB |||||
QY 448 ACTCNNTNTTCTTCGCGNNTNATAGTNTNTNCGCGGNTTCTTNCANATGCGCGAA 507
DB |||||
QY 1178 TGGCTACGTCATCGAAGACCTGTCACATCTTCGCGCTGCATCTACTCGATCGCATGG 1237
DB |||||
QY 508 TGGCTGTAACATTGNAGACCTGTCGNTTCTGCGGCCNNNTGTTCTCGTNGNGTGG 567
DB |||||
QY 1238 ACAACGTGCAATTACGCGCTCTCACTGCCATCGTTATTTCTCGGATCGCGCGGCTAG 1297
DB |||||
QY 568 NCNNGTCGNATNCGCGCTTCTCNCCTGCCATGTGNTCTTCTCGNCGCGCGCGGCTGG 627
DB |||||
QY 1298 AGCAGCCACAGCTAGTAGAAGATCCAGCGGTATTACCTGGAACACGCTCGGGGTGTACA 1357
DB |||||
QY 628 NGNNGGCCNNNTNGTCGNNCGNTCCNGAGCTNCTNCATCGNNAAGTNNGNATTWTA 687
DB |||||
QY 1358 TCATGAACACAGCAGCGCTCGCGCGTTCGCGCGTCACTACGCGAAGATTTCTGTCGG 1417
DB |||||
QY 688 TNCCTCAACCGGCATCGCGNGANTCAATGNGNCTGCTTCTTNGNANANTGCTCTCGN 747
DB |||||
QY 1418 TGCTTACCGAGTTGCGGACGCTGGGATGCGAATTCGAAACATGTGATCTCGCTGAAGC 1477
DB |||||
QY 748 T-CCTCCGGGCTGCGTNGCTGGGNNCCGNNANGGNGTGTTGTTCTCAC--TAAGN 803
DB |||||
QY 1478 TCAAGAACAGGAAGCTGCCCGCTTCTCGGAGGAGATCTGGG 1519
DB |||||
QY 804 TNNAGTCCGNNNCTGNCNNNGTTCTCGNGGNGNNTCTGG 845
DB |||||

RESULT 7

AI258616

LOCUS

DEFINITION

574 bp mRNA linear EST 19-APR-2001
LP01848, Sprime LP Drosophila melanogaster larval-early pupal p012
Drosophila melanogaster cDNA clone LP01848 Sprime similar to
M74078: ECR FBgn0000546 PID:gl57318 SWISS-PROT:P34021, mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AI258616.1 GI:3866141
Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephidroidae; Drosophilidae; Drosophila.
1 (bases 1 to 574)
Harvey D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.
BDGP/HMI Drosophila EST Project

JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu
hit genomic sequence DS05325
High quality sequence stop: 533.
Location/Qualifiers
1. 574
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="LP01848"
/sex="male and female"
/dev stage="larvae-pupae"
/lab_host="DH5-alpha"
/clone_lib="LP Drosophila melanogaster larval-early pupal
pOT2"
/note="Organ: whole body; Vector: pOT2; Site 1: EcoRI;
Site 2: XhoI; Sized fractionated cDNAs were directly
ligated into pOT2. Plasmid cDNA library."
"

ORIGIN
Query Match 10.5%; Score 159.6; DB 1; Length 574;
Best Local Similarity 61.1%; Pred. No. 1.2e-32;
Matches 280; Conservative 0; Mismatches 169; Indels 9; Gaps 1;
QY 753 GTTCTTAACGGAGACTTAATGGAGCAGAACAGACTGAAGATGTGACGCCCTGTGGC 812
Db 126 GCTACTACCTGATGAATATTGGCCAAAGTGTCAAGCGCGCAATATACCTTCTTAACGTA 185
QY 813 GAACAGAGTCCCTGATCGCAGGCTCGTGTGGTACAGGACGGATACGAGCGCTTC 872
Db 186 CAATCAGTTGGCGTTATATACAGTTAATTTGGTACAGGATGGCTATGACAGCCATC 245
QY 873 GGAAGAGTCTCAAAAGGGTGACGAGACTTTGGCAATCAGAGATGAAGAAGACGAAGA 932
Db 246 TGAAGAGGATCTCAGCGGTATATGATCA-----ACCGATGAGAAGCAGAGCCA 296
QY 933 CTCAGACATGCCATTCGGCGAGTACAGAAATGACCATCTCTCAGATCAGCTAATAGT 992
Db 297 AACGGACGTGAGTTTTCGGCATATAACCGAGATAACCATCTACCGGTCCAGTTGATTG 356
QY 993 CGAGTTTGGCAAGGCTACCTGGTTTTCAAAGATCTCACAACCTGACAGATCACATT 1052
Db 357 TGAGTTTGTAAAGGCTACCGAGTGTATGATGCTGCGTATGGCAGCGCTATGACACAG 416
QY 1053 ATTAAAGGATGCTCAAGCGAAGTATGATGCTGCGAGTAGCGAGCGGTACGACCGGT 1112
Db 417 ACTAAAGGCTGCTCGTGGAGTGTATGCTGCGTATGGCAGCGCTATGACACAG 476
QY 1113 GTCGATAGCGTTCTGTTTCGCCAAACCGAGCGGTACATCTCGGACAACTACCGAAGC 1172
Db 477 CTCGGACTCAATATCTTCGCGAATAATAGATCATATACGCGGATTTCTTACAAATGCG 536
QY 1173 GGCATGGCTACGTATCAAGACCTGCTGCACTTCT 1210
Db 537 CGGAATGGCTGATAACATTGAAGACCTGCTGCACTTCT 574

RESULT 8
BQ058428 1031 bp mRNA linear EST 29-MAR-2002
LOCUS AGENCOURT_6794704 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5814274
DEFINITION 5', mRNA sequence.
ACCESSION BQ058428
VERSION BQ058428.1 GI:19817768
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1031)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LUCM2067 row: k column: 11
High quality sequence stop: 634.
Location/Qualifiers
1. 1031
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5814274"
/tissue type="lymphoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 99"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and SuperScript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 9.2%; Score 140; DB 5; Length 1031;
Best Local Similarity 56.3%; Pred. No. 3.9e-27;
Matches 329; Conservative 0; Mismatches 240; Indels 15; Gaps 3;
QY 946 TTCCGCCAGATCACAGAATGACCATCTCTCAGTACAGTAAATAGTCGAGTTTGC AAA 1005
Db 194 TTTGCCCACTTCACGAGCTGGCCATCATCTCAGTCCAGAGATGCTGGACTTCGCTAAG 253
QY 1006 GGCCTACCTGTTTTTAAAGATCTCAACCTGACCAGATCACATTATTAAAGCATGC 1065
Db 254 CAAGTGCCTGTTTCTTCGAGCTGGCGGAGGACCATGATCGCCCTCTGAAGGATCC 313
QY 1066 TCAAGCGAAGTATGATGCTGCGAGTAGCGAGCGGTACGCGGTGTCGGATACGTT 1125
Db 314 ACTATGAGATCATGCTGTAGACAGCAGCGCGCTACAAACACGACAGAGTGTATC 373
QY 1126 CTGTTTCCGCAACCAACGAGCGGTACACTCCGCAAACTACCGAAGCGGGCAT---GGCC 1182
Db 374 ACCTTCTTGAAGACTTTCACCTACAGCAAGGACGACTTCCACCGTGCAGCGCTGCAGGTG 433
QY 1183 TAGCTCATCGAAGACCTGCTGCATCTTCTCCGCTGCATGTACTCGATGTCGATGGACAAC 1242
Db 434 GAGTTTCATCAACCCCATCTTTCGAGTTCTCGCGGCGCATCGCGGCTTGGACGAC 493
QY 1243 GTGCAATACGCGCTCTCTACTGCCATCGTTATATTCTCG---GATCGCGCGGCGCTTAGAG 1299
Db 494 GCTGAGTACGCCCTGCTCATCGCCATCAACATCTTCTCGCGCGACCGGCCAACGTCGAG 553
QY 1300 CAGCCACAGCTTAGTAGAAGATCCAGCGGTATTACCTGAAACACCGTTCGGGTGTTATCATC 1359
Db 554 GAGCGGGCGGTGGAGCGGTTCGACAGAGCCCTACGTGGAGCGCGTGTGTCTCTACAC- 612
QY 1360 ATGAACACAGACAGCGCGTTCGCGGCTTTCGCGGCTCATCTACCGAAGATTCTGTGGTG 1419
Db 613 -----GCGCATCAAGAGCGCGCAGGACCGAGCTCGGCTTCCCGCGCATGCTCATGAAG 664

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QY 1420 CTTACGAGTTCGGGACGCTGGCGATCGAGATTCGAACTGTCGCTCGCTGAAGCTC 1479
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 665 CTGGTGAGCTGGCGACGCTGAGCTCTGTGCACTCGGAGCAGGCTCTTCGCTTGGCGCTC 724
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1480 AAGAACGAGGAGCTGGCGGCTTCCTGGAGGAGACTGGGAGCT 1523
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 725 CAGGACAAGAGCTGGCGGCTCTGCTGTGGAGACTGGGAGCT 768
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
LOCUS CNS06JKC 842 bp DNA linear GSS 30-NOV-2001
DEFINITION T7 end of clone AS0AA029D12 of library AS0AA from strain CLIB 533
of Saccharomyces bayanus, genomic survey sequence.
ACCESSION AL401698
VERSION AL401698.1 GI:12159736
KEYWORDS GSS.
SOURCE Saccharomyces bayanus
ORGANISM Saccharomyces bayanus
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
REFERENCE 1 (bases 1 to 842)
AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malbertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaiia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
GENOMIC exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876
REFERENCE 2 (bases 1 to 842)
AUTHORS Bon,E., Neuveglise,C., Casaregola,S., Artiguenave,F., Wincker,P.,
Aigle,M. and Durrens,P.
GENOMIC exploration of the hemiascomycetous yeasts: 5.
Saccharomyces bayanus var. uvarum
JOURNAL FEBS Lett. 487 (1), 37-41 (2000)
MEDLINE 20584715
PUBMED 11152880
REFERENCE 3 (bases 1 to 842)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. [E-mail :
secref@genoscope.cns.fr - Web : www.genoscope.cns.fr]
COMMENT This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
FEATURES
source
1. 842
/organism="Saccharomyces bayanus"
/mol_type="genomic DNA"
/strain="CLIB 533"
/variety="uvarum"
/db_xref="taxon:4931"
/clone="AS0AA029D12"
/clone_lib="AS0AA"
/note="Tend : T7"
<4..>379
/note="similar to Saccharomyces cerevisiae ORF YPL247c [
similarity to human HAN11 protein and petunia an11 protein
]
2 putative frameshift(s) "

misc_feature
<419..>822
/note="similar to Saccharomyces cerevisiae ORF YPL248c [
GAL4 ; transcription factor ]"
/evidence=not_experimental

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misc_feature
/evidence=not_experimental
<619..>822
/note="similar to Saccharomyces cerevisiae ORF YPL248c [
GAL4 ; transcription factor ]"
/evidence=not_experimental

ORIGIN
Query Match 9.2%; Score 139.6; DB 9; Length 842;
Best Local Similarity 74.8%; Pred. No. 4.8e-27;
Matches 175; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 87 CTGTGTTTGGTGTACTCTGTGAGGATCGCCACCATGAGCTACTGTCTTCTATCGA 146
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 582 CTTTGTGAGATGCAAGCTGCAGACCTCGATACCAATGAGCTGTTCCTGCAATGGA 641
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 147 ACAAGCATGCGATATTTTCCGACCTTAAAGAGCTCAAGTGCTCCAAAGAAAACCGAAGTG 206
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 642 ACAGCTTGGACATATGCCGGCTCAAGAACTCAAGTGTCTCCAAAGAAAACCAAGTG 701
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 207 CGCAGATGTCGAAGAACCAACTGGGAGTGTGCTACTCTCCCAAAACCAAAAGGTCTCC 266
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 702 TTCCAAGTGTCTGAAGAACCAACTGGGAGTGTGCTATTTCCTTAAGACCAAAAGTCCCC 761
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 267 GCTGACTAGGCGCATCTGACAGAGTGGAACTCAAGCTAGAAAGACTGGACA 320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 762 CCTAACCCGGGTGCACCTGACAGAGTGCAGGTGGAAAGTTGGAACA 815
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
LOCUS CN309352 651 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000599937470 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN309352
VERSION CN309352.1 GI:47325766
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 651)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
TITLE Transcription characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 651 Std Error: 0.00.
FEATURES
source
1. 651
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_lib="GRN PREHEP"
/note="oligo dt-primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN
Query Match 9.1%; Score 138.4; DB 7; Length 651;
Best Local Similarity 56.2%; Pred. No. 9.6e-27;
Matches 328; Conservative 0; Mismatches 241; Indels 15; Gaps 3;

QY 946 TTCCGCCAGATCACAGAAATGACCATCTCCAGATACAGCTAATAGTCAGTTGCCAA 1005
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 77 TTTGCCCACTTCAAGGAGTGGCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCTAAG 136
QY 1066 GGCCTACCTGGTTTTCAAAGATCTCAACCTGACAGATCACATTAATAAGGCATGC 1065
Db 137 CAAAGTGCCTGGTTTCTCGAGCTGGCCGGAGGACCATGCGCTCTCTGAAGCATCC 196
QY 1066 TCAACGGAAGTATGATGATGCTGCGAGTACGAGCGGTACGAGCGGTGTGCGATAGCGTT 1125
Db 197 ACTATCGAGATCATGCTGCTAGACAGACCCAGCGCTACACCAAGACAGAGTGTATC 256
QY 1126 CTGTTTCCCAACCAACAGCGGTACACTCGCGAACAATCCGCAAGCGCGGCAT----GGCC 1182
Db 257 ACCTTCTTGAAGGACTTCACTTACAGCAAGGACGACTTCCACCGTGCAGGCTGCAGGTG 316
QY 1183 TAGGTATCGAAGACCTGCTGACATCTTCCCGCTGCATGATCTCATGTCGATGACACAC 1242
Db 317 GAGTTTCAACCCCATCTTTCAGTGTCTCGCGGCGCATCGCGGCTGGGCCCTGCAGCAC 376
QY 1243 GTGCATTACGCTCTCACTGCTCATCTGTTATATCTCG--GATCGCGCGGCTAGAG 1299
Db 377 GCTGAGTACGCTCTGCTCATCGCCATCAACATCTTCTCGCGCGACCGGCCCAAGTGCAG 436
QY 1300 CAGCCACAGCTAGTAGAAGATCCAGCGGTATTACCTGAACACGCTCGCGGTGATATC 1359
Db 437 GAGCCGGCGCGTGGAGCGTTGACAGACGCCCTAGCTGAGGCGCTGCTGCTTACAC- 495
QY 1360 ATGAACCAAGACAGCGCGTTCGCGGCTGCGCGCTCATCTACGCAAGATTTCTGTCGTTG 1419
Db 496 -----CGCATCAAGAGCGCGCAGGACCAAGTCTGCGCTTCCCGCGCATGCTCATGAAG 547
QY 1420 CTTACCGAGTTCGGAGCGTGGCGATGCAAGATTCGAACATGTGCATCTCGTGAAGCTC 1479
Db 548 CTGGTGAGCTGCGACGCTGAGCTCTGTGCATCTCGGACAGAGTCTTTCGCTTGGCTC 607
QY 1480 AAGAACAGGAAGTGGCGCGTTCCTCGAGGAGATCTGGGAGT 1523
Db 608 CAGGACAGAGTGGCGCTCTGCTGTCGGAGATCTGGGAGT 651

RESULT 11
CD673041 667 bp mRNA linear EST 24-JUN-2003
LOCUS f91905.y1 Human Iris cDNA (Normalized): fg Homo sapiens cDNA clone
DEFINITION f91905 5', mRNA sequence.
ACCESSION CD673041
VERSION CD673041.1 GI:32174772
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 667)
AUTHORS Wistow G., Bernstein S.L., Ray S., Wyatt M.K., Behal, A.,
Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.
TITLE Expressed sequence tag analysis of adult human iris for the NEIBank
Project: steroid-response factors and similarities with retinal
pigment epithelium
JOURNAL Mol. Vis. 8 (4), 185-195 (2002)
MEDLINE 22103462
PUBMED 12107412
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 19 row: g column: 05
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
FEATURES
source 1..667
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="fg1905"
/tissue_type="Iris"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Iris cDNA (Normalized): fg"
/notes="Organ: Eye; Vector: pCMVSPORT6; A human iris library (bx) was normalized by self-subtraction. One portion of double stranded plasmid DNA representing the library was linearized by NotI. This NotI digested library was used as a template for biotinylated RNA synthesis using SP6 RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (Cot 500) with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/ss-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN
Query Match 9.1%; Score 138.4; DB 6; Length 667;
Best Local Similarity 56.2%; Pred. No. 9.6e-27; Indels 15; Gaps 3;
Matches 328; Conservative 0; Mismatches 241;

QY 946 TTTCCGCCAGATCACAGAAATGACCATCTCACAGTACAGCTAATAGTCGAGTTTGCAA 1005
Db 13 TTTGCCCACTTCAAGGAGTGGCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCTAAG 72
QY 1006 GGCCTACCTGGTTTTCAAAGATCTCAACCTGACCGAGATCACATTAATAAGGATGC 1065
Db 73 CAAAGTGCCTGGTTTCTCGAGCTGGCGGAGGACCATGCGCTCTCTGAAGCATCC 132
QY 1066 TCAACGGAAGTATGATGCTGCGAGTAGCGAGCGGTACGAGCGGTGTCGATACCGTT 1125
Db 133 ACTATCGAGATCATGCTGCTAGAGACAGCCAGCGCTCAACACAGACAGAGTGTATC 192
QY 1126 CTGTTTCCCAACCAACAGCGGTACACTCGCGAACAATCCGCAAGCGCGGCAT---GGCC 1182
Db 193 ACCTTCTTGAAGACTTCACTACAGCAAGAGAGCTTCCACCGTGCAGCGCTGCAGGTG 252
QY 1183 TAGGTATCGAAGACCTGCTGCATCTTCCCGCTGCATGATCTCGATGTCGATGGAACAC 1242
Db 253 GAGTTTCAACACCCCATCTTCGAGTTCTCGCGGCGCATCGCGCGCTGCGCTTGAAGCAG 312
QY 1243 GTGCATTAGCGCTCTCTCATGCTGCTATATTTCTCG--GATCGCGCGGCTAGAG 1299
Db 313 GCTGAGTACGCTCTGCTCATCGCCATCAACATCTTCTCGCGCGACCGGCCCAACGTGCAG 372
QY 1300 CAGCCACAGCTAGTAGAAGATCCAGCGGTATTACCTGAACACGCTGGCGGTGTATCATC 1359
Db 373 GAGCCGGCGCGGTGGAGCGTTTGCAGAGCGCTACGTGGAGCGCTGCTGTCTTACAC- 431
QY 1360 ATGAACCAAGACAGCGCGTTCGCGGCTCATCTACGCGAGATTTCTGTCGTTG 1419
Db 432 -----CGCATCAAGAGCGCGCAGGACCAAGTCTGCGCTTCCCGCGCTGCTCATGAAG 483
QY 1420 CTTACCGAGTTCGGAGCGTGGCGATGCAAGATTCGAACATGTGCATCTCGCTGAAGCTC 1479
Db 484 CTGGTGAGCTGCGCACGCTGAGCTCTGTGCACTCGGAGCAGGTCTTTCGCTTTCGCGCTC 543
QY 1480 AAGAACAGGAAGTGGCGCGTTCCTCGAGGAGATCTGGGAGCT 1523
Db 544 CAGGACAGGAAGTGGCGCTCTGCTGTCGGAGATCTGGGAGCT 587

RESULT 12
BQ222200
LOCUS BQ222200
DEFINITION AGENCOURT_7503312 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6018964
5', mRNA sequence.
ACCESSION BQ222200

—

QY 1243 GTGCATTACGCGCTCTCACTGCCATCGTTATATCTCG---GATCGCGCGGCGCTAGAG 1299
DB 335 GCTGAGTACGCGCTCTCATCGCCATCAACATCTTCTCGCGCGAGCCGCGCCACAGCTGCGAG 394
QY 1300 CAGCCACAGCTAGTAGAAGATCAGCGCGTATTACCTGAACACACGCTCGGGGTGTACATC 1359
DB 395 GAGCGCGCGGCTGGAGCGTTGAGCAGCGCTACGTTGAGGCGCTGCTGTCTTACAG- 453
QY 1360 ATGAACACAGCAGCGCGTTCGCGCGTTCGCGCGTTCATCTACGGAAGATTTCTGTCGGTG 1419
DB 454 -----GCGCATCAAGAGGCGGAGGACCAAGCTGCGCTTCCGCGCATGCTCATGAAG 505
QY 1420 CTTACCGAGTTCGGGACGCTGGCGCATGCGAATTCGAACATGTCGCTGAAGCTC 1479
DB 506 CTGGTGAGCTTCGGACGCTGAGCTCTGTGCACTCGGACAGGCTTTCGCTTCGGGCTC 565
QY 1480 AAGAACAGGAGCTGCGCGCTTCCTGGAGGAGATCTGGGAGCT 1523
DB 565 CAGGACAGAGCTGCGCGCTCTGCTGTGCGAGATCTGGGAGCT 609
RESULT 14
LOCUS CR614375 1685 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DM011YE14 of Fetal liver of Homo sapiens (human).
ACCESSION CR614375
VERSION CR614375.1 GI:50495182
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1685)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1685)
REFERENCE 2 (bases 1 to 1685)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM011YE14"
/tissue_type="Fetal liver"
/plasmid="PCMVSPORT_6"
ORIGIN
Query Match 9.1%; Score 138.4; DB 3; Length 1685;
Best Local Similarity 56.2%; Pred. No. 1.2e-26;
Matches 328; Conservative 0; Mismatches 241; Indels 15; Gaps 3;
QY 946 TTCGCCAGATCAGAAATGACCATCTCACAGTACAGCTAATAGTCGAGTTTGCCAAA 1005
DB 734 TTTGCCCACTTCAGGAGCTGGCCATCTCAGTCCAGAGATCGTGGACTTCGCTAAG 793
QY 1006 GGCCTACTCGTTTTCAAAAGATCTCAACACCTGACCAGATCATATTATTAAGGCGATCG 1065
DB 794 CAAGTGTCTGTTTCTCTGCAGCTGGCGCGGAGGACCGAGATCGCCCTCTGGAAGGATCC 853

QY 1066 TCAAGCGAAGTGATGATGCTCGAGTAGCGAGGCGGTACGACGCGGTCTCGGATAGCGTT 1125
DB 854 ACTATCGAGATGATGCTGCTAGAGACAGCCAGGCGCTACAAACACAGACAGAGTGTATC 913
QY 1126 CTGTTGGCCAAACACAGGCGGTACTCTCGCAGCAACTACCGCAAGCGCGGCAT---GGCC 1182
DB 914 ACCTTCTTGAAGGACTTCACCTACAGCAAGGACGACTTCCACCGTGCAGGCGCTGAGGTG 973
QY 1183 TAGCTCATCGAAGACCTCTGCACATTCGCGCGTGCATGTACTCATGATGTGATGACAAAC 1242
DB 974 GAGTTTCATCAACCCCATCTTCAGTTCTCGCGGCGCATCGCGGCTGGCCCTGGACGAC 1033
QY 1243 GTGCATTACGCGCTCTCACTGCCATCGTTATATTTCTCG---GATCGCGCGGCGCTAGAG 1299
DB 1034 GCTGAGTAGCGCTCTCATGCCATCAACATCTTCTCGCGCGAGCCGCGCCAAACGTGCAG 1093
QY 1300 CAGCCACAGCTAGTAGAAGATCAGCGGTATTACCTGAACACACGCTCGGGGTGTACATC 1359
DB 1094 GAGCGCGCGCGTGGAGGCGTTGAGCAGAGCCCTACGTGGAGGCGCTGCTGTCTTACAC- 1152
QY 1360 ATGAACACAGCAGCGCGTTCGCGCGTTCATCTAGCGCAAGATTTCTGTCGGTG 1419
DB 1153 -----GCGCATCAAGAGGCGCGAGGACGAGCTGCGTTCGCGCATGCTCATGAAG 1204
QY 1420 CTTACCGAGTTCGCGGACGCTGGCGCATGCGAATTCGAACATGTCATCTCGTGAAGCTC 1479
DB 1205 CTGGTGAGCTTCGCGACGCTGAGCTCTGTGCACTCGGAGCAGGCTTTCGCTTGGCGCTC 1264
QY 1480 AAGAACAGGAGCTGCGCGCTTCCTGGAGGAGATCTGGGAGCT 1523
DB 1265 CAGGACAGAGCTGCGCGCTCTGCTGTGCGGAGATCTGGGAGCT 1308
RESULT 15
LOCUS CR610600 1763 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DJ010YB16 of T cells (Jurkat cell line) Cot 10-normalized of Homo sapiens (human).
ACCESSION CR610600
VERSION CR610600.1 GI:50491407
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1763)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1763)
REFERENCE 2 (bases 1 to 1763)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES
source Location/Qualifiers
1..1763
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ010YB16"
/tissue_type="T cells (Jurkat cell line) Cot 10-normalized"
/plasmid="PCMVSPORT_6"

Fri Apr 15 16:53:51 2005

ORIGIN

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Query Match      9.1%; Score 138.4; DB 3; Length 1763;
Best Local Similarity 56.2%; Pred. No. 1.2e-26;
Matches 328; Conservative 0; Mismatches 241; Indels 15; Gaps 3;

Qy 946 TTCGCCGAGATCAGCAAAATGACCATCTCTCAGTAGCAGCTAATAGTCGAGTTGGCCAAA 1005
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Db 820 TTGCCCCACTTCAGCGAGCTGCCCATCATCTCAGTCCAGGAGATCGTGGACTTCGCTAAG 879

Qy 1006 GGCCTACCTGTTTTCAAAGATCTCAACCTGCACAGATCACATTATTAAGGCATGC 1065
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Db 880 CAAGTGCCTGGTTTCTCAGCTGGCGCGGAGACCAGATCGCCCTCTGAAGGCATCC 939

Qy 1066 TCAAGCGAAGTAGATGCTCGAGTAGCGAGGCGGTACGACGCGGTGTCGGATAGCGTT 1125
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Db 940 ACTATCGAGATCATGCTGCTAGAGACAGCCAGGCGCTACAACACGACAGACAGAGTGTATC 999

Qy 1126 CTGTTTCGCCAACACACAGCGGTACACTCGGCACACTACCGCAAGCGCGGCAT---GGCC 1182
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Qy 1183 TAGGTCATCGAAGACTGCTGCACCTCTGCCGCTCATGTACTGATGTCGATGGACAAC 1242
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Db 1060 GAGTTCAATCAACCCCATCTTCGAGTTCTCGGGGCCATGCGGGCGCTGGGCTGGACGAC 1119

Qy 1243 GTGCATTACGCGCTCTCACTGCCCATCGTTATATTCTCG---GATCGCGCGGCGCTAGAG 1299
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Qy 1300 CAGCCACAGCTAGTAGAAGAGATCCAGCGGTATTACCTGAACACGCTCGCGGTGTACATC 1359
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Qy 1360 ATGAACCAACAGCGCGTTCGCGCGTTCGCGCGTCACTACGCGAAGATTCTGTTCGGTG 1419
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Db 1351 CAGGACAAGAAGCTGCCGCTCTGCTGTGCGAGATCTGGACGT 1394
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Search completed: April 14, 2005, 18:41:14
Job time : 5201.63 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	836	54.9	2126	4	US-09-393-839-1		Sequence 1, Appli
2	632.2	41.5	2711	3	US-08-891-298-2		Sequence 2, Appli
3	623.2	40.9	2745	3	US-08-653-648A-4		Sequence 4, Appli
4	623.2	40.9	2745	4	US-09-564-418-4		Sequence 4, Appli
5	621.6	40.8	1934	3	US-08-653-648A-2		Sequence 2, Appli
6	621.6	40.8	1934	4	US-09-564-418-2		Sequence 2, Appli
C 7	621.6	40.8	1934	4	US-09-564-418-61		Sequence 61, Appl
C 8	621.6	40.8	2463	3	US-08-653-648A-10		Sequence 10, Appl
9	621.6	40.8	2464	4	US-08-653-648A-3		Sequence 3, Appli
10	621.6	40.8	2464	4	US-09-564-418-3		Sequence 3, Appli
C 11	621.6	40.8	2464	4	US-09-564-418-62		Sequence 62, Appl
C 12	618.4	40.6	1934	3	US-08-653-648A-6		Sequence 6, Appli
13	617.2	40.5	948	3	US-08-653-648A-6		Sequence 6, Appli
14	617.2	40.5	948	4	US-09-564-418-6		Sequence 63, Appl
C 15	617.2	40.5	948	4	US-09-564-418-63		Sequence 64, Appl
C 16	614	40.3	948	3	US-08-653-648A-64		Sequence 2, Appli
17	445.6	29.2	545	3	US-08-477-493-2		Sequence 3, Appli
18	445.6	29.2	545	3	US-09-788-070-3		Sequence 3, Appli
19	445.6	29.2	546	4	US-10-142-373-3		Sequence 3, Appli
20	445.6	29.2	546	4	US-09-155-252A-3		Sequence 3, Appli
21	445.6	29.2	576	3	US-08-465-375-3		Sequence 3, Appli
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23	445.2	29.2	10060	3	US-09-479-122-25		Sequence 25, Appl
24	445.2	29.2	10060	4	US-09-484-397-25		Sequence 25, Appl
25	445.2	29.2	10060	4	US-09-481-355-25		Sequence 25, Appl
26	445.2	29.2	10060	4	US-09-481-282-25		Sequence 25, Appl
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RESULT 3

US-08-653-648A-4
 ; Sequence 4, Application US/08653648A
 ; Patent No. 6379945
 ; GENERAL INFORMATION:
 ; APPLICANT: Jepsen, Ian
 ; APPLICANT: Greenland, Andrew
 ; APPLICANT: Martinez, Alberto
 ; TITLE OF INVENTION: A Gene Switch
 ; FILE REFERENCE: PPD50047/US
 ; CURRENT APPLICATION NUMBER: US/08/653,648A
 ; PRIOR FILING DATE: 1996-05-24
 ; PRIOR APPLICATION NUMBER: GB 9510759.5
 ; PRIOR FILING DATE: 1995-05-26
 ; PRIOR APPLICATION NUMBER: GB 9605656.9
 ; PRIOR FILING DATE: 1996-03-18
 ; PRIOR APPLICATION NUMBER: GB 9513882.2
 ; PRIOR FILING DATE: 1995-07-07
 ; PRIOR APPLICATION NUMBER: GB 9517316.7
 ; PRIOR FILING DATE: 1995-08-24
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 2745
 ; TYPE: DNA
 ; ORGANISM: Heliothis virescens
 ; FEATURE:
 ; NAME/KEY: Unsure
 ; LOCATION: (2522)..(2522)
 ; OTHER INFORMATION: Unsure
 US-08-653-648A-4

Query Match 40.9%; Score 623.2; DB 3; Length 2745;
 Best Local Similarity 79.1%; Pred. No. 2e-177;
 Matches 777; Conservative 0; Mismatches 178; Indels 27; Gaps 2;

Qy 558 TGATATGACGCGTATGAGCGCGGAGTGTGCTGCCAGAGTCCACGTCGAGCAACAAAG 617
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 Db 1841 CCTCGAGGAGATCTGGGACGTG 1862

RESULT 4

US-09-564-418-4
 ; Sequence 4, Application US/09564418
 ; Patent No. 6610828
 ; GENERAL INFORMATION:
 ; APPLICANT: Syngenta
 ; APPLICANT: Jepsen, Ian
 ; APPLICANT: Martinez, Alberto
 ; APPLICANT: Greenland, Andrew James
 ; TITLE OF INVENTION: A GENE SWITCH
 ; FILE REFERENCE: 1392/4/3
 ; CURRENT APPLICATION NUMBER: US/09/564,418
 ; CURRENT FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: US 09/564,418

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; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 2745
; TYPE: DNA
; ORGANISM: Heliothis virescens
; NAME/KEY: misc
; LOCATION: (2522)..(2522)
; OTHER INFORMATION: n=a, c, g, or t
US-09-564-418-4

Query Match      40.9%; Score 623.2; DB 4; Length 2745;
Best Local Similarity 79.1%; Pred. No. 2e-177;
Matches 777; Conservative 0; Mismatches 178; Indels 27; Gaps 2;

QY 558 TGTATCGACGGTATGAGCGCGAGTGGTCTGCTCCAGAGTCCAGCTGCAAGAACAAAG 617
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DB 1193 GTGTACAGGAGGATATGAGCAACCTTCCGAGGAGAGCTTGAAGAGGTTACAG-- 1250
QY 903 TTGGCAATCAGCAGATGAAGAGAGAGAGAGAGTCCAGACATGCGCATTCGCCAGATCACA 962
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DB 1421 GCTCCGAGTGGCTCGCGCGGTATGACGCGCCACCGACAGCGTACTGTTTCGCAACACCA 1480
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DB 1841 CTTGAGGAGATCTGGGAGCTG 1862

RESULT 5
US-08-653-648A-2
; Sequence 2, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jenson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1934
; TYPE: DNA
; ORGANISM: Heliothis virescens
US-08-653-648A-2

Query Match      40.8%; Score 621.6; DB 3; Length 1934;
Best Local Similarity 79.0%; Pred. No. 4.9e-177;
Matches 776; Conservative 0; Mismatches 179; Indels 27; Gaps 2;

QY 558 TGTATCGACGGTATGAGCGCGAGTGGTCTGCTCCAGAGTCCAGCTGCAAGAACAAAG 617
DB 733 TCTTCGGTGGCATGAGCGCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 792
QY 618 AAGAGAAAGGAAGCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 677
DB 793 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 852
QY 678 CGATCATATGCTGCCATTAATGCAATGATGACCTCCGCCCCCAGAGCGGCAAGATT-- 735
DB 853 CGATCATATGCTGCCATTAATGCAATGATGACCTCCGCCCCCAGAGCGGCTAGAAATCT 912
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QY 783 CAGATGAGAGATGTAGCGCGCTGTGGCGAACAGAGTCCCTGATCGCGAGGCTCGT 842
DB 973 CAGATTGAAGAACTGCGCCCCCTCACTGCGCAATCAGAAAGTCTGTTGATCGCAAGCTCGT 1032
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1323	QY	CCAGCGGTATTAAGCTGAACACGCTGCGGGGTGTACATCATGAACAGACACAGCGGTGCGCC	1382
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1383	QY	CGGTTGGCGCGTCACTACCGGAGATTCCTGTCGGTCTTTACCGAGTTGCGGACGCTGGG	1442
1561	Db		
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1443	QY	CATGCAAAATTCGAACATGTGCATCTTCGCTGAAGCTCAAGAACAGGAACTGCGCGCGTT	1502
1621	Db		
1621	Db	CATGCAAACTCCAAACATGTGCATCTCCCTCAAGCTGAAGAACAGGAACTGCGCGCGTT	1680
1503	QY	CCTGGAGGAGATCTGGGACGTG	1524
1681	Db		
1681	Db	CCTCGAGGAGATCTGGGACGTG	1702

RESULT 6

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US-09-564-418-2
; Patent 2, Application US/09564418
; Sequence NO. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jepson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1934
; TYPE: DNA
; ORGANISM: Heliothis virescens
US-09-564-418-2

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Query Match 40.8%; Score 621.6; DB 4; Length 1934;

Query Match 40.8%; Score 621.0; DF 4; Mengen 1931;
Best Local Similarity 79.0%; Pred. No. 4.9e-177;
Matches 776; Conservative 0; Mismatches 179; Indels 27; Gaps 2;

558	TG	TATCGACGCGTATGAGGCCCGAGTGCCTGTTCCAGAGTCCA	CGTGCAGAAACA	AAAG	617
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618	AA	GAGAAAGGAAGACACAGAGAGAAAAAGCAAACTTGCCAGTCA	GTA	CGACGACAGTGA	677

RESULT 7

US-09-564-418-61/c
 ; Sequence 61, Application US/09564418
 ; Patent No. 6610828
 ; GENERAL INFORMATION:
 ; APPLICANT: Syngenta
 ; APPLICANT: Jepson, Ian
 ; APPLICANT: Martinez, Alberto
 ; APPLICANT: Greenland, Andrew James

Db	793	GAAGAGAAAAAGGCGCAGAGGAAAAAGACAAATTGCCCGTCAGTACGACGACAGTAGA	852
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Qy	736	-----CAGCAAGTGGTCCGAGGTTCTTAACGGAGAAGCTAATCGGACGAGAA	782
Db	913	GGAAATGTGTGCACGACGAGAGGTGTGCCACGATTCCTGAAATGAGAAGCTAATGGAAACAGAA	972
Qy	783	CAGACTGAAGAATGTGAGCCGCTGTCCGCGAAACAGAAAGTCCCTGATCGCAGGCTCGT	842
Db	973	CAGATTGAAGAACGTGCCCCCTCACTGCCAATCAGAAGTCGTTGATCGCAAGGCTCGT	1032
Qy	843	GTGGTACCAAGACGGATACGACGACCTTCGGAAGAGGATTCAAAAAGGGTGACGCAGAC	902
Db	1033	GTGGTACCAGGAAGGCTATGAACAACTTCGAGGAAGACCTGAAGAGGGTTACACAG--	1090
Qy	903	TTGGGCATCAGCAGATGAAGAAGACGAGACTCAGACATGCCATTCGCGCAGATCACAGA	962
Db	1091	-----TCGCGAGGAGCGACGAAGACTCGGATATGCCGTTCCGTCAGATTACCGA	1140
Qy	963	AATGACCATCTCACAGTACAGCTAATAGTCGAGTTTGCCAAAGGCTACCTGGTTTTTC	1022
Db	1141	GATGACGATTCTCACAGTGCAGCTCATCGTAGAATTCGCTAAGSGCCTCCCGGGCTTCG	1200
Qy	1023	AAAGATCTCAACCTGACCCAGATCACTATTAAAGGCATGCTCAGCGAAGTGNATGAT	1082
Db	1201	CAAGATCTCGAGTCGGACCGACAGATCACGTTATTAAAGGCGTGCTCAAGTGAGGTGATGAT	1260
Qy	1083	GCTCGAGTAGCGAGCGGTGACGCGCGTGTCCGATAGCGTTCTGTTCCGCCAACAAACA	1142
Db	1261	GCTCGAGTGGCTCGCGCGTATGACCGCGCCACCGACGCGTACTGTTCCGNACAAACA	1320
Qy	1143	GGCGTACACTCGCGCAAACTACCGCAAGCGGCGCATGGCTACGTCATCGAAGACCTGCT	1202
Db	1321	GGCGTACACTCGCGCAAACTACCGCAAGCGAGCATGGCGTACGTCATCGAGGACCTGCT	1380
Qy	1203	GCATTTCTCGGCTGCATGTACTCGATGTCGATGGACAAGTGCATTACGCGCTCTCAC	1262
Db	1381	GCATTTCTCGGTGTCATGTACTCCATGATGATGGATAACGTGCAATTATGCGCTGCTTAC	1440
Qy	1263	TGCCATCTGTTATATTCTCGGATCGGCGCGGCGCTTAGAGCAGCCACAGCTAGTAGAAGAT	1322
Db	1441	AGCATATGTCATCTTCTCAGACCGGCGCGGGCTTGAGCAACCCCTGTTGGTGAGGACAT	1500
Qy	1323	CCAGCGGTATTACCTGAAACAACGCTGCGGTGTATCATCATGAAACAGCAGCCGCTGCC	1382
Db	1501	CCAGAGATATTACCTGAAACAACGCTACGGGTGTATCATCTGAAACAGAACGCGCTGCC	1560
Qy	1383	CGGTTGCGCGGTCATCTACGCGAAGATTCGTCCGNGCTTACCAGGTTCGGACGCTGGG	1442
Db	1561	CCGCGCGCGGTCATCTTTCGGCGAGATCTTCGGGCACTACTGACGGAGATCCGACGCTGGG	1620
Qy	1443	CATGCAGAAATTCGAAACATGTGCATCTTCGTTGAGCTCAAGAACAGGAAGCTCCGCCGTT	1502
Db	1621	CATGCAGAACTCCAAATGTGCATCTCCCTCAAGCTGGAAGAACAGGAAGCTCCGCCGTT	1680
Qy	1503	CCTGGAGGAGATCTGGACGTG	1524
Db	1681	CCTCGAGGAGATCTGGACGTG	1702

RESULT 7

US-09-564-418-61/c
 ; Sequence 61, Application US/09564418
 ; Patent No. 6610828
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Syngenta
 ; APPLICANT: Jepson, Ian
 ; APPLICANT: Martinez, Alberto
 ; APPLICANT: Greenland, Andrew James


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QY 903 TTGGCAATCAGCAGATGAAGAAGACGAGAGACTCAGACATGCCATTCGCCGAGATCAGAGA 962
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QY 963 AATGACCATCTCAGCAGTACAGCTAATAGTCGAGTTTCCCAAAGGCCCTACCTGGTTTTC 1022
DB 1444 GATGACGATTTCTCAGAGTGAGCTCATCTGTAGATTTCGTAAGGGCTCCCGGGCTTCGC 1385
QY 1023 AAAGATCTCACAACCTGACAGATCACAATTATTAAGGCATCTCTCAAGCAAGTGATGAT 1082
DB 1384 CAAGATCTCGAGTCGGACCAAGATCACGTTATTAAGGCGTGCTCAAGTGAGGTGATGAT 1325
QY 1083 GCTCGAGTAGGAGCGGTACGACGCGGTGTGCGATAGCGTTCTGTTCGCCCAACCA 1142
DB 1324 GCTCGAGTTGGCTCGCGGTATGACGCGGTCACCGACAGCGTACTGTTCGGGAAACCA 1265
QY 1143 GCGGTACACTCGGACAACTACCGCAAGCGGGCATGCCCTACGTCATCGAAGACCTGCT 1202
DB 1264 GCGGTACACTCGGACAACTACCGCAAGCGGGCATGCCCTACGTCATCGAAGACCTGCT 1205
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DB 1084 CCAGAGATATTACCTGAACACGCTCGGGGTGATCATATGAACACGACAGCGCGCTCGCC 1025
QY 1383 GGGTTGCGCGCTCATCTACGCAAGATTCTGTGCGTGTCTTACCGAGTTTCGGAACGCTGG 1442
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QY 1443 CATGAGAAATCGAATGTGATCTCGTGAAGCTCAAGAAACAGAAAGCTCGCGCGTT 1502
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QY 1503 CTTGGAGGAGATCTGGGAGTG 1524
DB 904 CTTGGAGGAGATCTGGGAGTG 883

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RESULT 9

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US-08-653-648A-3
; Sequence 3, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jenson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 2464
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:

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; NAME/KEY: Unsure
; LOCATION: (2241)..(2241)
; OTHER INFORMATION: Unsure
; US-08-653-648A-3

Query Match      40.8%; Score 621.6; DB 3; Length 2464;
Best Local Similarity 79.0%; Pred. No. 5.7e-177;
Matches 776; Conservative 0; Mismatches 179; Indels 27; Gaps 2;

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QY 618 AAGAGAAAAGGAACACACAGAGAGAAAAGCAAACTCCAGTCACTAGTACGACGACAGTGA 677
DB 672 GAAAGAGAAAAGGCGCAGAGGGAAGAACAAATTCGCCGTAGTACGACGACAGTAGA 731
QY 678 CGATCATATGCTGCCATTAATGAATGACCTCCGCCGCCAGAGGGCGGCAAGATT-- 735
DB 732 CGATCATATGCTGCCATTAATGAATGACCTCCGCCGCCAGAGGGCGGCTAGAAATTCT 791
QY 736 -----CACGNAAGTGTCCGAGGTTCCTAACGGAGAGAGCTTAATGGAGCAGAA 782
DB 792 GGAATGTGTGACGACGAGGTGGTCCACGATTCCTGAATGAGAAAGCTTAATGGAACAGAA 851
QY 783 CAGACTGAAGAAATGTGACCGCGCTGTCCGCGAACCCAGAAAGTCCCTGTATCGCGAGGCTCGT 842
DB 852 CAGATTGAGAAAGTGTGCGCCGCCCTCACTGCCAATCAGAAAGTCTGTTGATCGCAAGGCTGT 911
QY 843 GTGGTACAGACGAGTACGAGACGCTTCGGAAGAGGATCTCAAAAGGTGACGACGAC 902
DB 912 GTGGTACAGACGAGTATGAACAACTTCGAGGAGAGACCTGAAGAGGGTTACACAG-- 969
QY 903 TTGGCAATCAGCAGATGAAGAAGACGAGATCAGACATGCCATTCGCCGAGATCAGAGA 962
DB 970 -----TCGGACGAGGACGAGAGACTCGGATATGCCGTTCCGTCAGATTACCGA 1019
QY 963 AATGACCATCTCAGCAGTACAGCTAATAGTCGAGTTTCCCAAAGGCCCTACCTGGTTTTC 1022
DB 1020 GATGACGATTTCTCAGAGTGAGCTCATCTGTAGATTTCGTAAGGGCTCCCGGGCTCGC 1079
QY 1023 AAAGATCTCACAACCTGACAGATCACAATTATTAAGGCATCTCTCAAGCAAGTGATGAT 1082
DB 1080 CAAGATCTCGAGTCCGACGAGATCACGTTATTAAGGGCGTCTCAAGTGAGGTGATGAT 1139
QY 1083 GCTCGAGTAGGAGCGGTGTCGAGTAGCGGTTCGATAGCGTTCTGTTCCGCAACACCA 1142
DB 1140 GCTCGAGTTGGCTCGCGGTATGACGCGGCGCACCGACAGCGTACTGTTCCGGAACACCA 1199
QY 1143 GCGGTACACTCGGACAACTACCGCAAGCGGGCATGCCCTACGTCATCGAAGACCTGCT 1202
DB 1200 GCGGTACACTCGGACAACTACCGCAAGCGGGCATGCCGTAAGTACGTCATCGAGGACCTGCT 1259
QY 1203 GCATTTCTGCGCTGCATGTACTCGATGTGATGGAACAACGTGCAATTCAGCGCTCTCAC 1262
DB 1260 GCATTTCTGCGCTGCATGTACTCGATGTGATGGAACAACGTGCAATTCAGCGCTCTCAC 1319
QY 1263 TGCCATCGTTATTTCTCGGATCGCGCGGCTTAGAGGAGCCACAGCTAGTAGAAGAT 1322
DB 1320 AGCCATTGTCTTCTCAGACCGCGCGGCTTAGAGCAACCCCTGTTGGTGGAGGACAT 1379
QY 1323 CCAGCGGTATTACCTGAACACGCTCGGGGTGATCATATGAACACGACGACGAGCGCTCGCC 1382
DB 1380 CCAGAGATATTACCTGAACACGCTAGCGGTGTACATCTCTGAACACGACGAGCGCTCGCC 1439
QY 1383 GCGTTGCGCGCTCATCTAGCGGAAGATTCTGTGCGTGTCTTACCGAGTTCGGAACGCTGG 1442
DB 1440 CCGCGCGCGCTCATCTTCCGCGAGATCTCTGGGCATCTAGCGGAGATCCGCAAGCTGG 1499
QY 1443 CATGAGAAATTCGAACATGTGATCTCGTGAAGCTCAAGAAACGAGAGCTCGCGCGTT 1502
DB 1500 CATGAGAAATTCGAACATGTGATCTTCCCTCAAGCTGAAGAAACGAGAGCTCGCGCGTT 1559

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Db	1733	CGATCATCATGCCTCCCATCATGCAATGTGACCTTCGCGCCCCCAGAGCGCGCTAGAATTCT	1674
Qy	736	-----CACCAGTGGTCCGAGGTTCCCTAAACGAGAGACTAATGAGCAGAA	782
Db	1673	GGATGTGTGCAGCAGAGGTGTGCCACGATTCCTGAATGAGAGCTAATGAAACAGAA	1614
Qy	783	CAGACTGAAGAAATGTGACGGCGTGTCCGGCGAACAGAAATCCCTGATCCGAGGCTCGT	842
Db	1613	CAGATTGAAGAAACGTGCGCCCGCTCACTGCGCAATCAGAAGTCGTGTGATCCAAAGGCTCGT	1554
Qy	843	GTGGTACACGAGCGGATACGAGCAGCTTCGGAAAGAGGATCTCAAAAGGCTGACGCGAC	902
Db	1553	GTGGTACACGAGGCTATGAAACACTTCGAGGAAGACCTGAGAGGTTACACAG--	1496
Qy	903	TTGGCAATCAGCAGATGAAGAGACGAAAGACTCAGACATGCGATTCCGCGCAGATCAGAA	962
Db	1495	-----TCGGACGAGGACGACGAAGACTCGGATATGCCGTTCGCTCAGATTACCGA	1446
Qy	963	AATGACCATCCTCAGCTACAGCTAATAGTCGAGTTTGCCAAAGCGCTACTCGTGTTTTC	1022
Db	1445	GATCAGGATTCCTCAGGTGACGCTCATCGTAGAAATTCGTAAAGGCGCTCCGGGCTTCG	1386
Qy	1023	AAAGATCTCAAACTGACACAGATCACAATATTAAAGGCGATGCTCAAGCGAAAGTGATGAT	1082
Db	1385	CAAGATCTCGCAGTCGGACACAGATCAGTTATTAAAGCGTGCTCAAGTGAGGTGATGAT	1326
Qy	1083	GCTCGGAGTAGCGAGCGGTACGACGGGTGCGATAGCGTTCTGTTCGCCACAACCA	1142
Db	1325	GCTCCGAGTGGCTCGCGGATGATGACGGGCGCACCGACAGCGTACTGTTCCGGAACAACCA	1266
Qy	1143	GGCGTACACTCGGACAACTACCAGCGGGGATGGCCCTACGTCATCGAAGACCTGCT	1202
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Qy	1203	GCATTTGCGCGCTGCATGTACTCGATGTGATGGAACAACTGATGAGGCTTCCTCAC	1262
Db	1205	GCACTTGTGCGTGCATGTACTCCATGATGGATAACTGATGATGCGCTGCTTAC	1146
Qy	1263	TGCCATCGTTATTTCTCGGATCGCGCGGCTAGAGCAGCCACAGCTAGTGAAGAGAT	1322
Db	1145	AGCCATGTGTATCTCTCAGACCGCGCGGCTTAGACACCCCTGTGTTGGTGGAGCAT	1086
Qy	1323	CCAGCGGTATTACCTGAAACAGCTGCGGGTGTACATCATGAACACGACAGCGGTGCC	1382
Db	1085	CCAGAGATATTACCTGAACACGCTACGCGTGTACATCTGAACACGAAACAGCGGTGCC	1026
Qy	1383	GGTTGCGCGCTCATCTACGCGAAGATTTCTGCGTGTCTTACCGAGTTGCGGACGCTGG	1442
Db	1025	CCGCGCGCGCTCATCTTTCGCGGAGATCCTGGGCATCTGACGGAGATCCCGACGCTGG	966
Qy	1443	CATGCAGAAATTCGAACATGTGATCTCGCTGAAGCTCAAGAACAGGAAAGCTGCCCGCTT	1502
Db	965	CATGCAGAACTCCACATGTGATCTCCCTCAAGCTGAAGAACAGGAAAGCTGCCCGCTT	906
Qy	1503	CCTGAGGAGATCTCGGACGTG	1524
Db	905	CCTCGAGGAGATCTCGGACGTG	884

RESULT 12

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US-08-653-648A-9/c
; Sequence 9, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PP050047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26

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Qy		
Db		
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Qy		
Db		
181	TTCCTGANTGAAAAGCTAATGGACAGACAAGGCTCAAGNATGTG--CCCCCTCACTGCC	238
Qy		
Db		
814	AACCAGAAATCCCTGATCGCGAGGCTGGTGTGTATCCAGGACGGATACGAGCAGCCTTCG	873
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Db		
874	GAAGAGGATCTCAAAGGGTGACGCAGACTTGCCAATCAGCACAGATGAAGAAGACGAGAC	933
Qy		
Db		
299	GAAGAGGATCTAAAAAGAGTFCACACAG-----TCGGATGAAGACGGAAGAAG	346
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Db		
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Qy		
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347	TCGGACATGCGGTTCGTGAGATCAACGAGATGACGNATCTTCACAGTGCAGCTCATTTGT	406
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Qy		
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647	ATGGATAACTGCTCCACTATGCACTGCTCACTGCCCATCGTCATTTTCTCAGACCGACCCGGG	706
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 : Sequence 63, Application US/09564418
 : Patent No. 6610828
 : GENERAL INFORMATION:
 : APPLICANT: Syngenta
 : APPLICANT: Jepson, Ian
 : APPLICANT: Martinez, Alberto
 : APPLICANT: Greenlead, Andrew James
 : TITLE OF INVENTION: A GENE SWITCH
 : FILE REFERENCE: 1392/4/3
 : CURRENT APPLICATION NUMBER: US/09/564,418
 : CURRENT FILING DATE: 2000-05-03
 : PRIOR APPLICATION NUMBER: US 09/564,418
 : PRIOR FILING DATE: 2000-05-03
 : NUMBER OF SEQ IDS: 63

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 63
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Spodoptera exigua
US-09-564-418-63

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Best Local Similarity 79.8%; Pred. No. 6.7e-176;
Matches 758; Conservative

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1828 ATTATGCAGTGTGATCCACCGCTCCAGAGCGCGCAAGAAATTCACGAGGTGGTCCACAGA 769
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1114 TCGGATAGCGTTCGTTTCGCGCAACAAACAGCGGTACACTCGGACAACTACCGCAAGCG 1173
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1414 TCGGTGCTTACCGAGTTTCGGAACGCTGGGATGAGAAATTCGAACATGTGCATCTCGCTG 1473
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Db 62 AAGCTGAAGAACAGGACGTGCCGCCGTTCTTCGAGGATATCTGGACGT 13

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.
OM nucleic - nucleic search, using sw model
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(without alignments)
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Total number of hits satisfying chosen parameters: 11245082
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Listing first 45 summaries

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SUMMARIES					
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2	1414.2	92.8	1782 16	US-10-087-167-124	Sequence 124, App
3	1332	87.4	1848 16	US-10-087-167-134	Sequence 134, App
4	1332	87.4	1863 16	US-10-087-167-136	Sequence 136, App
5	1332	87.4	3972 16	US-10-087-167-104	Sequence 104, App
6	1328.8	87.2	1767 16	US-10-087-167-122	Sequence 122, App
7	1311.2	86.0	1776 16	US-10-087-167-118	Sequence 118, App
8	1222.2	80.2	1800 16	US-10-087-167-126	Sequence 126, App
9	1209	79.3	1428 16	US-10-087-167-128	Sequence 128, App
10	1208.2	79.3	1809 16	US-10-087-167-142	Sequence 142, App
11	1073	70.4	1800 16	US-10-087-167-147	Sequence 147, App

12	955.6	62.7	1500	16	US-10-087-167-67	Sequence 67, Appl
13	848.8	55.7	1515	16	US-10-087-167-75	Sequence 75, Appl
14	836	54.9	2126	14	US-10-295-370-1	Sequence 1, Appl
15	836	54.9	2126	15	US-10-292-356-1	Sequence 1, Appl
16	836	54.9	2126	15	US-10-292-324-1	Sequence 1, Appl
17	763.6	50.1	1518	16	US-10-087-167-93	Sequence 93, Appl
18	763.6	50.1	2840	15	US-10-083-842A-6	Sequence 6, Appl
19	763.6	50.1	2840	16	US-10-087-167-1	Sequence 1, Appl
20	760.4	49.9	1500	16	US-10-087-167-69	Sequence 69, Appl
21	742.8	48.7	1509	16	US-10-087-167-65	Sequence 65, Appl
22	719.4	47.2	763	16	US-10-087-167-5	Sequence 5, Appl
23	656.8	43.1	1533	16	US-10-087-167-79	Sequence 79, Appl
24	638.6	41.9	838	16	US-10-087-167-7	Sequence 7, Appl
25	636	41.7	1524	16	US-10-087-167-77	Sequence 77, Appl
26	632.2	41.5	2711	9	US-09-952-559-2	Sequence 2, Appl
27	628	41.2	1110	9	US-09-965-703-2	Sequence 2, Appl
28	628	41.2	1110	17	US-10-239-134-2	Sequence 2, Appl
29	628	41.2	1288	9	US-09-965-703-1	Sequence 1, Appl
30	628	41.2	1288	17	US-10-239-134-1	Sequence 1, Appl
31	628	41.2	1288	17	US-10-468-199-59	Sequence 59, Appl
32	628	41.2	1542	9	US-09-965-703-58	Sequence 58, Appl
33	628	41.2	1542	17	US-10-239-134-49	Sequence 49, Appl
34	626.4	41.1	1290	9	US-09-965-697-4	Sequence 4, Appl
35	621.6	40.8	960	9	US-09-965-703-5	Sequence 5, Appl
36	621.6	40.8	960	17	US-10-239-134-5	Sequence 5, Appl
37	621.6	40.8	960	17	US-10-468-199-3	Sequence 3, Appl
38	621.6	40.8	1054	9	US-09-965-703-3	Sequence 3, Appl
39	621.6	40.8	1054	17	US-10-239-134-3	Sequence 3, Appl
40	621.6	40.8	1054	17	US-10-468-199-65	Sequence 65, Appl
41	621.6	40.8	1054	18	US-10-783-810-1	Sequence 1, Appl
42	621.6	40.8	1934	17	US-10-606-060A-2	Sequence 2, Appl
43	621.6	40.8	2464	17	US-10-606-060A-3	Sequence 3, Appl
44	621.6	40.8	2464	17	US-10-606-060A-4	Sequence 4, Appl
45	617.2	40.5	948	17	US-10-606-060A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-10-087-167-120
; Sequence 120, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1767)
; OTHER INFORMATION: Ecdysone receptor chimera G(M)EV
US-10-087-167-120
Query Match 100.0%; Score 1524; DB 16; Length 1767;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCAGCAGCTATGTGGATTTTATAGCCCTTCATACGCTATTATTGCTTGG 60
|||||

Fri Apr 15 16:53:51 2005

D	b	1	ATGCAGCAGCTATATGTGGAGTTTTTTTAGCCCTGCCTCTCATAGCTATTTATTTTCGTTGG	60
Q	y	61	TACTGTTCCTTTTGTTCGATGCTCACCTCTGTGTGTGGTGTACTTCTCGAGGATCCGCC	120
D	b	61	TACTGTTCCTTTTGTTCGATGCTCACCTCTGTGTGTGGTGTACTTCTCGAGGATCCGCC	120
Q	y	121	ACCATGAAGCTACTGTCTTCCTATCGAAACAGCATGCGATATTGTCCGACTTAAAAGCTC	180
D	b	121	ACCATGAAGCTACTGTCTTCCTATCGAAACAGCATGCGATATTGTCCGACTTAAAAGCTC	180
Q	y	181	AAGTGCTCCAAAGAAAAACCGAAGTGCGCCAAGTGTCTGAAGAAACAACTCGGAGTGTGCG	240
D	b	181	AAGTGCTCCAAAGAAAAACCGAAGTGCGCCAAGTGTCTGAAGAAACAACTCGGAGTGTGCG	240
Q	y	241	TACTCTCCCAAAACCAAAGGTCTCCGCTGACCTAGGGCACA	300
D	b	241	TACTCTCCCAAAACCAAAGGTCTCCGCTGACCTAGGGCACA	300
Q	y	301	AGGCTAGAAAGACTGGAAACAGCTATTTCTACTCATTTTTTCTCGAAGAACCTTGACATG	360
D	b	301	AGGCTAGAAAGACTGGAAACAGCTATTTCTACTCATTTTTTCTCGAAGAACCTTGACATG	360
Q	y	361	ATTTTGAATAATGGATTCTTTACAGGATATAAAAGCAATTTGTAAACAGGATTAATTGTACAA	420
D	b	361	ATTTTGAATAATGGATTCTTTACAGGATATAAAAGCAATTTGTAAACAGGATTAATTGTACAA	420
Q	y	421	GATTAATGTGAATAAAGATGCGGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCCCT	480
D	b	421	GATTAATGTGAATAAAGATGCGGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCCCT	480
Q	y	481	CTAACATTGTAGACAGCAGTAGAATAAGTGCACATCATCATCGGAAGAGAGTAGTAACAAA	540
D	b	481	CTAACATTGTAGACAGCAGTAGAATAAGTGCACATCATCATCGGAAGAGAGTAGTAACAAA	540
Q	y	541	GGTCAAAAGACAGTTGACTGTATCGACGGTATGAGGCCCGAGTGGTTCGCCAGAGTCC	600
D	b	541	GGTCAAAAGACAGTTGACTGTATCGACGGTATGAGGCCCGAGTGGTTCGCCAGAGTCC	600
Q	y	601	ACGTGCAGAACAAAGAGAGAAAGAGACAGAGAGAAAAAGACAAACTGCCAGTGC	660
D	b	601	ACGTGCAGAACAAAGAGAGAAAGAGAGACAGAGAGAAAAAGACAAACTGCCAGTGC	660
Q	y	661	AGTACGACGACAGTGGACGATCATATGCTGCCATAATGCAATGTGACCTCCGCCCCCA	720
D	b	661	AGTACGACGACAGTGGACGATCATATGCTGCCATAATGCAATGTGACCTCCGCCCCCA	720
Q	y	721	GAGGCGGCAAGGATTCAGAAAGTGGTCCGAGGTTCTTAACGAGAGAGCTAATGAGGACG	780
D	b	721	GAGGCGGCAAGGATTCAGAAAGTGGTCCGAGGTTCTTAACGAGAGAGCTAATGAGGACG	780
Q	y	781	AACAGACTGAAGAATGTGACGCCGTGTGGCGGAACAGAAAGTCCCTGTATCGGAGGCTC	840
D	b	781	AACAGACTGAAGAATGTGACGCCGTGTGGCGGAACAGAAAGTCCCTGTATCGGAGGCTC	840
Q	y	841	GTGTGGTACAGGACGGATACAGACGCTTCGGAAAGAGGATCTCAAAAGGGTGACGAG	900
D	b	841	GTGTGGTACAGGACGGATACAGACGCTTCGGAAAGAGGATCTCAAAAGGGTGACGAG	900
Q	y	901	ACTTGGCAATCAGCAGATGAAGAGACGAAGACTCAGACATGCCATTTCCGCGAGATCACA	960
D	b	901	ACTTGGCAATCAGCAGATGAAGAGACGAAGACTCAGACATGCCATTTCCGCGAGATCACA	960
Q	y	961	GAATGACCATCCTCACAGTACAGCTAATAGTTCGAGTTTGCCAAAGGCTACTCTGGTTTT	1020
D	b	961	GAATGACCATCCTCACAGTACAGCTAATAGTTCGAGTTTGCCAAAGGCTACTCTGGTTTT	1020
Q	y	1021	TCAAAGATCTCAACACTGACAGATCAATATTAAAGGCATGCTCAAGCGAGTCAATG	1080
D	b	1021	TCAAAGATCTCAACACTGACAGATCAATATTAAAGGCATGCTCAAGCGAGTCAATG	1080
Q	y	1081	ATGCTCGCAGTAGCAGGCGGTACGACCGGTGTCCGATAGCGTTTGTTCGCCAACAA	1140
D	b	1081	ATGCTCGCAGTAGCAGGCGGTACGACCGGTGTCCGATAGCGTTTGTTCGCCAACAA	1140

QY	1141	CAGGCGGTACACTCGCGACAACTACCGCAAGGCGGGCGATGGCCTACGTCATCGAAGACCTG	1200
Db	1141	CAGGCGGTACACTCGCGACAACTACCGCAAGGCGGGCGATGGCCTACGTCATCGAAGACCTG	1200
QY	1201	CTGCACCTTCCTGCGCGTGCATGTACTCGATGTCGATGGACAACGTCGCAATTACGGCGCTCCTC	1260
Db	1201	CTGCACCTTCCTGCGCGTGCATGTACTCGATGTCGATGGACAACGTCGCAATTACGGCGCTCCTC	1260
QY	1261	ACTGGCCATCGTTATATTTCTCGGATCGGCCGGGGCTAGAGCAGGCACACAGCTAGTAGAAGAG	1320
Db	1261	ACTGGCCATCGTTATATTTCTCGGATCGGCCGGGGCTAGAGCAGGCACACAGCTAGTAGAAGAG	1320
QY	1321	ATCCAGCGGTATTACCTGAAACAGCTGCGGGTGTACATCATGAACAGCAGACGCGCGTCG	1380
Db	1321	ATCCAGCGGTATTACCTGAAACAGCTGCGGGTGTACATCATGAACAGCAGACGCGCGTCG	1380
QY	1381	CCGCGTTGCCCGCTCATCTACGGCGAAGATTCTGTGCGGTGCTTACCGAGTTGCGGACGCTG	1440
Db	1381	CCGCGTTGCCCGCTCATCTACGGCGAAGATTCTGTGCGGTGCTTACCGAGTTGCGGACGCTG	1440
QY	1441	GGCATGCAGAAATTCGAAACATGTGTCATCTCGCTGAAGCTCAAGAACAGCAAGCTGCCGCG	1500
Db	1441	GGCATGCAGAAATTCGAAACATGTGTCATCTCGCTGAAGCTCAAGAACAGCAAGCTGCCGCG	1500
QY	1501	TTCTCTGGAGGAGATCTGGGACGTG	1524
Db	1501	TTCTCTGGAGGAGATCTGGGACGTG	1524

RESULT 2
 US-10-087-167-124
 ; Sequence 124, Application US/10087167
 ; Publication No. US20030154509A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pascal, Erica
 ; APPLICANT: Valentine, Scott
 ; APPLICANT: Brown, Jeffrey
 ; APPLICANT: Cockrell, Adam
 ; APPLICANT: Johnson, Brian
 ; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
 ; FILE REFERENCE: 500184
 ; CURRENT APPLICATION NUMBER: US/10/087,167
 ; PRIORITY FILING DATE: 2002-03-01
 ; PRIOR APPLICATION NUMBER: US 60/242,969
 ; PRIOR FILING DATE: 2000-10-24
 ; NUMBER OF SEQ ID NOS: 148
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 124
 ; LENGTH: 1782
 ; TYPE: DNA
 ; ORGANISM: Synthetic Construct
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1782)
 ; OTHER INFORMATION: Ecdysone receptor chimera G(E) EV
 US-10-087-167-124

	Query Match	92.8%;	Score 1414.2;	DB 16;	Length 1782;
	Best Local Similarity	95.6%;	Pred. No. 0;		
	Matches 1471;	Conservative	0;	Mismatches 53;	Indels 15; Gaps 1
QY	1	ATGCAGCAGCTATATGTGGATTTTTTTT	TAGCCCTGCCTTCATACGCTATTTATTTGCTTGG	60	
DB	1	ATGCAGCAGCTATATGTGGATTTTTTTT	TAGCCCTGCCTTCATACGCTATTTATTTGCTTGG	60	
QY	61	TACTCTTTTCTTTTGTGAGTCTACCCCTGTTGTTTGGTGTACTTCT	TGCAGGATCCGCC	120	
DB	61	TACTGTGTTCTTTGTGCGATGCTCACCCCTGTTGTTTGGTGTACTTCT	TGCAGGATCCGCC	120	
QY	121	ACCATGAAGCTACTGTCCTTCTATCGAACAGCATCGATATTTGCGACTTAAAAAGCTC	180		
DB	121	ACCATGAAGCTACTGTCCTTCTATCGAACAGCATCGGATATTTTGCAGCTTAAAAAGCTC	180		

181 AAGTCTCAAGAAACCGAAGTGGCCAAAGTGTCTGAAGAAACAACCTGGAGTGTGC 240
181 AAGTCTCAAGAAACCGAAGTGGCCAAAGTGTCTGAAGAAACAACCTGGAGTGTGC 240
241 TACTCTCCAAACCAAGAGTCTCCGCTGACTAGGGCAGCATCTGACAGAAAGTGAATCA 300
241 TACTCTCCAAACCAAGAGTCTCCGCTGACTAGGGCAGCATCTGACAGAAAGTGAATCA 300
301 AGGCTAGAAAGACTGGAACAGACTATTTCTACTGATTTTCTCTCGAAGAGACCTTGACATG 360
301 AGGCTAGAAAGACTGGAACAGACTATTTCTACTGATTTTCTCTCGAAGAGACCTTGACATG 360
361 ATTTTGAATAAGTATTTTACAGATATAAAGCAATTTTAAACAGGATTTTGTACAA 420
361 ATTTTGAATAAGTATTTTACAGATATAAAGCAATTTTAAACAGGATTTTGTACAA 420
421 GATAATGTGAATAAAGATGCCGTACAGATAGATTGGCTTCAAGTGGAGACTGATATGCT 480
421 GATAATGTGAATAAAGATGCCGTACAGATAGATTGGCTTCAAGTGGAGACTGATATGCT 480
481 CTAACATTGAGACAGCATAGATAAGTGGCAGCATCATCATCGGAAGAGAGTAGTAACAAA 540
481 CTAACATTGAGACAGCATAGATAAGTGGCAGCATCATCATCGGAAGAGAGTAGTAACAAA 540
541 GGTCAAAGACAGTTGACTGTATCGAGCGGTATGAGCCCGAGTGGTGGTCCAGAGTCC 600
541 GGTCAAAGACAGTTGACTGTATCGAGCGGTATGAGCCCGAGTGGTGGTCCAGAGAG 600
601 AGCTGCAAGCAACAAAGAGAGAGAAAGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 660
601 AGCTGCGCAACAAAGAGAGAGAAAGGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
661 AGTACGACGACAGTGGACGATCATATGCTGCGCATATGCAATGCAATGCAACCTCCGCCCA 720
661 AGCACAACGACAGTGGACGATCATATGCTGCGCATATGCAATGCAATGCAACCTCCGCC 720
721 GAGGCGGCAAGGATT-----CAGGAAGTGGTCCGAGGTTCTTAACGGAG 765
721 GAGGCGGCAAGGATTCTGGAATGTTTGCAGCATGAAGTGGTCCCGCGGTTCTCTCGGAG 780
766 AAGCTAATGGAGACAGACAGATGGAAGATGTGACGCCGCTGTGGCGGAACAGAGAGTCC 825
781 AAGCTGATGGAGAGAGATCGGCTGAAGAAACATACCCCTTACCCGCAACAGCAGTTC 840
826 CTGATCGCAGGCTCGTGTGGTACAGGACGGATACGAGCAGCTTTCGGAAGAGGATCTC 885
841 CTGATCGCAGGCTCGTGTGGTACAGGACGGATACGAGCAGCTTTCGGAAGAGGATCTC 900
886 AAAAGGCTGACGAGACTTGGCAATCAGCAGATGAAGAGAGAGAGAGAGAGAGAGAGAG 945
901 AAAAGGCTGACGAGACTTGGCAATCAGCAGATGAAGAGAGAGAGAGAGAGAGAGAGAG 960
946 TTCCGCCAGATCAGAGAAATGACCATCTCAGAGTACAGTATAGTTCGAGTTTGCCAAA 1005
961 TTCCGCCAGATCAGAGAAATGACCATCTCAGAGTACAGTATAGTTCGAGTTTGCCAAA 1020
1006 GGCTACCTGTTTTCAGAGATCTCACAACCTGACAGATCAATATTTAAAGGATGC 1065
1021 GGCTACCTGTTTTCAGAGATCTCACAACCTGACAGATCAATATTTAAAGGATGC 1080
1066 TCAAGGAAATGATGATGCTGGAGATGAGAGCGGCTGACAGCGGTGTCGATAGCGTT 1125
1081 TCAAGGAAATGATGATGCTGGAGATGAGAGCGGCTGACAGCGGTGTCGATAGCGTT 1140
1126 CTGTTGCGCAACAGAGGCTACACTCGCGCAACCTTACCGAGGCGGCTAGCGCTAC 1185
1141 CTGTTGCGCAACAGAGGCTACACTCGCGCAACCTTACCGAGGCGGCTAGCGCTAC 1200
1186 GTCATGGAAGACCTGCTGCACTTCTGCGGCTGATGTACTGATGTCGATGGAACAAGTGC 1245
1201 GTCATGGAAGACCTGCTGCACTTCTGCGGCTGATGTACTGATGTCGATGGAACAAGTGC 1260

1246 CATTACCGCTCTCTCACTGCGCATGTTATATTTCTCGATCGCCGGGCTTAGACAGCCA 1305
1261 CATTACCGCTCTCTCACTGCGCATGTTATATTTCTCGATCGCCGGGCTTAGACAGCCA 1320
1306 CAGCTAGTAGAAGAGATCCAGCGGTATTTACCTGAACAGCTGCGGGTGTACATCATGAAC 1365
1321 CAGCTAGTAGAAGAGATCCAGCGGTATTTACCTGAACAGCTGCGGGTGTACATCATGAAC 1380
1366 CAGCACAGCGCTGCGCGGTGCGCGTATCTACGCGAAGATTTCTGCTCGGTGCTTACC 1425
1381 CAGCACAGCGGTGCGCGGTGCGCGTATCTACGCGAAGATTTCTGCTCGGTGCTTACC 1440
1426 GAGTTGGGGAAGCTGCGCATGAGAAATTCGAACATGTGCATCTCGTGAAGCTCAAGAAC 1485
1441 GAGTTGGGGAAGCTGCGCATGAGAAATTCGAACATGTGCATCTCGTGAAGCTCAAGAAC 1500
1486 AGGAAGCTGCGCGGTCTCTGAGGAGATCTGGGACGTG 1524
1501 AGGAAGCTGCGCGGTCTCTGAGGAGATCTGGGACGTG 1539

RESULT 3

US-10-087-167-134
; Sequence 134, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 1848
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1848)
; OTHER INFORMATION: Bodyson receptor chimera G(M)MC
US-10-087-167-134

Query Match 87.4%; Score 1332; DB 16; Length 1848;
Best Local Similarity 92.1%; Pred No. 0;
Matches 1404; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
1 ATGCAGCAGCTATATGTGGATTTTTTAGCCCTGCTTCATACGCTATTTATTTGCTTGG 60
1 ATGCAGCAGCTATATGTGGATTTTTTAGCCCTGCTTCATACGCTATTTATTTGCTTGG 60
61 TACTGTTTCTTTTGTGATGCTCACCCCTGTTGTTGGTGTACTTCTGCGAGGATCCGCC 120
61 TACTGTTTCTTTTGTGATGCTCACCCCTGTTGTTGGTGTACTTCTGCGAGGATCCGCC 120
121 ACCATGAGCTACTGTTCTTATCGAAACAGCATGGATATTTTCCGACTTAAAAAGCTC 180
121 ACCATGAGCTACTGTTCTTATCGAAACAGCATGGATATTTTCCGACTTAAAAAGCTC 180
181 AAGTGTCTCAAAAGAAAAACCGAAGTGGCGCAAGTGTCTGAAGAAACAACCTGGAGTGTGC 240
181 AAGTGTCTCAAAAGAAAAACCGAAGTGGCGCAAGTGTCTGAAGAAACAACCTGGAGTGTGC 240
241 TACTCTCCAAACCAAAAGGTTCTCGCTGACTAGGGCAGCATCTGACAGAGTGGATCA 300
241 TACTCTCCAAACCAAAAGGTTCTCGCTGACTAGGGCAGCATCTGACAGAGTGGATCA 300

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QY 301 AGGCTAGAAAGACTGGAAACAGCTATTCTACTGATTTTCTCGAGAGACCTTGACATG 360
DB 301 AGGCTAGAAAGACTGGAAACAGCTATTCTACTGATTTTCTCGAGAGACCTTGACATG 360
QY 361 ATTTTGAANAATGGATTCTTTTACAGGATATAAAGCAATTTGTTAAACAGGATTTATTGTACAA 420
DB 361 ATTTTGAANAATGGATTCTTTTACAGGATATAAAGCAATTTGTTAAACAGGATTTATTGTACAA 420
QY 421 GATAATGTGAATAAAGATGCGGTTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCCT 480
DB 421 GATAATGTGAATAAAGATGCGGTTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCCT 480
QY 481 CTAACATTGAGACAGCATAGATAAGTCGCGACATCATCATCGAAGAGAGTAGTAACAAA 540
DB 481 CTAACATTGAGACAGCATAGATAAGTCGCGACATCATCATCGAAGAGAGTAGTAACAAA 540
QY 541 GGTCAAAAGACAGTTGACTGTATCGACGGTATGAGGCCCGAGTGGCTGCTCCAGAGTCC 600
DB 541 GGTCAAAAGACAGTTGACTGTATCGACGGTATGAGGCCCGAGTGGCTGCTCCAGAGTCC 600
QY 601 AGCTGCAAGAACAAAGAGAGAAAGAAAGCAACAGAGAGAAAGCAAACTGCCAGTC 660
DB 601 AGCTGCAAGAACAAAGAGAGAAAGAAAGCAACAGAGAGAAAGCAAACTGCCAGTC 660
QY 661 AGTACGACGACAGTGGACGATCATATGCTGCGATAATGCAATGTGACCTCCGCCCCCA 720
DB 661 AGTACGACGACAGTGGACGATCATATGCTGCGATAATGCAATGTGACCTCCGCCCCCA 720
QY 721 GAGGCGGCAAGGATTCAGGAAGTGTCCGAGGTTCTTAACGGAGAACTAATGGAGCAG 780
DB 721 GAGGCGGCAAGGATTCAGGAAGTGTCCGAGGTTCTTAACGGAGAACTAATGGAGCAG 780
QY 781 AACAGACTGAAGAAATGTGACGCGCTGTGCGGAAACAGAGTCCCTGATCGCAGGCTC 840
DB 781 AACAGACTGAAGAAATGTGACGCGCTGTGCGGAAACAGAGTCCCTGATCGCAGGCTC 840
QY 841 GTGTGTACACGAGCGGATACAGACAGCTTCGGAAGAGGATCTCAAAAGGGTGACGCGAG 900
DB 841 GTGTGTACACGAGCGGATACAGACAGCTTCGGAAGAGGATCTCAAAAGGGTGACGCGAG 900
QY 901 ACTTGGCAATCAGCAGATGAAGAAGACGAGACTCAGACATGCCATTCGCGCAGATACAA 960
DB 901 ACATGSCAGTTAGNAGNAGAAAGAGAGGAGAACTGACATGCCCTCCGTCAGATCACA 960
QY 961 GAATGACCATCTCAGACTAGCTATAGTCGAGTTTGCCAAAGGCTTACTCGGTTTT 1020
DB 961 GAGATGACCATCTTAAACAGTCAGCTTATGTAGAAATTCGAAAGGAGTACCGGATC 1020
QY 1021 TCAAGATCTCAACCTGACAGATCACAATTATTAAGGCAATGCTCAAGCGAAGTGATG 1080
DB 1021 TCCNAGATATCTCAGTCCGATCAAAATTACATTTATTAAGGCGTTCATCAAGCGAAGTGATG 1080
QY 1081 ATGCTGCGAGTAGCAGGCGGTACGACGCGGTGTCGGATAGCGTTCTGTTGCGCAACAC 1140
DB 1081 ATGCTGCGAGTAGCAGGCGGTACGACGCGGCGACGACAGCGGTGCTGTTGCGCAACAC 1140
QY 1141 CAGGCGTACACTCGCGACAACTACCGCAAGGCGGCGATCGTCAATCAAGACCTG 1200
DB 1141 CAGGCGTACACGCGCGACAACTACCGCAAGGCGGCGATGTCCTAGTCAATCGAGACCTG 1200
QY 1201 CTGCACTTCTGCGGTGTCATGTAATGATGTCGATGCAACAGTGCATTCACGCGTCTCTC 1260
DB 1201 CTGCACTTCTGCGGTGTCATGTAATGATGTCGATGCAACAGTGCATTCACGCGTCTCTC 1260
QY 1261 ACTGCCATCTGTTATATTCGGATCGCGCGGCTTAGACGACCCACAGTAGTAGAGAG 1320
DB 1261 ACCGCCATCGTTATATTCAGACCGCGCGGCTCGAGCAACCCCTTTTAGTGGAGGAA 1320
QY 1321 ATCCAGCGGTATTTACCTGAACAGCTGCGGGTGTACATCATGAACAGCAGACGCGCTCG 1380
DB 1321 ATCCAGAGATATCTATTGAAGACGCTGCGGGTTTACATTTTAAATCAGCAGACGCGCTCG 1380
QY 1381 CCGCGTTGCGCGCTCATCTACCGGAAGATTTCTGTGCGGTGCTTACCGAGTTGCGGAGCTG 1440
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DB 1381 CCTCGTGGCGGTGCTGTTCCGCAAGATCCTCGGCGTGTGACGGAACCTGCGCAGCTC 1440
QY 1441 GGATCAGAAATTCGAACATGTGCTCTGCTGAAGCTCAAGAAACAGGAGCTGCGCGCG 1500
DB 1441 GGCACGCAAACTCCAACTATGTCATCTCGTGAAGCTGAAGAAACAGGAAACTTCGCCCA 1500
QY 1501 TTCTCGAGGAGATCTGGGACGTG 1524
DB 1501 TTCTCGAGGAGATCTGGGACGTG 1524

RESULT 4
US-10-087-167-136
; Sequence 136, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 136
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1863)
; OTHER INFORMATION: Ecdysone receptor chimera G(M)M
US-10-087-167-136

Query Match 87.4%; Score 1332; DB 16; Length 1863;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 1404; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 1 ATGCAGCAGCTATATGTGGATTTTTTATGCGCTGCTTCATACGCTATTTATTTGCTTGG 60
DB 1 ATGCAGCAGCTATATGTGGATTTTTTATGCGCTGCTTCATACGCTATTTATTTGCTTGG 60
QY 61 TACTGTTTCTTTTGTGATGCTCACCTGTTGTTGTTGTTTACTTCTGCGGGATCGCC 120
DB 61 TACTGTTTCTTTTGTGATGCTCACCTGTTGTTGTTGTTTACTTCTGCGGGATCGCC 120
QY 121 ACCATGAAGCTACTGCTCTTCTATCGAAACAGCATGCCATATTTGCCGACTTTAAAGATC 180
DB 121 ACCATGAAGCTACTGCTCTTCTATCGAAACAGCATGCCATATTTGCCGACTTTAAAGATC 180
QY 181 AAGTGTCTCCAAAGAAAAACCGAAGTGGCCCAAGTGTCTGAAGAAACAACCTGGAGTGTGC 240
DB 181 AAGTGTCTCCAAAGAAAAACCGAAGTGGCCCAAGTGTCTGAAGAAACAACCTGGAGTGTGC 240
QY 241 TACTCTCCAAACCAAAAGGCTCTCCGCTGACTAGGCGACATCTGACAGAAGTGGAAATCA 300
DB 241 TACTCTCCAAACCAAAAGGCTCTCCGCTGACTAGGCGACATCTGACAGAAGTGGAAATCA 300
QY 301 AGGCTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTTTCTCGAGAGACCTTTGACATG 360
DB 301 AGGCTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTTTCTCGAGAGACCTTTGACATG 360
QY 361 ATTTTGAANAATGGATTTCTTTACAGGATATAAAGCAATTTGTTAAACAGGATTTATTGTACAA 420
DB 361 ATTTTGAANAATGGATTTCTTTACAGGATATAAAGCAATTTGTTAAACAGGATTTATTGTACAA 420
QY 421 GATAATGTGAATAAAGATGCGGTTCACAGATAGATTGGCTTCAGTGGAGACTGATATGCCT 480
```


Publication No. US20030154509A1		GENERAL INFORMATION:	
APPLICANT: Pascal, Erica		APPLICANT: Valentini, Scott	
APPLICANT: Brown, Jeffrey		APPLICANT: Cockrell, Adam	
APPLICANT: Johnson, Brian		TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS	
FILE REFERENCE: 50018A		CURRENT APPLICATION NUMBER: US/10/087,167	
CURRENT FILING DATE: 2002-03-01		PRIOR APPLICATION NUMBER: US 60/242,969	
PRIOR FILING DATE: 2000-10-24		NUMBER OF SEQ ID NOS: 148	
SOFTWARE: PatentIn version 3.1		SEQ ID NO 122	
LENGTH: 1767		TYPE: DNA	
ORGANISM: Synthetic Construct		FEATURE:	
NAME/KEY: CDS		LOCATION: (1)..(1767)	
OTHER INFORMATION: Ecdysone receptor chimera G(M)FV		US-10-087-167-122	
Query Match		Score 1328.8; DB 16; Length 1767;	
Best Local Similarity		92.0%; Pred. No. 0;	
Matches 1402; Conservative		0; Mismatches 122; Indels 0; Gaps 0;	
Qy	1	ATCGAGCAGCTATATGTGGATTTTATTTAGCCCTGCTTATACGCTATTTATTTGCTTGG	60
Db	1	ATCGAGCAGCTATATGTGGATTTTATTTAGCCCTGCTTATACGCTATTTATTTGCTTGG	60
Qy	61	TACTGTTCTTTTGTGATGCTCACCTGTTTGTGTTTGTGTTTCTTCTGAGGATCGCC	120
Db	61	TACTGTTCTTTTGTGATGCTCACCTGTTTGTGTTTGTGTTTCTTCTGAGGATCGCC	120
Qy	121	ACCATGAAGCTACTGTCTTCTATCGAACAAGCATGCGATATTTGCGACCTTAAAGACTC	180
Db	121	ACCATGAAGCTACTGTCTTCTATCGAACAAGCATGCGATATTTGCGACCTTAAAGACTC	180
Qy	181	AAGTGTCTCAAGAAAACCGAAGTGGCCAGTGTCTGAAGAACAACTGGAGTGTGCG	240
Db	181	AAGTGTCTCAAGAAAACCGAAGTGGCCAGTGTCTGAAGAACAACTGGAGTGTGCG	240
Qy	241	TACTCTCCCAAAACCAAAAGGTCTCCGCTGACTAGGACATCTGACAGAGTGAATCA	300
Db	241	TACTCTCCCAAAACCAAAAGGTCTCCGCTGACTAGGACATCTGACAGAGTGAATCA	300
Qy	301	AGGCTAGAAAAGCTGGAACAGCTATTTCTAGTATTTTCTCGAGAAGACCTTGAATG	360
Db	301	AGGCTAGAAAAGCTGGAACAGCTATTTCTAGTATTTTCTCGAGAAGACCTTGAATG	360
Qy	361	ATTTTGAATATGATTTCTTACAGGATATAAAGCATTTGTAACAGGATTTTGTACAA	420
Db	361	ATTTTGAATATGATTTCTTACAGGATATAAAGCATTTGTAACAGGATTTTGTACAA	420
Qy	421	GATAATGTGAATAAAGATGCGCTCACAGATAGATTGCTTCAAGTGGAGATGATGCT	480
Db	421	GATAATGTGAATAAAGATGCGCTCACAGATAGATTGCTTCAAGTGGAGATGATGCT	480
Qy	481	CTAATCTGAGACAGCATAGATTAAGTGGACATCATCATCGGAAGAGAGTAGTAACAA	540
Db	481	CTAATCTGAGACAGCATAGATTAAGTGGACATCATCATCGGAAGAGAGTAGTAACAA	540
Qy	541	GGTCAAGACAGTGTGACTGTATCGACGCTATGAGGCCGAGTGGCTGCTCCAGAGTCC	600
Db	541	GGTCAAGACAGTGTGACTGTATCGACGCTATGAGGCCGAGTGGCTGCTCCAGAGTCC	600
Qy	601	ACGTGCAAGAACAAAGAAAGAAAGAACGACAGAGAGAAAGAAAGAAAGAAAGAAAG	660
Db	601	ACGTGCAAGAACAAAGAAAGAAAGAACGACAGAGAGAAAGAAAGAAAGAAAGAAAG	660

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661 AGTACGACGACGACGATCATATGCTGTCATAAATGCAATGTGACCTCCGCCCCA 720
661 AGTACGACGACGACGATCATATGCTGTCATAAATGCAATGTGACCTCCGCCCCA 720
721 GAGCGGCAAGGATTCACGAAGTGTCCGAGGTTCTTAACGGAAGACTAATGAGCAG 780
721 GAGCGGCAAGGATTCACGAAGTGTCCGAGGTTCTTAACGGAAGACTAATGAGCAG 780
781 AACACATGAAGAATGTGACGCGCTGTGCGGACCAAGAGTCCCTGATCGGAGGCTC 840
781 AACACATGAAGAATGTGACGCGCTGTGCGGACCAAGAGTCCCTGATCGGAGGCTC 840
841 GTGTGTACACGACGACGATACGACGCTTCCGGAAGAGGATCTCAAAAGGATGACGAC 900
841 GTGTGTACACGAGGAGGTACGACGCTTCCGGAAGAGGATCTCAAAAGGATGACGAC 900
901 ACTTGGCAATCAGCAGATGAAGAAGACGAGACTCAGACATGCCATTCGCGCAGATACA 960
901 ACATGGCAGTTAGAAGAAGACGAGGAGGAACTGACATGCCCTTCGCTCAGATACA 960
961 GAAATGACCATCTCAGCAGTACGATTAATGTCGAGTTTGCACAAAGGCTTACCTGTTT 1020
961 GAGATGACCATCTTAACGATGCGCTTATTTGTAAGATTCGCAAGGGGACTACCGGATTC 1020
1021 TCAGAGATCTCAACCTGACGACATCAATTTAAAGGATGCTCAAGCGAAGTGTG 1080
1021 TCAAGATATCTCAGTCCGATCAATTTAAAGGATGCTCAAGCGAAGTGTG 1080
1081 ATGCTGCGAGTACGAGGCGGTACGACGCGGTGTCGATAGCGTTCTGTTCCCAACAAC 1140
1081 ATGCTGCGAGTACGAGGCGGTACGACGCGGTGTCGATAGCGTTCTGTTCCCAACAAC 1140
1141 CAGCGGTATACCTGCGGACAACTACGCAAGGCGGCTATGCTCATCGAAGCCTG 1200
1141 CAGCGGTATACCTGCGGACAACTACGCAAGGCGGCTATGCTCATCGGAGCCTG 1200
1201 CTGCACTTCTGCGGTGATGCTACGATGTCGATGCAAGCGTACGATGCTGCTC 1260
1201 CTGCACTTCTGCGGTGATGCTACGATGTCGATGCAAGCGTACGATGCTGCTC 1260
1261 ACTGCCATCGTTATTTCTCGGATCGCGGCGCTAGACGACCCACAGCTAGTAGAAG 1320
1261 ACCGCCATCGTTATTTCTCAGACGCGCCAGGCTCGACCAACCCCTTTAGTGGAGAA 1320
1321 ATCCAGCGTATTAACGCAAGCTGCGGCTGATCATATGAAACGACGACGCGCTG 1380
1321 ATCCAGGATATCTACTTGAAGACGCTGCGGTTTACATTTAAATCAGTACAGCGCTG 1380
1381 CCGGTTGCGCGCTCATCTACGCAAGATTTCTGCGTGTCTTACGAGTTGCGGACGCTG 1440
1381 CCGGTTGCGCGCTCATCTACGCAAGATTTCTGCGTGTCTTACGAGTTGCGGACGCTG 1440
1441 GGCATCGAATTCGAACATGTGCTATCTCGCTGAAGCTCAAGAACGAGGAGCTGCGCG 1500
1441 GGCATCGAATTCGAACATGTGCTATCTCGCTGAAGCTCAAGAACGAGGAGCTTCCGCCA 1500
1501 TTCTCGAGGAGATCTGGGACGCTG 1524
1501 TTCTCGAGGAGATCTGGGACGCTG 1524

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RESULT 7

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US-10-087-167-118
; Sequence 118, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A

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; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 118
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1776)
; OTHER INFORMATION: Ecdysone receptor chimera G(M)BV
US-10-087-167-118

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Query Match      86.0%; Score 1311.2; DB 16; Length 1776;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1398; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

QY 1 ATGCAGCAGCTATATGTGGATTTTGTAGCCCTGCCCTTCATACGCTATTTATTTGCTTGG 60
DB 1 ATGCAGCAGCTATATGTGGATTTTGTAGCCCTGCCCTTCATACGCTATTTATTTGCTTGG 60
QY 61 TACTGTTTCTTTTGTGATGCTCACCCCTGTTTGTGTTTACTTCTCGAGGATCCGCC 120
DB 61 TACTGTTTCTTTTGTGATGCTCACCCCTGTTTGTGTTTACTTCTCGAGGATCCGCC 120
QY 121 ACCATGAAGCTTACTGTTCTTCTATGMAACAGATGCGATATTTGCCGACTTAAAAAGCTC 180
DB 121 ACCATGAAGCTTACTGTTCTTCTATGMAACAGATGCGATATTTGCCGACTTAAAAAGCTC 180
QY 181 AAGTGTCTCCAAAGAAAACCCGAGTGCSCCAAGTGTCTGAAGAACAACTGGGAGTGTGCG 240
DB 181 AAGTGTCTCCAAAGAAAACCCGAGTGCSCCAAGTGTCTGAAGAACAACTGGGAGTGTGCG 240
QY 241 TACTCTCCAAAACCCAAAGGTTCTCCGCTGACTAGGGCACAATCTGACAGAAAGTGAATCA 300
DB 241 TACTCTCCAAAACCCAAAGGTTCTCCGCTGACTAGGGCACAATCTGACAGAAAGTGAATCA 300
QY 301 AGGCTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTCTCGAGAGAGACTTGCATG 360
DB 301 AGGCTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTCTCGAGAGAGACTTGCATG 360
QY 361 ATTTTGAAGATGGATTTCTTACAGGATATAAAGCATTGTTAAACAGGATTTTCTGACAA 420
DB 361 ATTTTGAAGATGGATTTCTTACAGGATATAAAGCATTGTTAAACAGGATTTTCTGACAA 420
QY 421 GATATGTGAATAAAGATGCCGTCAAGATAGATTGGCTTCAGTGGAGACTGATATGCT 480
DB 421 GATATGTGAATAAAGATGCCGTCAAGATAGATTGGCTTCAGTGGAGACTGATATGCT 480
QY 481 CTAACTTGAAGACAGCATAGATAAAGTGGCAGCATCATCTCGAAGAGAGTAGTAACAA 540
DB 481 CTAACTTGAAGACAGCATAGATAAAGTGGCAGCATCATCTCGAAGAGAGTAGTAACAA 540
QY 541 GGTCAAGACAGTTCGACTGTATCGACGCGTATGAGCCCGGAGTGGTGTCTCCAGAGTCC 600
DB 541 GGTCAAGACAGTTCGACTGTATCGACGCGTATGAGCCCGGAGTGGTGTCTCCAGAGTCC 600
QY 601 ACCTGCAAGAACAAAAGAGAGAAAGAACGACAGAGAGAAAAAGACAAACTGCCAGTTC 660
DB 601 ACCTGCAAGAACAAAAGAGAGAAAGAACGACAGAGAGAAAAAGACAAACTGCCAGTTC 660
QY 661 AGTACGACGACAGTGGACGATCATATGCTGCTGATTAATGCAATGTGACCTCCGCCCA 720
DB 661 AGTACGACGACAGTGGACGATCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 GAGGCGGCAAGGATTCACGAAGTGTCCGAGGTTCTTAACGGAAGACTAATGAGCAG 780
DB 721 GAGGCGGCAAGGATTCACGAAGTGTCCGAGGTTCTTAACGGAAGACTAATGAGCAG 780
QY 781 AACACATGAAGAATGTGACGCGCTGTGCGGACCAAGAGTCCCTGATCGGAGGCTC 840

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Db 901 AAGAGGTTACACAGACATGCGAGTTAGAGAGAGAGAGAGAGAGAACTGACATGCC 960
Qy 946 TTCCGCCAGATCACAGAAATGACCATCTCCAGATGACAGTAAATGTCGAGTTGCCAAA 1005
Db 961 TTCCGTCAGATCACAGAGATGACGATCTTAACAGTGCAGCTTATTTGTAGAATTGCAAG 1020
Qy 1006 GGCCTACCTGGTTTTCAGAGATCTCAACACTGACACAGATCACATTTATAAGGCGATGC 1065
Db 1021 GACATACCGGGAATCTCCAGANATCTCAGTCCGATCAANTTACATTTAAAGGCGTCA 1080
Qy 1066 TCAAGCGAAGTATGATGCTCGAGTAGCGAGGCGGTACGACGCGGTTCGAGTAGCGTT 1125
Db 1081 TCAAGCGAAGTATGATGCTCGAGTAGCGAGGCGGTACGACGCGCGGCGAGCAGCGTG 1140
Qy 1126 CTGTTCCGCAACACAGCGGTACACTCGGACAACTACCGCAAGCGGCGGCGATGCGCTAC 1185
Db 1141 CTGTTCCGCAACACAGCGGTACACGCGGCAAACTACCGCAAGCGGCGGCGATGCTCTAC 1200
Qy 1186 GTCATCGAAGACCTCTGCACTTCTGCGCTGCTGATGCTGATGCGATGGAACAACGTG 1245
Db 1201 GTCATCGAAGACCTCTGCACTTCTGCGCTGCTGATGCTGATGCGATGGAACAACGTG 1260
Qy 1246 CATTACGGGCTCCTCACTGCCATCGTTATTTCTCGATCGCGCGGCTAGAGAGCCA 1305
Db 1261 CACTACGCGCTCTCACCGCATCGTTATTTCTCAGACCGGCGGCGCTCGAGCAACC 1320
Qy 1306 CAGCTAGTAGAAGAGATCCAGCGGTATTACCTGAACACGCTCGCGGTGTACATGAAC 1365
Db 1321 CTTTGTAGTGGAGAAATCCAGAGATACTACTTTGAAGACGCTCGCGGTGTACATTTAAAT 1380
Qy 1366 CAGCACAGCGCTCGCGGTTGCGCGCTCATCTACGCGAAGATCTGTGCGTGTCTACC 1425
Db 1381 CAGCACAGCGCTCGCGGTTGCGCGCTCATCTACGCGAAGATCTGTGCGTGTCTACC 1440
Qy 1426 GAGTTGCGGACGCTCGGATCGAGAAATCGAAATGTGATCTCGCTGAGATCTGAGAAC 1485
Db 1441 GAACTGCGGACGCTCGGACGAGAACTCCAACATGTGATCTCGCTGAGATCTGAGAAC 1500
Qy 1486 AGGAAGTCCGCGGTTCTCGGAGAGATCTGGGAGTG 1524
Db 1501 AGGAAGTCCGCGGTTCTCGGAGAGATCTGGGAGTG 1539

RESULT 9
US-10-087-167-128
; Sequence 128, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Eric
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1428)
; OTHER INFORMATION: G(M)M (GAL4 DNA Binding Domain fused to the Manduca Ecr Hinge and
; OTHER INFORMATION: Ligand Binding Domain)
US-10-087-167-128
Query Match 79.3%; Score 1209; DB 16; Length 1428;
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Best Local Similarity 91.4%; Pred. No. 0; Mismatches 120; Indels 0; Gaps 0;
Matches 1281; Conservative
Qy 124 ATGAGCTACTGCTCTTATCGAACAGCATGCGATATTTGCCGACTTAAAGAGCTCAAG 183
Db 1 ATGAGCTACTGCTCTTATCGAACAGCATGCGATATTTGCCGACTTAAAGAGCTCAAG 60
Qy 184 TGCTCCAAAGAAAACCGAAGTGCCTGAAGAAACAATGCGAGTGTGCGTAC 243
Db 61 TGCTCCAAAGAAAACCGAAGTGCCTGAAGAAACAATGCGAGTGTGCGTAC 120
Qy 244 TCTCCCAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAGTGCMAATCAAG 303
Db 121 TCTCCCAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAGTGCMAATCAAG 180
Qy 304 CTAGAAAGACTTGGAAACAGCTATTTCTACTGATTTTCTCGAGAGAGACTTGGACATGAT 363
Db 181 CTAGAAAGACTTGGAAACAGCTATTTCTACTGATTTTCTCGAGAGAGACTTGGACATGAT 240
Qy 364 TTGAAATGGATTTCTTTACAGGATATAAAGCATTTGTTAAACAGGATTTTGTACAAGAT 423
Db 241 TTGAAATGGATTTCTTTACAGGATATAAAGCATTTGTTAAACAGGATTTTGTACAAGAT 300
Qy 424 AATGTGAATAAGATGCCGTCAAGATAGATTGGCTTCACTGGAGACTGATATGCTCTA 483
Db 301 AATGTGAATAAGATGCCGTCAAGATAGATTGGCTTCACTGGAGACTGATATGCTCTA 360
Qy 484 ACATTGGACAGCATAGAAATAGTGGACATCATCATCGAAGAGAGTAGTAACAAGGT 543
Db 361 ACATTGGACAGCATAGAAATAGTGGACATCATCATCGAAGAGAGTAGTAACAAGGT 420
Qy 544 CAAAGACAGTTGACTGTATCGACGCTATGAGGCGCGAGTGCCTGCCAGAGTCCACG 603
Db 421 CAAAGACAGTTGACTGTATCGACGCTATGAGGCGCGAGTGCCTGCCAGAGTCCACG 480
Qy 604 TGCAGAAACAAAGAGAGAAAGAGAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 663
Db 481 TGCAGAAACAAAGAGAGAGAAAGAGAACACAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy 664 AGCAGCAGTGGACGATCATATGCTGCCATATGCAATGTCACCTCCGCGCCCCAGAG 723
Db 541 AGCAGCAGTGGACGATCATATGCTGCCATATGCAATGTCACCTCCGCGCCCCAGAG 600
Qy 724 GCGGCAAGGATTCAGAAAGTGTGTCGCGAGGTTCTTAACGAGAGAGAGAGAGAGAG 783
Db 601 GCGGCAAGGATTCAGAAAGTGTGTCGCGAGGTTCTTAACGAGAGAGAGAGAGAGAG 660
Qy 784 AGACTGAAGAAATGTGACGCGCTGTGCGGGAACCAAGAGTCCCTGATCGCGAGGTCGTG 843
Db 661 AGACTGAAGAAATGTGACGCGCTGTGCGGGAACCAAGAGTCCCTGATCGCGAGGTCGTG 720
Qy 844 TGGTACCAAGGAGGATACGAGCAGCTTTCGGAAGAGGATCTCAAAGGGTGCAGCAGACT 903
Db 721 TGGTACCAAGGAGGATACGAGCAGCTTTCGGAAGAGGATCTCAAAGGGTGCAGCAGACT 780
Qy 904 TGGCAATCAGCAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 963
Db 781 TGGCAGTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Qy 964 ATGACATCTCTCAGAGTACAGTAAATAGTTCGAGTTTGCAGAGGCTTACCTGGTTTCA 1023
Db 841 ATGACATCTCTCAGAGTACAGTAAATAGTTCGAGTTTGCAGAGGCTTACCTGGTTTCA 900
Qy 1024 AAGATCTCAACCTGACAGATCATATTTAAAGGAGGATGCTCAAGCGAGTGTGATG 1083
Db 901 AAGATCTCAACCTGACGATCAAAATTTAAAGGCGCTCATCAAGCGAGTGTGATG 960
Qy 1084 CTGCGAGTAGCGAGGCGGTACGACGCGGTGTCGAGTAGCGTTCTGTTCGCCAACACAG 1143
Db 961 CTGCGAGTAGCGGCGAGGCTGACGCGGCGGACGAGCAGCGTGTGTTCGCCAACACAG 1020
Qy 1144 GGTACACTCGGACAACTACCGCAAGGCGGCGATGGCTTACGTCTATCGAAGACCTGCTG 1203
Db 1144 GGTACACTCGGACAACTACCGCAAGGCGGCGATGGCTTACGTCTATCGAAGACCTGCTG 1203
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QY 1312 GTAGAAGAGATCCAGCGGTATTACTGAAACCGCTGGGGTGTATCATCATCAACACGAC 1371
DB 1561 GTGGAGGAATCCAGAGATCTACTTGAAGACGCTGCGGGTTTACATTTTAAATTCAGCAC 1620
QY 1372 AGCGGCTCGCGCGTTCGCGCGTCTATCTACCGGAAGATTCTGCGGTCTTACCGAGTTG 1431
DB 1621 AGCGGCTCGCGCGTTCGCGCGTCTGCTGTTCCGGAAGATCTCTCGCGGTGCTGACGGA 1680
QY 1432 CGGAGCTGGGATGTCAGAAATTCGAACATGTGCAATCTGCTGAAGCTCAAGAACAGGAAG 1491
DB 1681 CGCAGCTCGGCAGCAGCAACTCCAAATGTGCAATCTGCTGAAGCTGAAGAACAGGAAA 1740
QY 1492 CTGCGCGCTTCCTGGAGAGATCTGGGACGTG 1524
DB 1741 CTTCCGCCATTCTCTCGAGGAGATCTGGGACGTG 1773

RESULT 12
US-10-087-167-67
; Sequence 67, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 1500
; TYPE: DNA
; ORGANISM: Synthetic construct
; FEATURE:
; LOCATION: (1)..(1500)
; OTHER INFORMATION: Ecdysone Receptor Chimera MEV
US-10-087-167-67

Query Match 62.7%; Score 955.6; DB 16; Length 1500;
Best Local Similarity 99.6%; Pred. No. 2.9e-276;
Matches 958; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 563 CGACGGTATGAGGCCGAGTGGTGGTCCAGAGTCCACGTGCAAGAACAAAAGAGAG 622
DB 296 CGGTGGCATGAGGCCGAGTGGTGGTCCAGAGTCCACGTGCAAGAACAAAAGAGAG 355
QY 623 AAAAGAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 682
DB 356 AAAAGAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 415
QY 683 ATATGCTGCCATATGCAATGTGACCTCCGCCCCAGAGCGGCGGAGGATTCAGAG 742
DB 416 ATATGCTGCCATATGCAATGTGACCTCCGCCCCAGAGCGGCGGAGGATTCAGAG 475
QY 743 TGGTCCCGAGGTTCTTAACCGAGAGAGTAAATGAGCAGAGACAGACTGAAGAAATGTGAGCG 802
DB 476 TGGTCCCGAGGTTCTTAACCGAGAGAGTAAATGAGCAGAGACAGACTGAAGAAATGTGAGCG 535
QY 803 CGCTGTCCGGAACACAGAGAGTCCCTGATCGGAGGCTCTGTGTGTTACAGAGCGGATAGC 862
DB 536 CGCTGTCCGGAACACAGAGAGTCCCTGATCGGAGGCTCTGTGTGTTACAGAGCGGATAGC 595
QY 863 AGCAGCTTCGGAAGAGGATCTCAAAAGGTCAGCAGACTTGGCAATCAGCAGATGAG 922
DB 596 AGCAGCTTCGGAAGAGGATCTCAAAAGGTCAGCAGACTTGGCAATCAGCAGATGAG 655
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QY 923 AAGACGAAGACTCAGACATGCCATTCCGCCAGATCACAGAAATGACCATCTCAGAGTAC 982
DB 656 AAGACGAAGACTCAGACATGCCATTCCGCCAGATCACAGAAATGACCATCTCAGAGTAC 715
QY 983 AGCTAATAGTCTGAGTTTGCCTAAGGCTTACCTGGTTTTCCTCAAGATCTCAGAACCTGACC 1042
DB 716 AGCTAATAGTCTGAGTTTGCCTAAGGCTTACCTGGTTTTCCTCAAGATCTCAGAACCTGACC 775
QY 1043 AGATCAATATTAAAGGATGCTCAAGGAAAGTGTATGCTGCGAGTAGCGAGCGGT 1102
DB 776 AGATCAATATTAAAGGATGCTCAAGGAAAGTGTATGCTGCGAGTAGCGAGCGGT 835
QY 1103 ACAGCGCGTGTGCGATAGCGTTCTGTTCCCAACCAACAGCGGTACATCTCGGCAACT 1162
DB 836 ACAGCGCGTGTGCGATAGCGTTCTGTTCCCAACCAACAGCGGTACATCTCGGCAACT 895
QY 1163 ACCGCAAGCGGCGATGGCTTACGTATCGAAGACCTGTGCACTTCTGCGCGTGCATGT 1222
DB 896 ACCGCAAGCGGCGATGGCTTACGTATCGAAGACCTGTGCACTTCTGCGCGTGCATGT 955
QY 1223 ACTCGATGTGATGGAACAACGTGCAATTACGCGCTCTCTCACTGCCATCGTTATTTCTCGG 1282
DB 956 ACTCGATGTGATGGAACAACGTGCAATTACGCGCTCTCTCACTGCCATCGTTATTTCTCGG 1015
QY 1283 ATCGCGCGGCGCTAGAGCAGCCACAGCTAGTAGAAGAGATCCAGCGGTATTACCTGAACA 1342
DB 1016 ATCGCGCGGCGCTAGAGCAGCCACAGCTAGTAGAAGAGATCCAGCGGTATTACCTGAACA 1075
QY 1343 CGTGGCGGTGTACATCATGAAACAGCAGCGCGTTCGCGCGTTCGCGCGTCTATCTACG 1402
DB 1076 CGTGGCGGTGTACATCATGAAACAGCAGCGCGTTCGCGCGTTCGCGCGTCTATCTACG 1135
QY 1403 CGAAGATTCTGCGGTCTTACCGAGTTGCGGACGCTGCGGATTCGGAATTCGGAACATGT 1462
DB 1136 CGAAGATTCTGCGGTCTTACCGAGTTGCGGACGCTGCGGATTCGGAATTCGGAACATGT 1195
QY 1463 GCATCTCGTGAAGCTCAAGAACAGAGAGTTCGCGCGTTCCTGGAGGAGATCTGGGACG 1522
DB 1196 GCATCTCGTGAAGCTCAAGAACAGAGAGTTCGCGCGTTCCTGGAGGAGATCTGGGACG 1255
QY 1523 TG 1524
DB 1256 TG 1257

RESULT 13
US-10-087-167-75
; Sequence 75, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Synthetic construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1515)
; OTHER INFORMATION: Ecdysone Receptor Chimera BEV
US-10-087-167-75
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Query Match		55.7%;	Score 848.8;	DB 16;	Length 1515;
Best Local Similarity		90.9%;	Pred. No. 4.1e-244;	Indels 15;	Gaps 1;
Matches 920;		Conservative 0;	Mismatches 77;		
QY	528	GAGTAGTAAAGAGTCAAGACAGCTTGACTGTGTATCGACGGGTATGAGCCCGAGTGCCT	587		
DB	261	GAATGTCAAGATGTCGGTGAAGAGTGTGTAGCGGTGGCGATGAGCCCGAGTGCCT	320		
QY	588	GTCCAGAGTCCAGTCAAGAGCAAAAGAGAGAAAAGGAGACACAGAGAGAAAAGA	647		
DB	321	GGTCCAGAGACGAGTGTGCGCAAAAAGGAGAGAGAAAGACACAGAGAGAAAAGA	380		
QY	648	CAAACTGCGAGTCACTAGACACAGTGAACCATCATATGCTGCTGCATTAATCAATGTGA	707		
DB	381	CAAACTACAGTGAACACACAGTGAACCATCATATGCTGCTGCATTAATCAATGTGA	440		
QY	708	CCCTCGGCCCCAGAGGGCGCAAGGATT-----CACGAAGTGGTCCCGAG	752		
DB	441	TCACACACCCCGAGGACGAGGATTCTGGAATGTTTGACGATGAAGTGTCCCGCG	500		
QY	753	GTTCCTAACGAGAGAGTAAATGGAGCAAGACAGTGAAGAAATGTGAAGCCGCTGCGC	812		
DB	501	GTTCCTCTCGGAGAGCTGATGGAGCAGAAATCGGCTGAAGAACATACCCCGCTCACCGC	560		
QY	813	GAACCAAGTCCCTGATCGGAGGCTCGTGTGTACCAAGGACGATACGACAGCCTTC	872		
DB	561	CAACCAGCAGTTCTGATCGCAGGCTGTGTGTACCAAGGACGATACGACAGCCTTC	620		
QY	873	GGAAGAGGATCTCAAAAGGTCACGACACTTTGGCAATCAGCAGATGAAGAGACGAAGA	932		
DB	621	GGAAGAGGATCTCAAAAGGTCACGACACTTTGGCAATCAGCAGATGAAGAGACGAAGA	680		
QY	933	CTCAGACATGCCATTCGCCAGATCAAGAAATGACCATCTCAAGTACAGTAAATAGT	992		
DB	681	CTCAGACATGCCATTCGCCAGATCAAGAAATGACCATCTCAAGTACAGTAAATAGT	740		
QY	993	CGAGTTTGCACAAAGGCTACCTGGTTTTTCAAGATCTCACAACTGACAGATCAATT	1052		
DB	741	CGAGTTTGCACAAAGGCTACCTGGTTTTTCAAGATCTCACAACTGACAGATCAATT	800		
QY	1053	ATTAAAGGATGCTCAAGCGAGTATGATGCTGCGAGTAGCGAGCGGTACGACCGGT	1112		
DB	801	ATTAAAGGATGCTCAAGCGAGTATGATGCTGCGAGTAGCGAGCGGTACGACCGGT	860		
QY	1113	GTGCGATAGCGTTCTGTTCCGCAACAAACAGGCGGTACATCTGCGCAAACTACCGCAAGGC	1172		
DB	861	GTGCGATAGCGTTCTGTTCCGCAACAAACAGGCGGTACATCTGCGCAAACTACCGCAAGGC	920		
QY	1173	GGCGATGGCTAGCTCATCGAAGACCTGTGCACTTCTGCGCTGCTACTCGATGTC	1232		
DB	921	GGCGATGGCTAGCTCATCGAAGACCTGTGCACTTCTGCGCTGCTACTCGATGTC	980		
QY	1233	GATGGACAAGCTGCTTACGCGCTCTCTACTGCGATCGTTATATTCTCGGATCGGCGGG	1292		
DB	981	GATGGACAAGCTGCTTACGCGCTCTCTACTGCGATCGTTATATTCTCGGATCGGCGGG	1040		
QY	1293	CCTAGAGCACCACAGCTAGTAGAAGAGATCCAGCGGTATTACTGAAACGCTGCGGGT	1352		
DB	1041	CCTAGAGCACCACAGCTAGTAGAAGAGATCCAGCGGTATTACTGAAACGCTGCGGGT	1100		
QY	1353	GTACATCATGAACAGACAGCGGTGCGCGCTTGGCGCTCATCTACGCGAGATTCT	1412		
DB	1101	GTACATCATGAACAGACAGCGGTGCGCGCTTGGCGCTCATCTACGCGAGATTCT	1160		
QY	1413	GTGCGTCTTACCGAGTTGCGAGCGCTGGCGATGCAAAATTCGAAATGTGCAATCTCGCT	1472		
DB	1161	GTGCGTCTTACCGAGTTGCGAGCGCTGGCGATGCAAAATTCGAAATGTGCAATCTCGCT	1220		
QY	1473	GAAGCTCAAGAACAGGAGCTGCGCGCTTCTTGAGAGAGATCTGGGACGCTG	1524		
DB	1221	GAAGCTCAAGAACAGGAGCTGCGCGCTTCTTGAGAGAGATCTGGGACGCTG	1272		

RESULT 14

US-10-295-370-1
; Sequence 1, Application US/10295370
; Publication No. US2003008890A1
; GENERAL INFORMATION:
; APPLICANT: Albertsen, Marc C.
; APPLICANT: Brooke, Catherine D.
; APPLICANT: Garnaat, Carl W.
; APPLICANT: Roth, Bradley A.
; TITLE OF INVENTION: NOVEL ECDYSONE RECEPTORS AND METHODS FOR THEIR USE
; FILE REFERENCE: 5718-26
; CURRENT APPLICATION NUMBER: US/10/295,370
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/393,839
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2126
; TYPE: DNA
; ORGANISM: Ostrinia nubilalis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (368)..(2005)
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence and deduced amino acid
; OTHER INFORMATION: sequence of Ecdysone receptor
US-10-295-370-1

Query Match		54.9%;	Score 836;	DB 14;	Length 2126;
Best Local Similarity		90.1%;	Pred. No. 3.6e-240;	Indels 15;	Gaps 1;
Matches 912;		Conservative 0;	Mismatches 85;		
QY	528	GAGTAGTAAAGAGTCAAGACAGCTTGACTGTGTATCGACGGGTATGAGCCCGAGTGCCT	587		
DB	940	GAATGTCAAGATGTCGGTGAAGAGTGTGTAGCGGTGGCGATGAGCCCGAGTGCCT	999		
QY	588	CCTCCAGAGTCCAGTCAAGAGCAAAAGAGAGAGAAAAGGAGCAACAGAGAGAAAAGA	647		
DB	1000	GGTCCAGAAAGCGAGTGTGCGCAAAAGGAGAGAGAAAAGGAGCAACAGAGAGAAAAGA	1059		
QY	648	CAAACTGCGAGTCACTAGACACAGTGAAGTATATGCTGCTGCCATTAATGCAATGTGA	707		
DB	1060	CAAACTGCGAGTCACTAGACACAGTGAAGTATATGCTGCTGCCATTAATGCAATGTGA	1119		
QY	708	CCCTCGGCCCCAGAGGGCGCAAGGATT-----CACGAAGTGGTCCCGAG	752		
DB	1120	TCGCGCACCCCGAGGAGCGAGGATTCTGGAATGTTTGCAGCATGAAGTGTCCCGCG	1179		
QY	753	GTTCCTTAACGAGAGAGTAAATGGAGCAGAAACAGACTGAAGAAATGTGACCGCGCTGTCGC	812		
DB	1180	GTTCCTTCTCGAGAGAGTGAAGCAGAAATCGGTTGAAGACATACCCCGCTCACCGC	1239		
QY	813	GAACCAAGAGTCCCTGATCGGAGGCTCGTGTGTTACAGGACGATACGAGCAGCCTTC	872		
DB	1240	CAACAGCAGATTCCTGATCGGAGGCTGGTGTGTACCAAGGACGATACGAGCAGCCTTC	1299		
QY	873	GGAAGAGGATCTCAAAAGGTCACGACACTTTGGCAATCAGCAGATGAAGAGACGAAGA	932		
DB	1300	GGAAGAGGATCTCAAAAGGTCACGACACTTTGGCAATCAGCAGATGAAGAGACGAAGA	1359		
QY	933	CTCAGACATGCCATTCGCGCAGATCAAGAAATGACCATCTCTCACAGTACAGCTAATAGT	992		
DB	1360	CTCAGACATGCCATTCGCGCAGATCAAGAAATGACCATCTCTCACAGTACAGCTAATAGT	1419		
QY	993	CGAGTTTGCACAAAGGCTACCTGGTTTTTCAAGATCTCAAACTGACAGATCAATT	1052		
DB	1420	CGAGTTTGCACAAAGGCTACCTGGTTTTTCAAGATCTCAAACTGACAGATCAATT	1479		
QY	1053	ATTAAAGGATGCTCAAGCGAGTATGATGCTGCGAGTAGCGGCGGTACGACCGGT	1112		
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[illegible]

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RESULT 15
US-10-292-356-1
; Sequence 1, Application US/10292356
; Publication No. US20030110528A1
; GENERAL INFORMATION:
; APPLICANT: Albertsen, Marc C.
; APPLICANT: Brooke, Catherine D.
; APPLICANT: Garmaat, Carl W.
; APPLICANT: Roch, Bradley A.
; TITLE OF INVENTION: NOVEL ECDYSONE RECEPTORS AND METHODS FOR THEIR USE
; FILE REFERENCE: 5718-26
; CURRENT APPLICATION NUMBER: US/10/292,356
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/393,839
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2126
; TYPE: DNA
; ORGANISM: Ostrinia nubilalis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (368)..(2005)
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence and deduced amino acid
; OTHER INFORMATION: sequence of Ecdysone receptor
US-10-292-356-1

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	Query Match	54.9%	Score 836;	DB 15;	Length 2126;
	Best Local Similarity	90.1%	Pred. No. 3.6e-240;		
	Matches 912;	Conservative 0;	Mismatches 85;	Indels 15;	Gaps 1;
Qy	528	GAGTAGTAAACAAGGTCAAAGACAGTTGACTGTATCGACGCGTATGAGGCCGAGTCCGT	587		
Db	940	GAATATGTCAAGAAATGCCGGTTTGAAGAAGTGTGTTAGCGTGGCATGAGGCCGAGTCCGT	999		
Qy	588	CGTCCCAGAGTCCAGTCCAAAGAAACAAAAGAGAGAAAGCAAGCACAGAGAGAAAAGA	647		
Db	1000	GGTGCCAGAAACGCGAGTGTGCGCAAAAAGAAAGAGAGAAAGCAACAGAGAGAAAAGA	1059		
Qy	648	CAAACTGCCAGTCAGTACGACACAGTGGACGATCATATGCTGCCAATTAATGCAATGTGA	707		
Db	1060	CAAACTACAGTGAACAAACAGATGACGATGACATATGCCCCCAATCATGTCAGTGTGA	1119		

Qy	708	CCCTCCGCCGCCCCAGAGCGCGCAAGGATTT-----CAGCAGTAGTGTCCCGAG	752
Db	1120	TCGCCCAACCCCGGAGCGACGAGGATTTCTGGAAATGTTTTCAGCATGAAGTGTGCCGCG	1179
Qy	753	GTTCCTTAACGGAGAGCTAATGAGCAGAGAACACAGACTGAAGAAATGTGACGCCGTGTCCGGC	812
Db	1180	GTTCCTCTCGGAGAGAGCTGATGAGCAGAGATCGGTTGAGAAATATACCCCCCTCACCGC	1239
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Qy	873	GGAGAGGAGTCTCAAAAGGCTGACGAGACTTGGCAATCAGCAGATGAAGAAACGAAAGA	932
Db	1300	GGAGAGGAGTCTCAAAAGGCTGACGAGACTTGGCAATCAGCAGATGAAGAAACGAGNAGA	1359
Qy	933	CTCAGACATGCCAATTCGCGCAGAGTACAGAAATGACCATCCTCACAGTACAGCTAATAGT	992
Db	1360	CTCAGACATGCCAATTCGCGCAGAGTACAGAAATGACCATCCTCACAGTACAGCTAATAGT	1419
Qy	993	CGAGTTTTCGCAAGGCCCTA	1052
Db	1420	CGAGTTTTCGCAAGGCCCTA	1479
Qy	1053	ATTAAAGGCATGCTCAAGCGAAGTGATGCTCGAGTAGCAGAGGCGGTACGACGCGGT	1112
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Qy	1113	GTCCGATAGCGGTTCTGTTTCGCCAACCAACACGAGGCGGTACACTCGCGACAACTACCGCAAGGC	1172
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Qy	1233	GATGGACAAAGTGTGATTAACGCGCTCCTCACTCGCCATCGTTATATTTCTCGGATCGGCGCGG	1292
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Qy	1353	GTACATCATGAACACAGCACGCGGTTCGCGCGTTCGCGTCACTATCTACGCGAAGATTCT	1412
Db	1780	GTACATCATGAACACAGCACGCGGTTCGCGCGTTCGCGTCACTATCTACGCGAAGATTCT	1839
Qy	1413	GTCCGCTGCTTACCGAGTTTGGGACGCTTGGGCATGAGAAATTCGAAACATGTGCACTCTCGCT	1472
Db	1840	GTCCGCTGCTTACCGAGTTTGGGACGCTTGGGCATGAGAAATTCGAAACATGTGCACTCTCGCT	1899
Qy	1473	GAAGCTCAAGAACAGGAAGCTGCCCGGTTCTCTGGAGGAGATCTGGGACGTG	1524
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Job time : 922.505 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 09:56:57 ; Search time 7226.52 Seconds
(without alignments)
11144.035 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_ev.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1612.8	97.0	1767	6	AX555370 Sequence
3	1552.2	93.4	1800	6	AX555374 Sequence
4	1441.6	86.7	1776	6	AX555366 Sequence
5	1431.8	86.1	1863	6	AX555384 Sequence
6	1426.6	85.8	1848	6	AX555382 Sequence
7	1425	85.7	1428	6	AX555376 Sequence
8	1424	85.7	1767	6	AX555368 Sequence
9	1422	85.6	1809	6	AX555390 Sequence
10	1314.2	79.1	1782	6	AX555372 Sequence
11	1316.6	73.2	1518	6	AX555341 Sequence
12	1167.4	70.2	1500	6	AX555317 Sequence
13	1166	70.2	1800	6	AX555395 Sequence
14	1109.8	66.8	1533	6	AX555327 Sequence
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ALIGNMENTS

RESULT 1
AX555352
LOCUS AX555352 3972 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 104 from Patent WO02061102.
ACCESSION AX555352
VERSION AX555352.1 GI:25898871
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.
TITLE Control of gene expression in plants
JOURNAL Patent: WO 02061102-A 104 08-AUG-2002;
Syngenta Participations AG (CH)
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/db_xref="taxon:32630"

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ORIGIN

Query Match	100.0%;	Score 1662;	DB 6;	Length 3972;
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Matches 1662;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps 0;				
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2127	TCTCCCAAAACCAAAAGGTCCTCCGTGACTAGGCGACATCTGCAGAAAGTGGAAATCAAGG	2185		
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361	ACATTGAGACAGATAGAATAAGTCGACATCATCTCGAAGAGAGTAGTAAACAAGGT	420		
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2547	ACGACGACAGTGACCGCATCATATGCTCGCCATAATGCAATGTGACCTTCGCGCCCCCAGAG	2605		
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Qy	1081	CACTTCTGTCGGTGATGTACTCCATGAGCATGGACAATGTCACCTACGCGTGTCTCACC	1140
Db	3087	CACTTCTGTCGGTGATGTACTCCATGAGCATGGACAATGTCACCTACGCGTGTCTCACC	3146
Qy	1141	GCATCGTTATATTTCTCAGACCGGCAGCGCTCGAGCAACCCCTTTTGTGGAGGAAATC	1200
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Qy	1261	CGTCGCGCGTCGTGTTTCGGCAAGATCCTCGGCGTCTGACGGAATCGCGACGCTCGGC	1320
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Qy	1621	ATGTTTACCGATGCCCTTGGAAATTGACGAGTACGGTGGTAG	1662
Db	3627	ATGTTTACCGATGCCCTTGGAAATTGACGAGTACGGTGGTAG	3668

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RESULT 2
AX555370
LOCUS linear PAT 27-NOV-2002
DEFINITION 1767 bp DNA
Sequence 122 from Patent WO02061102.
ACCESSION AX555370
VERSION AX555370.1 GI:25898889
synthetic construct
other sequences; artificial sequences.
ORGANISM
1
Pascal, E.J., Valentine, S.A., Brown, J.A., Cockrell, A.S. and
Johnson, B.D.
Control of gene expression in plants
Patent: WO 02061102-A 122 08-AUG-2002;
Syngenta Participations AG (CH)
Location/Qualifiers
1. 1767
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
1. 1767
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G(M)FV"
/codon_start=1
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FEATURES
source
CDS

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KGLPFSKISQSDQITLLKASSSEVMRLVARYDAATDSVLFANNOAYTRDNYRKAG
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ORIGIN

Query Match 97.0%; Score 1612.8; DB 6; Length 1767;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1642; Conservative 0; Mismatches 2; Indels 18; Gaps 1;

QY 1 ATGAAGCTACTGTCTTCTATCGAACAGCATGCCGATATTTCCGACTTTAAAAAGCTCAAG 60
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QY 61 TGCTCCAAAGAAAACCGAAGTGCAGGCTGTCTGAAGAACAACTGGAGTGTGCTTAC 120
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QY 241 TTGAAAATGGAATCTTTACAGATATTAAGCAATGTTTAAACAGGATTTATTTGACAAAT 300
DB 364 TTGAAAATGGAATCTTTACAGATATTAAGCAATGTTTAAACAGGATTTATTTGACAAAT 423

QY 301 ATGTGTAATAGATGCGCTGACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTA 360
DB 424 ATGTGTAATAGATGCGCTGACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTA 483

QY 361 ACATTGAGACAGCATAGATAAGTGCACATCATCATCGAAGAGAGTAGTAACAAAGGT 420
DB 484 ACATTGAGACAGCATAGATAAGTGCACATCATCATCGAAGAGAGTAGTAACAAAGGT 543

QY 421 CAAAGACAGTTGATGATTCGACGCGTATGAGCCCGAGTGGTGTCCACAGTCCAG 480
DB 544 CAAAGACAGTTGATGATTCGACGCGTATGAGCCCGAGTGGTGTCCACAGTCCAG 603

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QY 661 AGACTGAGNATGTGACGCGCTGCGGCAACCAAGTCCCTGATCGCGAGGTCGTG 720
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QY 781 TGGCAGTTAGAAAGAAAGAGAGAGGAAACTGACATGCTTCCGTTCAGATCAGAG 840
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DB 964 ATGACCATCTTAACAGTGCAGCTTATTTGTAGAAATTCGAAAGGAGCTACCGGGATTTCTCC 1023

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DB 1024 AAGATATCTCAGTCCGATCAAAATTTACATATTAAAGCGCTCATCAAGCGAAGTATGATG 1083

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QY 1021 GCGTACACGCGCGACAACTACCGGACGCGGCGATGCTCTACGTCATCGAGGACTGCTG 1080

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DB 1384 CGCTGCGCGGCTGTTTCGCAAGATCTCCTGCGCTGTGACGGAACCTCGCACGCTCGGC 1443

QY 1321 ACGCAGAACTCCAACTATGTGATCTCGCTGAAGCTGAAGAACAGGAACTTTCCGCAATTC 1380

DB 1444 ACGCAGAACTCCAACTATGTGATCTCGCTGAAGCTGAAGAACAGGAACTTTCCGCAATTC 1503

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QY 1621 ATGTTTACCGATGCGCTTGGAAATTCACGAGTACGCTGGGTAG 1662

DB 1726 ATGTTTACCGATGCGCTTGGAAATTCACGAGTACGCTGGGTAG 1767

RESULT 3

AX555374
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

AX555374
Sequence 126 from Patent WO02061102.
AX555374
AX555374.1 GI:25898893
synthetic construct
synthetic construct
other sequences; artificial sequences.
1
Pascal, E.J., Valentine, S.A., Brown, J.A., Cockrell, A.S. and
Johnson, B.D.
Control of gene expression in plants
Patent: WO 02061102-A 126 08-AUG-2002;
Syngenta Participations AG (CH)
Location/Qualifiers

AX555374
1800 bp
DNA
linear
PAT 27-NOV-2002

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CDS	1. .1800 /note="unnamed protein product; Ecdysone receptor chimera G(E)MV" /codon_start=1 /transl_table=11 /protein_id="CAD58258.1" /db_xref="GI:25898894"	706	ATCGCGAGGCTCGTGTGGTACCAAGAGGGGTACGAGCAGCGCTCGAGGAGAAAGATCTCAAG	765
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		766	AGAGTTTACACAGACATGGCAGTTTAGAAGAAAGAGAGGAGAACTGACATGCCCTTC	825
		904	AGAGTTTACACAGACATGGCAGTTTAGAAGAAAGAGAGGAGAACTGACATGCCCTTC	963
		826	CGTCAGATCACAGAGATGACGATCTTTAAAGTGCAGCTTATTGTAGAAATTCGAAAGGGA	885
		964	CGTCAGATCACAGAGATGACGATCTTTAAAGTGCAGCTTATTGTAGAAATTCGAAAGGGA	1023
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		1024	CTACCCGGGATCTCCAAAGATATCTCAGTCCGATCAAAATTACATTTATTAAGGCGTCATCA	1083
		946	AGCGAAGTATGATGTCTGCGAGTGGCGCGACCGGTACGACGCGCGACGACAGCGGTGCTG	1005
		1084	AGCGAAGTATGATGTCTGCGAGTGGCGCGACCGGTACGACGCGCGCGACGACAGCGGTGCTG	1143
		1006	TTCCGGAACAAACAGCGGTACACGCGCGACAACTACCGCAAGCGGGCATGTCTTACGCTC	1065
		1144	TTCCGGAACAAACAGCGGTACACGCGCGACAACTACCGCAAGCGGGCATGTCTTACGCTC	1203
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		1324	TTAGTGGAGAAATCCAGAGATACCTACTTTGAAGACGCTGCGGGTTTACATTTTAAATCAG	1383
		1246	CACAGCGCTCGCTCGCTGCGCGCTGTCTGTTTCGGCAAGATCTCTCGGCGTGTGACGGAA	1305
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		1366	AAACTTCCGCGCATTCCTCGAGGAGATCTGGGACGTGGCCGGAAGTGTGACGACGAGCTT	1425
		1504	AAACTTCCGCGCATTCCTCGAGGAGATCTGGGACGTGGCCGGAAGTGTGACGACGAGCTT	1563
		1426	GCCCCCGGACCGATGTGAGCTGGGGGACGAGCTCCACTTAGACGCGGAGGACGTGGCG	1485
		1564	GCCCCCGGACCGATGTGAGCTGGGGGACGAGCTCCACTTAGACGCGGAGGACGTGGCG	1623
		1486	ATGGCGCATCGCGACGCGCTAGACGATTTTCGATCTGGAATGTTGGGGGACGGGGATTC	1545
		1624	ATGGCGCATCGCGACGCGCTAGACGATTTTCGATCTGGAATGTTGGGGGACGGGGATTC	1683
		1546	CCGGGTCGGGATTTTACCCCGCCAGCTCCGCCCCCTACGCGCTCTGGATATGGCGGAC	1605
		1684	CCGGGTCGGGATTTTACCCCGCCAGCTCCGCCCCCTACGCGCTCTGGATATGGCGGAC	1743
		1606	TTCCAGTTTGAACAGATGTTTACCGATGCCCTTGGAAATTTGACGAGTACGGTGGGTAG	1662
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		AX555366	1776 bp	DNA linear PAT 27-NOV-2002
		LOCUS	Sequence 118 from Patent WO02061102.	
		DEFINITION		
		ACCESSION		

VERSION	AX555366.1	GI:25898885	
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	other sequences; artificial sequences.		
REFERENCE	1		
AUTHORS	Pascal, E.J., Valentine, S.A., Brown, J.A., Cockrell, A.S. and Johnson, B.D.		
TITLE	Control of gene expression in plants		
JOURNAL	Patent: WO 02061102-A 118 08-AUG-2002;		
	Syngenta Participations AG (CH)		
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	Best Local Similarity 92.6%; Pred. No. 3.7e-297;		
	Matches 1539; Conservative 0; Mismatches 114; Indels 9; Gaps 2;		
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QY	61	TGCTCCAAAGAAAACCGCAAGTCGCGCAAGTGTCTGAAGAACAACTGGGAGTGTCCCTAC	120
DB	184	TGCTCCAAAGAAAACCGCAAGTCGCGCAAGTGTCTGAAGAACAACTGGGAGTGTCCCTAC	243
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DB	244	TCTCCCAAAACCAAAAGGTCCTCGCTGACTAGGCGCACATCTGACAGAGTGGGAATCAAGG	303
QY	181	CTAGAAGAGTGGAAACAGCTATTTCTACTGATTTTCTCGAGAAGACCTTGACATGAT	240
DB	304	CTAGAAGAGTGGAAACAGCTATTTCTACTGATTTTCTCGAGAAGACCTTGACATGAT	363
QY	241	TTGAAAATGATTTCTTTACAGGATATATAAGCATTTGTTAAACAGATTTTGTGTACAGAT	300
DB	364	TTGAAAATGATTTCTTTACAGGATATATAAGCATTTGTTAAACAGATTTTGTGTACAGAT	423
QY	301	AATGTGAATAAGATCGCTGACAGATAGATTCGCTTTCAGTGGAGACTGATATGCTCTCTA	360
DB	424	AATGTGAATAAGATCGCTGACAGATAGATTCGCTTTCAGTGGAGACTGATATGCTCTCTA	483
QY	361	ACATTGAGACAGCATAGATAAGTGGACATCATCATCGAAGAGAGTAGTAAACAAGGT	420
DB	484	ACATTGAGACAGCATAGATAAGTGGACATCATCATCGAAGAGAGTAGTAAACAAGGT	543
QY	421	CAAAGACAGTTGACTGTATCGACGCTATGAGGCCCGAGTGCCTCCAGAGTCCACG	480
DB	544	CAAAGACAGTTGACTGTATCGACGCTATGAGGCCCGAGTGCCTCCAGAGTCCACG	603
QY	481	TGCAAGAACAAAGAGAGAAAAGGAGACACAGAGAGAAAAGACAAACTGCCAGTCAGT	540

DB	604	TGCAAGAACAAAGAGAGAAAAGGAGACACAGAGAGAAAAGACAAACTGCCAGTCAGT	663
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DB	664	ACGACGACAGTGGAGCATATATGCTCCATATATGCAATATGCACTCCGCCCCCAGAG	723
QY	601	CGCGCAAGGATTTACGAAGTGTGTCGAGGTTCTTAACGGAGAAAGCTAATGAGAGAGAAC	660
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QY	661	AGACTGAAGATGTGACCGCTGTGCGGACACAGAGTCCCTGATCGCGAGGTCGCG	720
DB	784	AGACTGAAGATGTGACCGCTGTGCGGACACAGAGTCCCTGATCGCGAGGTCGCG	843
QY	721	TGGTACACAGGAGGTTACGACGCGTCGGAGGAAGATCTCAAGAGAGTATTACACAGACA	780
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QY	781	TGGCAGTTAGAGAGAGAGAGAGGAGAACTGACATGCCCTTCCGTTCAGATCAACAGAG	840
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QY	1021	GGGTACACGCGGACAACTACCGGAAAGCGGCGCATGTCTAGTCTATCGAGGACCTGCTG	1080
DB	1141	GGGTACTCTCCGCGACAACTACCGGAAAGCGGCGCATGTCTAGTCTATCGAGGATCTCTTG	1200
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DB	1261	GCCATGTCATTTTCTCAGACCGGCGCTCGAGCAACCCCTTTTGTGGAGGAAATC	1320
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DB	1381	CGCTGCGGCTGCTGTTCGCGAAGATCTTCGCGGCTGCTGACGCACTCGCGAGCTCGGC	1440
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QY	1441	GTGAGCTGGGAGACGAGTCTTACCTAGACGCGGAGGAGTGGCGATGGCGATGCCGAC	1500
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QY	1501	GGCTAGACGATTTTCCATCTGACACATTTTGGGGACGCGGATTTCCCGGGTCCGGATTT	1560
DB	1615	GGCTAGACGATTTTCCATCTGACACATTTTGGGGACGCGGATTTCCCGGGTCCGGATTT	1674
QY	1561	ACCCCCCAGCTCCCGGCTCTGATATCGGCGCTCTGATATGGCGGACTTCAGGTTTGAGCA	1620

Db	1675	ACCCCCACGACTCGCGCCCTACGCGCTCTGGATATGGCCGACTTCGAGTTTGAGCAG	1734
Qy	1621	ATGTTTACCGATGCCCTTTGGAATTGACGAGTACGGTGGGTAG	1662
Db	1735	ATGTTTACCGATGCCCTTTGGAATTGACGAGTACGGTGGGTAG	1776
RESULT 5			
AX555384			
LOCUS	AX555384	1863 bp	DNA linear PAT 27-NOV-2002
DEFINITION	Sequence 136 from Patent WO02061102.		
ACCESSION	AX555384		
VERSION	AX555384.1	GI:25898903	
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	other sequences; artificial sequences.		
REFERENCE	1		
AUTHORS	Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.		
TITLE	Control of gene expression in plants		
JOURNAL	Patent: WO 02061102-A 136 08-AUG-2002;		
	Syngenta Participations AG (CH)		
FEATURES	Location/Qualifiers		
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ORIGIN			
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Best Local Similarity	99.2%; Pred. No. 4.6e-295;		
Matches 1439; Conservative	0; Mismatches 12; Indels 0; Gaps 0;		
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Qy	61	TGCTCCAAAGAAAACCGAGTCCGCAAGTGCTCTGAAGAACAACTGGGAGTGCCTAC	120
Db	184	TGCTCCAAAGAAAACCGAGTCCGCAAGTGCTCTGAAGAACAACTGGGAGTGCCTAC	243
Qy	121	TCTCCCAAACCAAAAGGTCCTCGCTGACTAGGGCACATCTGACAGAAGTGGAAATCAAGG	180
Db	244	TCTCCCAAACCAAAAGGTCCTCGCTGACTAGGGCACATCTGACAGAAGTGGAAATCAAGG	303
Qy	181	CTAGAAGACTGAAACAGCTATTTCTACTGATTTTTTCTCGAGAGACCTTCACATGATT	240
Db	304	CTAGAAGACTGAAACAGCTATTTCTACTGATTTTTTCTCGAGAGACCTTCACATGATT	363
Qy	241	TTGAAATGATTTCTTTACAGGATATAAAGCAATTCGTTAAACAGGATTTTGTGACAAAT	300
Db	364	TTGAAATGATTTCTTTTACAGGATATAAAGCAATTCGTTAAACAGGATTTTGTGACAAAT	423
Qy	301	AATGTGAATAAAGATGCGCGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCGCTCTA	360

Db 1504 CTCGAGGAGATCTGGACGTGSCCGAAGTGTGACGACGAAGCTTGAGCTCGCCACCGCG 1563

QY 1441 GTCAGCCTGGG 1451

Db 1564 GCCGACCCAGG 1574

RESULT 6

AX555382

LOCUS AX555382 1848 bp DNA linear PAT 27-NOV-2002

DEFINITION Sequence 134 from Patent WO02061102.

ACCESSION AX555382

VERSION AX555382.1 GI:25898901

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1

AUTHORS Pascal, E.J., Valentine, S.A., Brown, J.A., Cockrell, A.S. and Johnson, B.D.

TITLE Control of gene expression in plants

JOURNAL Patent: WO 02061102-A 134 08-AUG-2002;

Syngenta Participations AG (CH)

FEATURES

Location/Qualifiers

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ORIGIN

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Best Local Similarity 97.3%; Pred. No. 6e-294;

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Db 124 ATGAAGCTACTGCTCTATCGAACAGCATGCGATATTTGCCGACTTAAAAAGCTCAAG 183

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QY 181 CTAGAAAGACTGGAACAGTATTTCTACTGATTTTCTCTCGAGAAGACCTTGCATGATT 240

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LOCUS	AX555376	Sequence 128 from Patent WO02061102.	linear
DEFINITION	AX555376		
ACCESSION	AX555376		
VERSION	AX555376.1	GI:25898895	
KEYWORDS		synthetic construct	
SOURCE		synthetic construct	
ORGANISM		other sequences; artificial sequences.	
REFERENCE	1		
AUTHORS	Pascal E.J., Valentine, S.A., Brown, J.A., Cockrell, A.S. and Johnson, B.D.		
TITLE	Control of gene expression in plants		
JOURNAL	Patent: WO 02061102-A 128 08-AUG-2002;		
	Syngenta Participations AG (CH)		
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Db	61	TGCTCCAAAGAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTTCGCTAC	120
Qy	121	TCTCCAAACCAAAAGGCTCGGTGACTAGGGACATCTGACAGAGTGAATCAAGG	180
Db	121	TCTCCAAACCAAAAGGCTCGGTGACTAGGGACATCTGACAGAGTGAATCAAGG	180
Qy	181	CTAGAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAGAGACCTTCGACATGATT	240
Db	181	CTAGAAGACTGGAACAGCTATTTCTACTGATTTTCTCGAGAGACCTTCGACATGATT	240
Qy	241	TTGAAATGGATTTCTTTACAGGATATAAAAGCATTTGTTAAAGGATTTTGTACAGAT	300

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Qy	361	ACATTCGAGACAGCATAGAATAAGTGGGACATCATCATCGGAAGAGAGTAGTAAACAAAGT	420
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Db	541	ACGACGACAGTGGACGATCATATGCTGCGCATATGCAATGTGACCCCTCGCCCCCAGAG	600
Qy	601	CGCGCAAGGATTCACGAAGTGGTCCGAGGTTCTTAAACGAGAGAGCTTAATGGAGCAGAC	660
Db	601	CGCGCAAGGATTCACGAAGTGGTCCGAGGTTCTTAAACGAGAGAGCTTAATGGAGCAGAC	660
Qy	661	AGACTGAGAGTGTGACGCGCTGTCGGGAGACACAGAGTCCCTGATCGGAGGCTCGTG	720
Db	661	AGACTGAGAGTGTGACGCGCTGTCGGGAGACACAGAGTCCCTGATCGGAGGCTCGTG	720
Qy	721	TGGTACCAGGAGGTACGACGACGCGTTCGAGAGAGATCTCAAGAGAGTTACACAGACA	780
Db	721	TGGTACCAGGAGGTACGACGACGCGTTCGAGAGAGATCTCAAGAGAGTTACACAGACA	780
Qy	781	TGGCAGTTAGAGAGAGAGAGAGGAGGAGAACTGACATGCCCTTCGTCAGATCAGAGAG	840
Db	781	TGGCAGTTAGAGAGAGAGAGAGGAGGAGAACTGACATGCCCTTCGTCAGATCAGAGAG	840
Qy	841	ATGACGATCTTAAACAGTGCAGCTTATTGTAGAAATTCGAAAAGGAGCTACCGGATTCCTC	900
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Qy	901	AAGATATCTCAGTCCGATCAAAATTTACATTTAATAAGCGCTCATCAAGCGAAGTATGATG	960
Db	901	AAGATATCTCAGTCCGATCAAAATTTACATTTAATAAGCGCTCATCAAGCGAAGTATGATG	960
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Db	1021	GCGTACACGCGGACAACTACCGCAAGCGGCGATGTCCTACGTCATCGAGGACCTGCTG	1080
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Qy	1261	CGCTGCGCGTGTCTGTCGGCAAGATCCTCGGCGTGTGACGGAACCTGCGCACCGCTCGGC	1320
Db	1261	CGCTGCGCGTGTCTGTCGGCAAGATCCTCGGCGTGTGACGGAACCTGCGCACCGCTCGGC	1320
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Db	1321	ACGAGAGAACTCCAAACATGTGATCTCGCTGAAGCTGAAGAACAGGAAACTTCCGCCATTC	1380

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Db	484	ACATTGAGACAGCATAGAATAAGTGCACATCATCATCGGAAGAGAGTAGTAAACAAGGT	543	
Qy	421	CAAAGACAGTTGACTGTATCGACCGGTATGAGGCCCGAGTGCCTCGTCCAGAGTCCACG	480	
Db	544	CAAAGACAGTTGACTGTATCGACCGGTATGAGGCCCGAGTGCCTCGTCCAGAGTCCACG	603	
Qy	481	TGCAAGAACAAAGACAGAGAAAGGAAGCACAGAGAGAAAAAGACAAACTGCCAGTCAGT	540	
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Qy	1321	ACGCAAGACTCACAATGTGCAATCTGCTGGAAGCTGGAAGAACAGGAACTTCGCGCATTC	138	
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QY	1621	ATGTTTACCGATGCCCTTGGAAATTCAGCAGTACGGTGGGTAG	1662
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LOCUS			
Sequence 142 from Patent WO02061102.			
AX555390			
ACCESSION			
AX555390.1			
VERSION			
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KEYWORDS			
synthetic construct			
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other sequences; artificial sequences.			
ORGANISM			
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Pascal, E. J., Valentine, S. A., Brown, J. A., Cockrell, J. A. S. and			
Johnson, B. D.			
Control of gene expression in plants			
Patent: WO 02061102-A 142 08-AUG-2002;			
Syngenta Participations AG (CH)			
Location/Qualifiers			
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Db	445	TCCAAAGAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTGCTACTCT	504
QY	124	CCCAAAACCAAAGGTTCTCGCTGACTAGGGCACATCTGCAGAGAGTGAATCAAGGCTA	183

Oy	1264	TGCGCGTGTCTTGGCAAGATCTCTCGCGTGTCTGACGGAACCTGCGCAACGCTGGGACG	1323
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LOCUS	AX555372	Sequence 124 from Patent WO02061102.	linear
DEFINITION	AX555372		PAT 27-NOV-2002
ACCESSION	AX555372.1	GI:25898891	
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
synthetic construct			
other sequences; artificial sequences.			
REFERENCE			
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AUTHORS	Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.		
TITLE	Control of gene expression in plants		
JOURNAL	Patent: WO 02061102-A 124 08-AUG-2002;		
Syngenta	Participations AG (CH)		
FEATURES			
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ORIGIN			
Query Match	79.1%;	Score 1314.2;	DB 6; Length 1782;
Best Local Similarity	87.7%;	Pred. No. 6e-270;	
Matches 1471;	Conservative	0; Mismatches 173;	Indels 33; Gaps 2;
Oy	1	ATCAAGCTACTGCTTCTATCGAACAGCATGCGATATTTGCCGACTTAAAGAGCTCAAG	60
Db	124	ATGAAGCTACTGCTTCTATCGAACAGCATGCGATATTTGCCGACTTAAAGAGCTCAAG	183
Oy	61	TGCTCCAAAGAAAACCGAAGTGGCCAGTGTCTGAAGAACAACTGGGAGTGTCTGCTAC	120
Db	184	TGCTCCAAAGAAAACCGAAGTGGCCAGTGTCTGAAGAACAACTGGGAGTGTCTGCTAC	243
Oy	121	TCTCCCAAAACCAAAAGGTCTCGCTGACTAGGGCACATCTGCAGAGTGGGAATCAAG	180
Db	244	TCTCCCAAAACCAAAAGGTCTCGCTGACTAGGGCACATCTGCAGAGTGGGAATCAAG	303
Oy	181	CTAGAAGACTGGACAGCTATTTCTACTATTTTCTCGAGAAAGACCTTGCATGAT	240

QY	1306	CTGGCCAGCTCGGACGACAGAACTCCAACATGTGCATCTCGTGAAGCTGAAGAACAGG	1365
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QY	1366	AAATCTCGGCATCTCTCGAGAGATCTGGGACATGTGGCCGAGTGTGCAGCAGCAAGCTT	1425
Db	1504	AAGCTGCCGCGTCTCTGGAGGAGATCTGGACGT-----GAAGCTT	1545
QY	1426	CCCCCCCCGACGATGTGAGCTCTGGGACGAGCTCCACATTAGACGGCGAGGACGTGGCG	1485
Db	1546	CCCCCCCCGACGATGTGAGCTCTGGGACGAGCTCCACATTAGACGGCGAGGACGTGGCG	1605
QY	1486	ATGGCGCATCGGACGCGCTAGACGATTCGATCTGGACATGTTGGGGACGGGGATTCC	1545
Db	1606	ATGGCGCATCGGACGCGCTAGACGATTCGATCTGGACATGTTGGGGACGGGGATTCC	1665
QY	1546	CGGGTCCGGATTTACCCCCACGACTCCGCCCTTACGGCGCTCTGGATATGCCGAC	1605
Db	1666	CGGGTCCGGATTTACCCCCACGACTCCGCCCTTACGGCGCTCTGGATATGCCGAC	1725
QY	1606	TTGAGAGTTTGGACGATGTTTACCGATGCCCTTGGAAATTGACGATGCGTGGGTAG	1662
Db	1726	TTGAGAGTTTGGACGATGTTTACCGATGCCCTTGGAAATTGACGATGCGTGGGTAG	1782
RESULT 11			
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LOCUS	AX555341	Sequence 93 from Patent WO02061102.	linear
DEFINITION	AX555341		PAT 27-NOV-2002
ACCESSION	AX555341		
VERSION	AX555341.1	GI:25898860	
KEYWORDS		synthetic construct	
SOURCE		synthetic construct	
ORGANISM		other sequences; artificial sequences.	
REFERENCE			
AUTHORS	Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.		
TITLE	Control of gene expression in plants		
JOURNAL	Patent: WO 02061102-A 93 08-AUG-2002;		
	Syngenta Participations AG (CH)		
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ORIGIN			
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		0; Gaps	0;
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REFERENCE	1	Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.	
AUTHORS		Control of gene expression in plants	
TITLE		Patent: WO 02061102-A 147 08-AUG-2002;	
JOURNAL		Syngenta Participations AG (CH)	
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ORIGIN			
Query Match	70.2%;	Score 1166;	DB 6; Length 1800;
Best Local Similarity	85.1%;	Pred. No. 2.7e-238;	
Matches 1425;	Conservative 0;	Mismatches 0;	Indels 249; Gaps 1;
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DB	124	ATGAAGCTACTGCTCTTCTATCGAACAAAGTCGCGATATTTCGCCGACTTAAAAAGCTCAAG	183
QY	61	TGCTCCAAAGAAAAACCGAAGTGCAGGCTGCTGAAGAAACAACCTGGAGGTGCGCTAC	120
DB	184	TGCTCCAAAGAAAAACCGAAGTGCAGGCTGCTGAAGAAACAACCTGGAGGTGCGCTAC	243
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DB	244	TCTCCAAACCAAAAGGTCTCGCTGACTAGGACACATCTGACAGAAAGTGAATCAAGG	303
QY	181	CTAGAAAGACTGGAACAGCTATTTCTACTGATTTTCTCTCGAGAAAGACCTTGACATGAT	240
DB	304	CTAGAAAGACTGGAACAGCTATTTCTACTGATTTTCTCTCGAGAAAGACCTTGACATGAT	363
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DB	364	TTGAAATGGATCTTTTACAGATATAAAGCATTTGTTAAACAGGATTAATTTGTACAGAT	423
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DB	424	AATGTGAATAAGATGCCGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTA	483
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DB	484	ACATTGAGACAGCATAGAATAAGTGCACATCATCATCGAAAGAGAGTAGTAACAAAGGT	543
QY	421	CAAAAGACAGTTGATTCGACGGGTATGAGCCCGAGTGGTCCGACAGTCTCCAGAGTCT	476
DB	544	CAAAAGACAGTTGATTCGACGGGTATGAGCCCGAGTGGTCCGACAGTCTCCAGAGTCTCC	603
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DB	604	TGCAAGCTTGGCCCCCGACCGATGTGACGCTGGGGGACGAGCTCCACTTAGACGGGAG	663
QY	477	-----	476

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QY	477	-----	476
Db	724	GGGGATTCCCAGGTCCGGATTTTACCCCCACGACTCCGCCCTTACGGCGCTCTGGAT	783
QY	477	-----	476
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QY	477	-----CACGTGCAAGAACAAAAAGAGAAAGCAAGAGAAAAAGAAAGCAAACTG	531
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QY	1192	GAGGAATCCAGAGATACCTTGAAGACGCTCGGGTGTACATTTTAAATCAGCACAGC	1251
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QY	1252	CGCTCGCTCGCTCGCGCGTGTCTGTCGCAAGATCTCTCGCGGTGTGACGGAATCTGCC	1311
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RESULT 14
AX555327
LOCUS
DEFINITION
AX555327
ACCESSION
VERSION
AX555327.1 GI:25898846
KEYWORDS
SYNTHETIC CONSTRUCT
ORGANISM
Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and
Johnson,B.D.
TITLE
Control of gene expression in plants
JOURNAL
Patent: WO 02061102-A 79 08-AUG-2002;
Syngenta Participations AG (CH)
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AX555327
Sequence 79 from Patent WO02061102.
PAT 27-NOV-2002
linear
1533 bp
DNA
AX555327
GI:25898846
synthetic construct
synthetic construct
other sequences; artificial sequences.

AX555327
Sequence 79 from Patent WO02061102.
PAT 27-NOV-2002
linear
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DNA
AX555327
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PAT 27-NOV-2002
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Sequence 79 from Patent WO02061102.
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AX555327
Sequence 79 from Patent WO02061102.
PAT 27-NOV-2002
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AX555327
Sequence 79 from Patent WO02061102.
PAT 27-NOV-2002
linear
1533 bp
DNA
AX555327
GI:25898846
synthetic construct
synthetic construct
other sequences; artificial sequences.

QY 810 AACTGACATGCCCTTCGGTCAGATCACAGAGATGACGATCTTAAACAGTGCAGCTTATTGT 869
DB 881 AACTGACATGCCCTTCGGTCAGATCACAGAGATGACGATCTTAAACAGTGCAGCTTATTGT 740
QY 870 AGAATTCGAAAGGAGACTACCGGATCTTCAAGATATCTCAGTCCGATCAATACATTT 929
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DB 801 ATTAAGCGCTCATCAAGCGAAGTGATGCTCGAGTGGCGACGGTACGACGCGCGC 860
QY 990 GACGACAGCGTCTGTTTCGCGAACAACCGAGCGGTACACGCGCGCACTACCGCAAGC 1049
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RESULT 15
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LOCUS
DEFINITION
Sequence 65 from Patent WO02061102.
ACCESSION
AX555313
VERSION
AX555313.1 GI:25898832
KEYWORDS
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
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ORIGIN

Query Match 66.8%; Score 1109.8; DB 6; Length 1533;
Best Local Similarity 92.8%; Pred. No. 2.7e-226;
Matches 1181; Conservative 0; Mismatches 77; Indels 15; Gaps 1;
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QY 465 COTCCAGAGTCCAGTCAAGAACAAAGAGAGAGAAAGAGAGACAGAGAGAAAGA 524
DB 321 GGTGCCAGAAACGACAGTGTGCGCAAAAGAGAGAGAAAGAGAGAGAGAGAAAGA 380
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QY 690 GAACAGAGTCTCTGATCCGAGGCTCGTGTGCTACGAGGAGGAGTACGAGCAGCGCTC 749
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QY 750 GGAGGAGAGTCTCAAGAGAGTTACACAGCATGCGCAGTTAGAGAGAGAGAGAGAGGA 809
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Qy	1520	TGACATGTTTGGG	GACGGGATTCGCCGGGTCCGGATTTACCCCGACGACTCCGCC	1579
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Search completed: April 14, 2005, 15:39:53				
Job time : 7234.52 secs				

AUTHORS Pascal,E.J., Valentine,S.A., Brown,J.A., Cockrell,A.S. and Johnson,B.D.
TITLE Control of gene expression in plants
JOURNAL Patent: WO 02061102-A 65 08-AUG-2002; Syngenta Participations AG (CH)
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ORIGIN
 Query Match 59.9%; Score 996.2; DB 6; Length 1509;
 Best Local Similarity 89.6%; Pred. No. 4.9e-202;
 Matches 1096; Conservative 0; Mismatches 118; Indels 9; Gaps 2;
 Qy 440 CGACGGCGTATGAGGCCGCGAGTCGGTCGTCCAGAGTCCACGTCAAGAAACAAAGAAGAG 499
 Db 296 CGTGGGCATGAGGCCGCGAGTCGGTCGTCCAGAGTCCACGTCAAGAAACAAAGAAGAG 355
 Qy 500 AAAAGGAAGCACAGAGAGAAAAAGACAACTGCCAGTACGACAGCAGTGGACGATC 559
 Db 356 AAAAGGAAGCACAGAGAGAAAAAGACAACTGCCAGTACGACAGCAGTGGACGATC 415
 Qy 560 ATATGCTCGCATAATGCAATGTGACCTCCGCCCCAGAGGGCGGAAGATTACGAAG 619
 Db 416 ATATGCTCGCATAATGCAATGTGACCTCCGCCCCAGAGGGCGGAAGATTACGAAG 475
 Qy 620 TGGTCCCGAGGTTCTCTAAGCAGGAAGCTAATGAGCAGAGAAACAGACTGTGAACGC 679
 Db 476 TGGTCCCGAGGTTCTCTAAGCAGGAAGCTAATGAGCAGAGAAACAGACTGTGAACGC 535
 Qy 680 CGCTGTCCGGCAACCAAGTCCCTGATCCGAGGCTCGTGTGTTACAGAGGGGGGTACG 739
 Db 536 CGCTGTCCGGCAACCAAGTCCCTGATCCGAGGCTCGTGTGTTACAGAGGGGGGTATG 595
 Qy 740 AGCAGCCGTCCGGAGGAAGATCTCAAGAGAGTTTACAGACATGGCAGTTTGAAGAAGAAG 799
 Db 596 AACAACTTTCAGAGGAAGACTCAAGAGGGGTGACGAGACTTGGCAGTCGACAGGATG 655
 Qy 800 AAGAGGAGGAAACTGACATGCCCTTCGTCAGATCAAGAGATGACATCTTAAACAGTGC 859
 Db 656 AAGAGGAGTCA---GATATGCCGTTCCGCCAGATCACCGAGATGACGATCCTGACAGTTC 712
 Qy 860 AGCTTTATTGTAGAAATTCGAAAGGAGCTACCGGATTTCTCAAAGATATCTCAGTCCGATC 919
 Db 713 AACTCATGCTAGAATTCGAAAGAGCCCTGCCAGGCTTCGCCAAGATCTGCAGTCGATC 772
 Qy 920 AAATTACATTATTAAAGCGGTCAACAGCGAAGTGATGATGCTGCGAGTGGCGGACGGT 979
 Db 773 AAATCAGTGTACTTAAAGCGGTGTTTCAAGTGAGGTGATGATGCTCCGAGTGGCCCGCGGT 832
 Qy 980 ACAGCGGGCGGACGACAGCGTGTGTTTTCGCGAAACAACAGGGCGTACACGCGGCAACAAC 1039
 Db 833 ACGACGGGGCCACCGACAGCGTACTGTTTCGCGCAACAACAGGGCGTACTCCGCGGCAACAAC 892
 Qy 1040 ACCGCAAGGGCGGCGATGCTCTACGTCATCGAGGACCTGTGTCATCTCTGTGGGTGTATGT 1099

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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 08:10:36 ; Search time 914.987 Seconds
(without alignments)
10752.734 Million cell updates/sec

Title: US-10-087-167-104_COPY_2007_3668
Perfect score: 1662
Sequence: 1 atgaagctactgtcttctat.....ttgacgagtagcgggtag 1662

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 16Dec04: *
1: Geneseqn1980s: *
2: Geneseqn1990s: *
3: Geneseqn2000s: *
4: Geneseqn2001as: *
5: Geneseqn2001bs: *
6: Geneseqn2002as: *
7: Geneseqn2002bs: *
8: Geneseqn2003as: *
9: Geneseqn2003bs: *
10: Geneseqn2003cs: *
11: Geneseqn2003ds: *
12: Geneseqn2004as: *
13: Geneseqn2004bs: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1662	100.0	3972	6	ABT07353 Ecdysone
2	1662	100.0	3972	10	ADF49176 Ecdysone
3	1612.8	97.0	1767	6	ABT07368 Chimeric
4	1612.8	97.0	1767	10	ADF49194 Ecdysone
5	1552.2	93.4	1800	6	ABT07370 Chimeric
6	1552.2	93.4	1800	10	ADF49198 Ecdysone
7	1441.6	86.7	1776	6	ABT07366 Chimeric
8	1441.6	86.7	1776	10	ADF49190 Ecdysone
9	1431.8	86.1	1863	6	ABT07377 Chimeric
10	1431.8	86.1	1863	10	ADF49208 Ecdysone
11	1426.6	85.8	1848	6	ABT07376 Chimeric
12	1426.6	85.8	1848	10	ADF49206 Ecdysone
13	1425	85.7	1428	6	ABT07371 Chimeric
14	1425	85.7	1428	10	ADF49200 Ecdysone
15	1424	85.7	1767	6	ABT07367 Chimeric
16	1424	85.7	1767	10	ADF49192 Ecdysone
17	1422	85.6	1809	6	ABT07382 Chimeric
18	1422	85.6	1809	10	ADF49214 Ecdysone
19	1314.2	79.1	1782	6	ABT07369 Chimeric
20	1314.2	79.1	1782	10	ADF49196 Ecdysone

21	1216.6	73.2	1518	6	ABT07344
22	1216.6	73.2	1518	10	ADF49165 Ecdysone
23	1167.4	70.2	1500	6	ABT07332 Chimeric
24	1167.4	70.2	1500	10	ADF49141 Ecdysone
25	1166	70.2	1800	6	ABT07386 Chimeric
26	1166	70.2	1800	10	ADF49219 Ecdysone
27	1109.8	66.8	1533	6	ABT07337 Chimeric
28	1109.8	66.8	1533	10	ADF49151 Ecdysone
29	996.2	59.9	1509	6	ABT07330 Chimeric
30	996.2	59.9	1509	10	ADF49137 Ecdysone
31	978.6	58.9	1500	6	ABT07331 Chimeric
32	978.6	58.9	1500	10	ADF49139 Ecdysone
33	976.6	58.8	2840	6	ABT07274 Manduca s
34	976.6	58.8	2840	10	ADF49073 Manduca s
35	976.6	58.8	2840	12	ADI33132 Tobacco h
36	954.6	57.4	1551	6	ABT07333 Chimeric
37	954.6	57.4	1551	10	ADF49143 Ecdysone
38	954.6	57.4	1566	6	ABT07342 Chimeric
39	954.6	57.4	1566	10	ADF49161 Ecdysone
40	951.8	57.3	1464	6	ABT07339 Chimeric
41	951.8	57.3	1464	10	ADF49155 Ecdysone
42	893.4	53.5	1524	6	ABT07336 Chimeric
43	893.4	53.5	1524	10	ADF49149 Ecdysone
44	871.8	52.5	1515	6	ABT07335 Chimeric
45	871.8	52.5	1515	10	ADF49147 Ecdysone

ALIGNMENTS

RESULT 1
ABT07353
ID ABT07353 standard; DNA; 3972 BP.

AC ABT07353;

DT 07-NOV-2002 (first entry)

DE Ecdysone receptor containing vector pCGS202 DNA SEQ ID NO: 104.

XX Plant; gene expression control; insect; hormone receptor; fertility;
KW ecdysone receptor; gene; ds.

XX Synthetic.

PN WO200261102-A2.

PD 08-AUG-2002.

PF 24-OCT-2001; 2001WO-US051417.

PR 24-OCT-2000; 2000US-0242969P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

XX WPI; 2002-619259/66.

XX P-PSDB; ABJ05371.

XX New receptor cassette encoding a chimeric receptor polypeptide, useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility.

XX Claim 28; Page 255-258; 319pp; English.

XX The present invention relates to a receptor cassette encoding a chimeric receptor polypeptide comprising at least one DNA binding domain, a hinge domain of an ecdysone receptor (ECR) of an insect, a ligand binding domain of an insect ECR, where the ligand binding domain is heterologous with respect to the hinge domain and an activation domain. The chimeric insect hormone receptors and receptor cassettes are useful in regulating expression of target polypeptides in plants in the presence of

CC	appropriate ligands that may be used in controlling plant fertility. The	
CC	method is useful for decreasing or increasing plant gene expression. The	
CC	present sequence is a coding sequence described in the exemplification of	
CC	the invention	
XX		
SQ	Sequence 3972 BP; 1027 A; 895 C; 929 G; 1121 T; 0 U; 0 Other;	
	Query Match 100.0%; Score 1662; DB 6; Length 3972;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 1662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ATGAAGCTACTGCTCTCTATCGAACAGCATGCGATATTGCGGACCTTAAAGAGCTCAAG 60	
DB	2007 ATGAAGCTACTGCTCTCTATCGAACAGCATGCGATATTGCGGACCTTAAAGAGCTCAAG 2066	
QY	61 TGCTCCAAAGAAAACCGAAGTGGCCAAAGTGTCTGAAGAACAACTGGGAGTGTGCTAC 120	
DB	2067 TGCTCCAAAGAAAACCGAAGTGGCCAAAGTGTCTGAAGAACAACTGGGAGTGTGCTAC 2126	
QY	121 TCTCCAAAACCAAAGTCTCGCTGACTAGGGGACATCTGACAGAAAGTGGATCAAGG 180	
DB	2127 TCTCCAAAACCAAAGTCTCGCTGACTAGGGGACATCTGACAGAAAGTGGATCAAGG 2186	
QY	181 CTGAAGACACTGGAACAGCTATTTCTACTGATTTTCTCGAGAGACCTTTGACATGATT 240	
DB	2187 CTGAAGACACTGGAACAGCTATTTCTACTGATTTTCTCGAGAGACCTTTGACATGATT 2246	
QY	241 TTGAAAATGGATTCTTTTACAGGATATAAAGCATTTGTTAAACAGGATTTTGTACAAGAT 300	
DB	2247 TTGAAAATGGATTCTTTTACAGGATATAAAGCATTTGTTAAACAGGATTTTGTACAAGAT 2306	
QY	301 AATGTGAATAAAGATGCGGTACAGATAGATTGGCTTCAGTGGAGACTGATGCTCTTA 360	
DB	2307 AATGTGAATAAAGATGCGGTACAGATAGATTGGCTTCAGTGGAGACTGATGCTCTTA 2366	
QY	361 ACATTGAGACACATAGATAAGTCCGACATCATCTCGAAGAGAGTAGTAACAAGGT 420	
DB	2367 ACATTGAGACACATAGATAAGTCCGACATCATCTCGAAGAGAGTAGTAACAAGGT 2426	
QY	421 CAAAGACAGTTGACTGTATCGACGGTATAGAGCCCGAGTGGTCCGACAGATCCACG 480	
DB	2427 CAAAGACAGTTGACTGTATCGACGGTATAGAGCCCGAGTGGTCCGACAGATCCACG 2486	
QY	481 TCGAAGAACAAAGAGAGAAAGAACACACAGAGAGAAAGACAAACTGCCAGTCAGT 540	
DB	2487 TCGAAGAACAAAGAGAGAGAAAGAACACACAGAGAGAAAGACAAACTGCCAGTCAGT 2546	
QY	541 ACGACACAGTGGACGATCATATGCTGCTAATATGCAATGTGACCTCCGCCCCCAGAG 600	
DB	2547 ACGACACAGTGGACGATCATATGCTGCTAATATGCAATGTGACCTCCGCCCCCAGAG 2606	
QY	601 GCGGCAAGGATTACGAAGTGTCCGAGGTTCTTAAACGAGAGACTAATGGAGCAGAAC 660	
DB	2607 GCGGCAAGGATTACGAAGTGTCCGAGGTTCTTAAACGAGAGACTAATGGAGCAGAAC 2666	
QY	661 AGACTGAAGAAATGTACGCGGCTGTGCGGAAACCAAGAGTCCCTGATCGGAGGTCGTG 720	
DB	2667 AGACTGAAGAAATGTACGCGGCTGTGCGGAAACCAAGAGTCCCTGATCGGAGGTCGTG 2726	
QY	721 TGTGTACAGAGGGGTACGAGCAGCGCTCGGAGGAAGATCTCAAGAGAGTTTACACAGACA 780	
DB	2727 TGTGTACAGAGGGGTACGAGCAGCGCTCGGAGGAAGATCTCAAGAGAGTTTACACAGACA 2786	
QY	781 TGGCAGTTAGAGAAAGAGAGAGGAGAACTGACATGCCCTTCGTCAGATTCACAGAG 840	
DB	2787 TGGCAGTTAGAGAAAGAGAGAGGAGAACTGACATGCCCTTCGTCAGATTCACAGAG 2846	
QY	841 ATGACCATCTTACAGTGCAGCTTATTGTAGAAATTCGCAAGAGGACTACCGGATTTCTCC 900	
DB	2847 ATGACCATCTTACAGTGCAGCTTATTGTAGAAATTCGCAAGAGGACTACCGGATTTCTCC 2906	
QY	901 AAGATATCTCAGTCCCATCAAAATTACATTTATTAAGGCGCTCATCAAGCGAAGTGTATG 960	

Db	2907 AAGATATCTCAGTCCGATCAAAATTATTAAGGCGCTCATCAAGCGAAGTGTATGATG 2966
QY	961 CTGCGAGTGGCGGACGGTACGACGGCGGACGGACAGCGTGTGTTCCGAAACACACAG 1020
Db	2967 CTGCGAGTGGCGGACGGTACGACGGCGGACGGACAGCGTGTGTTCCGAAACACACAG 3026
QY	1021 GGTTACACGCGGACAACTACCGCAAGGCGGCGATGTCTCTAGCTCATCAGGACCTGCTG 1080
Db	3027 GGTTACACGCGGACAACTACCGCAAGGCGGCGATGTCTCTAGCTCATCAGGACCTGCTG 3086
QY	1081 CACTTCTGCGGTATGATCTCATATGAGCATGGAACAATGTGCATCTACGGCTGCTCACC 1140
Db	3087 CACTTCTGCGGTATGATCTCATATGAGCATGGAACAATGTGCATCTACGGCTGCTCACC 3146
QY	1141 GCCATCGTTATATTTCTCAGACCGGCGGCGCTCGAGCAACCCCTTTTAGTGAGGAAATC 1200
Db	3147 GCCATCGTTATATTTCTCAGACCGGCGGCGCTCGAGCAACCCCTTTTAGTGAGGAAATC 3206
QY	1201 CAGAGATACCTACTTGAAGACGCTGCGGGTTTACATTTTAAATCAGCACAGCGGCTGCT 1260
Db	3207 CAGAGATACCTACTTGAAGACGCTGCGGGTTTACATTTTAAATCAGCACAGCGGCTGCT 3266
QY	1261 CGTGGCGGCTGCTGTTCCGCAAGATCTCGGCGTCTGACGAACTGCGCACGCTCGGC 1320
Db	3267 CGTGGCGGCTGCTGTTCCGCAAGATCTCGGCGTCTGACGAACTGCGCACGCTCGGC 3326
QY	1321 ACCGAGAACTCCAAACATGTGCATCTCGCTGAAGTCAAGAACAGGAAACTTCCGCCATT 1380
Db	3327 ACCGAGAACTCCAAACATGTGCATCTCGCTGAAGTCAAGAACAGGAAACTTCCGCCATT 3386
QY	1381 CTCGAGGAGATCTGGGACGTGGCCGAAGTGTGACGACGAAGCTTGCCGCCCGCCGCGAT 1440
Db	3387 CTCGAGGAGATCTGGGACGTGGCCGAAGTGTGACGACGAAGCTTGCCGCCCGCCGCGAT 3446
QY	1441 GTCAGCTGGGGACGACGCTCCACTTAGACGGCGAGACGTGCGCATGGCGCATGCCGAC 1500
Db	3447 GTCAGCTGGGGACGACGCTCCACTTAGACGGCGAGACGTGCGCATGGCGCATGCCGAC 3506
QY	1501 GCGCTAGACCATTTCCGATCTGGACATGTTGGGGGACGGGATTTCCCGGGTCCGGGATTT 1560
Db	3507 GCGCTAGACCATTTCCGATCTGGACATGTTGGGGGACGGGATTTCCCGGGTCCGGGATTT 3566
QY	1561 ACCCCCCACACGACTCCGCCCCCTACGGCGCTCTGGATATGGCCGACTTCGAGTTTGAGCAG 1620
Db	3567 ACCCCCCACACGACTCCGCCCCCTACGGCGCTCTGGATATGGCCGACTTCGAGTTTGAGCAG 3626
QY	1621 ATGTTTACCGATGCCCTTGAATTTGACGAGTACGTTGGGTAG 1662
Db	3627 ATGTTTACCGATGCCCTTGAATTTGACGAGTACGTTGGGTAG 3668

RESULT 2

ADF49176

ID ADF49176 standard; DNA; 3972 BP.

XX

AC ADF49176;

XX AC

DT 12-FEB-2004 (first entry)

XX

DE Ecdysone receptor/VP16 transactivation domain DNA seq id 104.

XX

KW receptor cassette; chimeric receptor polypeptide; DNA binding domain;

KW hinge domain; ecdysone receptor; Ecr; ligand binding domain;

KW activation domain; transgenic seed; transgenic plant; plant line;

KW herbicide; pesticide; chimeric ecdysone receptor; Ecr;

KW yeast GAL4 DNA binding domain; VP16 transactivation domain; ds; gene.

XX Synthetic.

OS Manduca sexta.

OS Ascomycota.

OS Herpes simplex virus unknown type.

XX

PN US2003154509-A1.

||||| 3567 ACCCCACGACTCGGCCCTACGGGCTCTGGATATGGCCGACTTCGAGTTTGACGAG 3626
Db
||||| 1621 ATGTTTACCGATGCCCTTGGAAATTGACGAGTACGGTGGTAG 1662
Qy
||||| 3627 ATGTTTACCGATGCCCTTGGAAATTGACGAGTACGGTGGTAG 3668
Db

RESULT 3
ID ABT07368
XX ABT07368 standard; DNA; 1767 BP.
AC ABT07368;
XX
DT 29-AUG-2003 (revised)
DT 07-NOV-2002 (first entry)
XX
XX Chimeric ecdysone receptor coding sequence SEQ ID NO: 122.
XX
XX Plant; gene expression control; insect; hormone receptor; fertility;
KW ecdysone receptor; gene; ds.
XX
XX Manduca sexta.
OS Spodoptera frugiperda.
OS Chimeric.
XX
XX WO200261102-A2.
XX
XX 08-AUG-2002.
XX
XX 24-OCT-2001; 2001WO-US051417.
XX
XX 24-OCT-2000; 2000US-0242969P.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX WPI; 2002-619259/66.
XX P-PSDB; ABJ05374.
DR
XX
XX
XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
PT regulating expression of target polypeptides in plants in the presence of
PT appropriate ligands that may be used in controlling plant fertility.
XX
XX Example 23; Page 275-278; 319pp; English.
XX
XX The present invention relates to a receptor cassette encoding a chimeric
CC receptor polypeptide comprising at least one DNA binding domain, a hinge
CC domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
CC domain of an insect Ecr, where the ligand binding domain is heterologous
CC with respect to the hinge domain and an activation domain. The chimeric
CC insect hormone receptors and receptor cassettes are useful in regulating
CC expression of target polypeptides in plants in the presence of
CC appropriate ligands that may be used in controlling plant fertility. The
CC method is useful for decreasing or increasing plant gene expression. The
CC present sequence is a coding sequence described in the exemplification of
CC the invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX
SQ Sequence 1767 BP; 476 A; 431 C; 477 G; 383 T; 0 U; 0 Other;

Query Match 97.0%; Score 1612.8; DB 6; Length 1767;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1642; Conservative 0; Mismatches 2; Indels 18; Gaps 1;

Qy 1 ATGAAGCTACTGCTTCTATCGAACCAAGCATGCGATATTTGCGGACTTAAAAGCTCAAG 60
Db 124 ATGAAGCTACTGCTTCTATCGAACCAAGCATGCGATATTTGCGGACTTAAAAGCTCAAG 183
Qy 61 TGTCTCAAGAAACCGAGTGCCTCAAGTGTCTGAAGAACCACTGGGAGTGTGCTAC 120
Db 184 TGTCTCAAGAAACCGAGTGCCTCAAGTGTCTGAAGAACCACTGGGAGTGTGCTAC 243

Qy 121 TCTCCCAAAACCAAAAGGTCTCGCTGACTAGGCGACATCTGACAGAAGTGAATCAAG 180
Db 244 TCTCCCAAAACCAAAAGGTCTCGCTGACTAGGCGACATCTGACAGAAGTGAATCAAG 303
Qy 181 CTAGAAAGACTGGAAACAGCTATTTCTGAATTTTCTCGAGAAACCTTGACATGATT 240
Db 304 CTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTCTCGAGAAACCTTGACATGATT 363
Qy 241 TTGAAAATCGATCTTTTACAGGATATAAAGCATTTGTTAAACAGGATTTATTGTACAAGAT 300
Db 364 TTGAAAATCGATCTTTTACAGGATATAAAGCATTTGTTAAACAGGATTTATTGTACAAGAT 423
Qy 301 AATGTGAATAAAGATGCCGTACAGATAGATTGGCTTTCAGTGGAGACTGATATGCCCTCTA 360
Db 424 AATGTGAATAAAGATGCCGTACAGATAGATTGGCTTTCAGTGGAGACTGATATGCCCTCTA 483
Qy 361 ACATTGAGACAGCATAGAATAAGTGCAGATCATCATTCGGAAGAGAGTAGTAAACAAGGT 420
Db 484 ACATTGAGACAGCATAGAATAAGTGCAGATCATCATTCGGAAGAGAGTAGTAAACAAGGT 543
Qy 421 CAAAGACAGTTGACTGTATCGACGCGTATGAGGCCGAGTGCCTGCTCCAGAGTCCACG 480
Db 544 CAAAGACAGTTGACTGTATCGACGCGTATGAGGCCGAGTGCCTGCTCCAGAGTCCACG 603
Qy 481 TGCAAGAAACAAAGAGAGAGAAAAGGAAGCAACAGAGAGAAAACAAACTGCCAGTCAGT 540
Db 604 TGCAAGAAACAAAGAGAGAGAAAAGGAAGCAACAGAGAGAAAACAAACTGCCAGTCAGT 663
Qy 541 ACAGACAGTGGACGATCATATGCTGCCATATGCTGCAATATGCAATGTCACCTCCGCCAGAG 600
Db 664 ACAGACAGTGGACGATCATATGCTGCCATATGCTGCAATATGCAATGTCACCTCCGCCAGAG 723
Qy 601 GCGCAAGGATTCCAGAAAGTGGTCCCGAGGTTCTTAACGGAGAGAGTAAATGGAGCAAGAC 660
Db 724 GCGCAAGGATTCCAGAAAGTGGTCCCGAGGTTCTTAACGGAGAGAGTAAATGGAGCAAGAC 783
Qy 661 AGACTGAAGAAATGTGACCGCGCTGTGCGCGAAACAGAAAGTCCCTGATCGGAGGCTCGTG 720
Db 784 AGACTGAAGAAATGTGACCGCGCTGTGCGCGAAACAGAAAGTCCCTGATCGGAGGCTCGTG 843
Qy 721 TGCTACAGAGGGGTACGAGCAGCGCTCGGAGAGAGATCTCAAGAGAGTTTACACAGACA 780
Db 844 TGCTACAGAGGGGTACGAGCAGCGCTCGGAGAGAGATCTCAAGAGAGTTTACACAGACA 903
Qy 781 TGGCAGTTAGAAAGAAAGAGAGAGGAGAACTGCATGCGCTTCCGTCAGATCACAAG 840
Db 904 TGGCAGTTAGAAAGAAAGAGAGAGGAGAACTGCATGCGCTTCCGTCAGATCACAAG 963
Qy 841 ATGACGATCTTAACAGTGCAGCTTATTTGTAAGATTTCGAAAGGAGTACCGGGATTTCTCC 900
Db 964 ATGACGATCTTAACAGTGCAGCTTATTTGTAAGATTTCGAAAGGAGTACCGGGATTTCTCC 1023
Qy 901 AAGATATCTCAGTCCGATCAAAATTTACATTTAAAGCGCTCATCAAGCGAAGTGATGATG 960
Db 1024 AAGATATCTCAGTCCGATCAAAATTTACATTTAAAGCGCTCATCAAGCGAAGTGATGATG 1083
Qy 961 CTGCGAGTGGCGGACGCGTACGACGCGGCGAGCAGAGCGTGTGTTTCGCGAAACCAACG 1020
Db 1084 CTGCGAGTGGCGGACGCGTACGACGCGGCGAGCAGAGCGTGTGTTTCGCGAAACCAACG 1143
Qy 1021 GCGTACAGCGCGCAACTACCGCAGCGGCGATGCTTACGTCATCGAGAGCTGCTG 1080
Db 1144 GCGTACAGCGCGCAACTACCGCAGCGGCGATGCTTACGTCATCGAGAGCTGCTG 1203
Qy 1081 CACTTCTGTCGGTGTATGTACTCCATGAGCATGGACAATGTGCACTACGCGCTGCTACC 1140
Db 1204 CACTTCTGTCGGTGTATGTACTCCATGAGCATGGACAATGTGCACTACGCGCTGCTACC 1263
Qy 1141 GCGATCGTATATTTCTAGACCGCGCGCTCCAGCAACCCCTTTTAGTGGAGGAAATC 1200
Db 1264 GCGATCGTATATTTCTAGACCGCGCGCTCCAGCAACCCCTTTTAGTGGAGGAAATC 1323
Qy 1201 CAGAGATACTACTTGAAGACGCTCGGGGTTTACATTTTAAATCAGACAGCGCGCTCGCT 1260

Db 1324 CAGAGATACTACTTGAAGACGCTGGGGTTTACATTTTAAATCAGTACAGCGCTCGCT 1383
Qy 1261 CGCTGGCGCTGCTGTTGGCAAGATCTCTGGCGTGTGACGGAACCTGGGACGCTCGGC 1320
Db 1384 CGCTGGCGCTGCTGTTGGCAAGATCTCTGGCGTGTGACGGAACCTGGGACGCTCGGC 1443
Qy 1321 AGCGAGAACTCAACATGTCATCTGCTGAAGCTGMAAGACAGGAACTTCCGCCATTTC 1380
Db 1444 AGCGAGAACTCAACATGTCATCTGCTGAAGCTGMAAGACAGGAACTTCCGCCATTTC 1503
Qy 1381 CTCGAGGAGATCTGGGACGCTGGCGAAGTGTGACGACGAACTTGGCCCCCGACCGAT 1440
Db 1504 CTCGAGGAGATCTGGGACGCT-----GAACTTGGCCCCCGACCGAT 1545
Qy 1441 GTGAGCTGGGGACGAGCTTCACTTAGACGCGGAGAGCTGGCGATGCGGATCGGAC 1500
Db 1546 GTGAGCTGGGGACGAGCTTCACTTAGACGCGGAGAGCTGGCGATGCGGATCGGAC 1605
Qy 1501 GGGCTAGACGATTCGATCTGACATGTTGGGGGACGGGATTCGCCGGTCCGGGATTT 1560
Db 1606 GGGCTAGACGATTCGATCTGACATGTTGGGGGACGGGATTCGCCGGTCCGGGATTT 1665
Qy 1561 ACCCCACGACTCGGCCCTTACGCGCTCTGGATATGCGCGACTTCGAGTTTGAGCAG 1620
Db 1666 ACCCCACGACTCGGCCCTTACGCGCTCTGGATATGCGCGACTTCGAGTTTGAGCAG 1725
Qy 1621 ATGTTTACCGATGCCCTTGGAAATTGACGAGTACGGTGGGTAG 1662
Db 1726 ATGTTTACCGATGCCCTTGGAAATTGACGAGTACGGTGGGTAG 1767

RESULT 4
ADP49194
ID ADP49194 standard; DNA; 1767 BP.
XX AC ADP49194;
XX AC
XX AC
DT 12-FEB-2004 (first entry)
XX Ecdysone receptor/VP16 transactivation domain DNA seq id 122.
DE receptor cassette; chimeric receptor polypeptide; DNA binding domain;
KW hinge domain; ecdysone receptor; ECR; ligand binding domain;
KW activation domain; transgenic seed; transgenic plant; plant line;
KW herbicide; pesticide; chimeric ecdysone receptor; ECR;
KW yeast GAL4 DNA binding domain; VP16 transactivation domain; ds; gene.
XX
OS Synthetic.
OS Manduca sexta.
OS Ascomycota.
OS Spodoptera frugiperda.
OS Herpes simplex virus unknown type.
XX US2003154509-A1.
PN
XX 14-AUG-2003.
PD
XX 24-OCT-2001; 2001US-00087167.
XX 24-OCT-2001; 2001US-00087167.
PR
XX (PASC/) PASCAL E J.
PA (VALE/) VALENTINE S A.
PA (BROW/) BROWN J A.
PA (COCK/) COCKRELL A S.
PA (JOHN/) JOHNSON B D.
XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
PI WPI; 2003-897756/82.
XX P-PSDB; ADP49195.

PT New receptor cassette encoding a chimeric receptor polypeptide, useful
PT for regulating the expression of target polypeptides in plants in the
PT presence of appropriate chemical ligands.
XX Example 23; SEQ ID NO 122; 186pp; English.
XX
CC The invention describes a receptor cassette encoding a chimeric receptor
CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
CC (D) domain of an ecdysone receptor (ECR) of an insect, a ligand binding
CC (E) domain that is heterologous with respect to the D domain, and an
CC activation domain. The receptor cassette and method are useful in
CC regulating the expression of target polypeptides in plants in the
CC presence of appropriate chemical ligands. The transgenic seeds and plants
CC can be used for the breeding of improved plant lines that, for e.g.,
CC increase the effectiveness of conventional methods such as herbicide or
CC pesticide treatment. This sequence encodes an ecdysone receptor-VP16
CC transactivation domain fusion protein.
XX
SQ Sequence 1767 BP; 476 A; 431 C; 477 G; 383 T; 0 U; 0 Other;
Query Match 97.0%; Score 1612.8; DB 10; Length 1767;
Best Local Similarity 98.8%; Pred No. 0;
Matches 1642; Conservative 0; Mismatches 2; Indels 18; Gaps 1;
Qy 1 ATGAAGCTACTGTCTTCTATCGAACCAAGCATGCGATATTTGCCGACTTAAAAAGCTCAAG 60
Db 124 ATGAAGCTACTGTCTTCTATCGAACCAAGCATGCGATATTTGCCGACTTAAAAAGCTCAAG 183
Qy 61 TGCTCCAAAGAAAAACCGAAGTGCCTCAAGTGTCTGMAAGAACACTGGGAGTGCCTAC 120
Db 184 TGCTCCAAAGAAAAACCGAAGTGCCTCAAGTGTCTGMAAGAACACTGGGAGTGCCTAC 243
Qy 121 TCTCCCAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGCAGAACTGGAATCAAGG 180
Db 244 TCTCCCAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGCAGAACTGGAATCAAGG 303
Qy 181 CTAGAAAGACTGGAACAGCTATTTCTACTGATTTTCTCTGAGAGAGACTTGCATGATTT 240
Db 304 CTAGAAAGACTGGAACAGCTATTTCTACTGATTTTCTCTGAGAGAGACTTGCATGATTT 363
Qy 241 TTGAAATGGATTTCTTACAGGATATAAAGCATTTTAAACAGGATTTTGTACAGAT 300
Db 364 TTGAAATGGATTTCTTACAGGATATAAAGCATTTTAAACAGGATTTTGTACAGAT 423
Qy 301 AATGTGAATAAAGATGCGCTGACAGATAGATTTGGCTTCACTGGAGACTGATATGCTCTA 360
Db 424 AATGTGAATAAAGATGCGCTGACAGATAGATTTGGCTTCACTGGAGACTGATATGCTCTA 483
Qy 361 ACATTTGAGACAGCATAGATAAAGTGCACATCATCATATCGAAGAGAGATGATAAAGGT 420
Db 484 ACATTTGAGACAGCATAGATAAAGTGCACATCATCATCGAAGAGAGATGATAAAGGT 543
Qy 421 CAAAGACAGTTGACTGTATTCGACGGTATGAGCCCGAGTGGCTCTCCAGAGTCCACG 480
Db 544 CAAAGACAGTTGACTGTATTCGACGGTATGAGCCCGAGTGGCTCTCCAGAGTCCACG 603
Qy 481 TGCAGAAACAAAGAGAGAGAAAGGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 604 TGCAGAAACAAAGAGAGAGAGAAAGGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 663
Qy 541 ACAGCAGAGTGGACGATCATATGCTGCGCATATGCAATGTGACCTCGCCCCCAGAG 600
Db 664 ACAGCAGAGTGGACGATCATATGCTGCGCATATGCAATGTGACCTCGCCCCCAGAG 723
Qy 601 GCGGCAAGGATTCAGAAAGTGGTCCGAGGTTCTTAACCGAGAGAGCTTAATGGAGCAGAC 660
Db 724 GCGGCAAGGATTCAGAAAGTGGTCCGAGGTTCTTAACCGAGAGAGCTTAATGGAGCAGAC 783
Qy 661 AGACTGAAGAAATGTGACGCGCTGTGCGGGAACAGAGAGTCCCTGATCGCGAGCTCGTG 720
Db 784 AGACTGAAGAAATGTGACGCGCTGTGCGGGAACAGAGAGTCCCTGATCGCGAGGCTCGTG 843
Qy 721 TGTATCAGAGAGGGGTACGAGCAGCGGTGCGAGAGAGAGATCTCAAGAGAGATTACAGACA 780

Db 484 ACAATTGAGACAGCATAGATTAAGTCCGACATCATCTCGAAGAGAGTAGTAACAAGGT 543
QY 421 CAAGACAGTTGACTGTATCGACGGTATGAGGCCGAGTGCCTCCAGAGTCCACG 480
Db 544 CAAGACAGTTGACTGTATCGACGGTATGAGGCCGAGTGCCTCCAGAGTCCACG 603
QY 481 TCAAGAACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTCAAGT 540
Db 604 TGTGCGCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTCAAGT 663
QY 541 AGCAGCAGATGACGATCATATGCTCCATAATGCAATGTGACCCCTCCGCCCCCAGAG 600
Db 664 ACACAGCAGATGACGATCATATGCCCAATCATGCAAGTGTGATCCACCAACCCCGGAG 723
QY 601 CGCGCAAGGATT-----CACGAAGTGTGTCGCCAGGTTTCTTAACGAGAGAG 645
Db 724 GCAGCGAGGATTCTGGAATGTTTGACGATGAAGTGTGTCGCCGCGTTCTCTCGGAGAG 783
QY 646 CTAATGGAGCAGACAGACTGAAGATGTGACCGCGCTGTGCGGCGAACCAGAGTCCCTG 705
Db 784 CTGATGGAGCAGAACTCGGCTGAAGAACATACCCCCCTCACCGCAACAGAGTTCCTG 843
QY 706 ATCGCGAGGCTGTGTGGTACAGAGGGGTACGAGAGCCCTCGAGGAAGATCTCAAG 765
Db 844 ATCGCGAGGCTGTGTGGTACAGAGGGGTACGAGAGCCCTCGAGGAAGATCTCAAG 903
QY 766 AGAGTTACACAGACATGCGAGTTAGAAAGAAAGAGAGAGAACTGACATGCCCCCTC 825
Db 904 AGAGTTACACAGACATGCGAGTTAGAAAGAAAGAGAGAGAACTGACATGCCCCCTC 963
QY 826 CTTAGATCACAGATGACGATCTTAACAGTGCAGCTTATTTAGATTTCCCAAGGGA 885
Db 964 CGTCAGATCACAGATGACGATCTTAACAGTGCAGCTTATTTAGATTTCCCAAGGGA 1023
QY 886 CTACCGGGATTCTCAAGATATCTCAGTCCGATCAAAATPACATTTATTAAGCGCTCATCA 945
Db 1024 CTACCGGGATTCTCAAGATATCTCAGTCCGATCAAAATPACATTTATTAAGCGCTCATCA 1083
QY 946 AGCGAAGTGATGATGCTGCGAGTGGCGGACGGTACGACGCGCGGACGACGCGTGTG 1005
Db 1084 AGCGAAGTGATGATGCTGCGAGTGGCGGACGGTACGACGCGCGGACGACGCGTGTG 1143
QY 1006 TTGCGGAACAACAGCGGTACAGCGCGCAACTACCGCAAGCGCGGCGATGCTTACGTC 1065
Db 1144 TTGCGGAACAACAGCGGTACAGCGCGCAACTACCGCAAGCGCGGCGATGCTTACGTC 1203
QY 1066 ATCGAGGACCTGCTGACCTTCTGTCGGTGTATGCTTCCATGAGCATGACATGTGCAC 1125
Db 1204 ATCGAGGACCTGCTGACCTTCTGTCGGTGTATGCTTCCATGAGCATGACATGTGCAC 1263
QY 1126 TAGCGCTGCTCACCGCCATCGTTATATTCTACAGCCGCCAGGCTTCGAGCAACCCCTT 1185
Db 1264 TAGCGCTGCTCACCGCCATCGTTATATTCTACAGCCGCCAGGCTTCGAGCAACCCCTT 1323
QY 1186 TTAGTGGAGAAATCAGAGATCTACTTGAAGACGCTGCGGTTTACATTTTAAATCAG 1245
Db 1324 TTAGTGGAGAAATCAGAGATCTACTTGAAGACGCTGCGGTTTACATTTTAAATCAG 1383
QY 1246 CACAGCGCTGCTGCTGCGCGCTGCTTTCGGAAGATCTTCGCGGTGCTGACGGAA 1305
Db 1384 CACAGCGCTGCTGCTGCGCGCTGCTTTCGGAAGATCTTCGCGGTGCTGACGGAA 1443
QY 1306 CTCGCAAGCTGCGCAGCGAGAACTCCAAATGTGATCTTCGTGAAGTGAAGAAACAGG 1365
Db 1444 CTCGCAAGCTGCGCAGCGAGAACTCCAAATGTGATCTTCGTGAAGTGAAGAAACAGG 1503
QY 1366 AAATCTCGCCATCTCTGAGGAGATCTGGAGTGGCCGAAGTGTGACGAGAGAGCTT 1425
Db 1504 AAATCTCGCCATCTCTGAGGAGATCTGGAGTGGCCGAAGTGTGACGAGAGAGCTT 1563
QY 1426 GCCCCCCCAGCAGTGTACGCTGGGGAGCAGCTCCACTTACAGCGCGAGGAGCTGGCG 1485

Db 1564 GCCCCCCCAGCAGGATGTGATGCTGGGGACAGGCTCCACTTAGACGGGAGACGTGGCG 1623
QY 1486 ATGCGGATCCGACGCGCTAGACGATTTTCGATCTGGACATGTTGGGGGACGGGATTC 1545
Db 1624 ATGCGGATCCGACGCGCTAGACGATTTTCGATCTGGACATGTTGGGGGACGGGATTC 1683
QY 1546 CCGGTCGCGGATTTTACCCCCACGACTCCGCCCTTACGGCGCTCTGGATATGCCGAC 1605
Db 1684 CCGGTCGCGGATTTTACCCCCACGACTCCGCCCTTACGGCGCTCTGGATATGCCGAC 1743
QY 1606 TTCGATTTGACGAGATGTTTACCGATGCCCTTGGAAATGACGATACGGTGGGTAG 1662
Db 1744 TTCGATTTGACGAGATGTTTACCGATGCCCTTGGAAATGACGATACGGTGGGTAG 1800

RESULT 6
ADF49198
ID ADF49198 standard; DNA; 1800 BP.
XX
AC ADF49198;
XX
DT 12-FEB-2004 (first entry)
XX
DE Ecdysone receptor/VP16 transactivation domain DNA seq id 126.
XX
KW receptor cassette; chimeric receptor polypeptide; DNA binding domain;
KW hinge domain; ecdysone receptor; Ecr; ligand binding domain;
KW activation domain; transgenic seed; transgenic plant; plant line;
KW herbicide; pesticide; chimeric ecdysone receptor; Ecr;
KW yeast GAL4 DNA binding domain; VP16 transactivation domain; ds; gene.
XX
OS Synthetic.
OS Ostrinia nubilalis.
OS Ascomycota.
OS Manduca sexta.
OS Herpes simplex virus unknown type.
XX
PN US2003154509-A1.
XX
PD 14-AUG-2003.
XX
PF 24-OCT-2001; 2001US-00087167.
XX
PR 24-OCT-2001; 2001US-00087167.
XX
PA (PASC/) PASCAL E. J.
PA (VALE/) VALENTINE S. A.
PA (BROW/) BROWN J. A.
PA (COCK/) COCKRELL A. S.
PA (JOHN/) JOHNSON B. D.
XX
PI Pascal BJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
XX WPI; 2003-897756/82.
XX P-PSDB; ADF49199.
XX
PT New receptor cassette encoding a chimeric receptor polypeptide, useful
PT for regulating the expression of target polypeptides in plants in the
PT presence of appropriate chemical ligands.
XX
PS Example 23; SEQ ID NO 126; 186pp; English.
XX
CC The invention describes a receptor cassette encoding a chimeric receptor
CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
CC (D) domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
CC (E) domain that is heterologous with respect to the D domain, and an
CC activation domain. The receptor cassette and method are useful in
CC regulating the expression of target polypeptides in plants in the
CC presence of appropriate chemical ligands. The transgenic seeds and plants
CC can be used for the breeding of improved plant lines that, for e.g.,
CC increase the effectiveness of conventional methods such as herbicide or
CC pesticide treatment. This sequence encodes an ecdysone receptor-VP16
CC transactivation domain fusion protein.

XX	Sequence	1800 BP; 482 A; 444 C; 485 G; 389 T; 0 U; 0 Other;
QQ	Query Match	93.4%; Score 1552.2; DB 10; Length 1800;
QQ	Best Local Similarity	95.9%; Pred. No. 0;
QQ	Matches 1609; Conservative	0; Mismatches 53; Indels 15; Gaps 1;
QY	1	ATGAAGCTACTGTTCTTATCGAACAAGCATGCGATATTTGCCGACCTTAAAGACTCAAG 60
DB	124	ATGAAGCTACTGTTCTTATCGAACAAGCATGCGATATTTGCCGACCTTAAAGACTCAAG 183
QY	61	TGCTCCAAAGAAACCGAAGTGCAGAGTGTCTGAAGAACAACTGGAGTGTGCGTAC 120
DB	184	TGCTCCAAAGAAACCGAAGTGCAGAGTGTCTGAAGAACAACTGGAGTGTGCGTAC 243
QY	121	TCTCCAAAACCAAAAGGTCTCCGTGACTAGGGCACATCTGACAGAAGTGGAAATCAAG 180
DB	244	TCTCCAAAACCAAAAGGTCTCCGTGACTAGGGCACATCTGACAGAAGTGGAAATCAAG 303
QY	181	CTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTCTCGAAGAACCTTGCATGATT 240
DB	304	CTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTCTCGAAGAACCTTGCATGATT 363
QY	241	TTGAAATGGATCTTTTACAGATATAAAAGCATTTGTTAACAGGATTTATTTGTACAAGAT 300
DB	364	TTGAAATGGATCTTTTACAGATATAAAAGCATTTGTTAACAGGATTTATTTGTACAAGAT 423
QY	301	AATGTGAATAAGATGCCGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCCTCTA 360
DB	424	AATGTGAATAAGATGCCGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCCTCTA 483
QY	361	ACATTGAGACAGCATAGATAAGTCCGACATCATCTCGAAGAGAGTAGTAACAAGGT 420
DB	484	ACATTGAGACAGCATAGATAAGTCCGACATCATCTCGAAGAGAGTAGTAACAAGGT 543
QY	421	CAAGACAGTTGACTGTATCGACGGGTATGAGGCCGAGTGGTCCGAGAGTCCACG 480
DB	544	CAAGACAGTTGACTGTATCGACGGGTATGAGGCCGAGTGGTCCGAGAGTCCACG 603
QY	481	TGCAAGAAACAAAGAGAGAAAGAAAGACACAGAGAGAAAGACAACTGCCAGTCAAGT 540
DB	604	TGTGCGCAAAAGAAAGAGAGAAAGACACAGAGAGAAAGACAACTACCAGTGAAGC 663
QY	541	ACGACAGAGTGCAGCATATGCTGCCATATGCAATGTGACCTCCGCCCCCGAG 600
DB	664	ACGACAGAGTGCAGCATATGCTGCCATATGCAATGTGACCTCCGCCCCCGAG 723
QY	601	GGCGCAAGGATT-----CACGAAGTGGTCCGAGGTTCTTAAACGAGAAAG 645
DB	724	GGCGCAAGGATTCTGGAAATGTTTGACGATGAAGTGGTCCGCGGTTCTCTCGAGAAAG 783
QY	646	CTAATGGAGCAGACAGACTGAAGATGTGAGCCGCTGTGGCGAAGCAGAGTCCCTG 705
DB	784	CTAATGGAGCAGACAGACTGAAGATGTGAGCCGCTGTGGCGAAGCAGAGTCCCTG 843
QY	706	ATCGCGAGGCTCGTGTGTACAGAGGGGTACGAGCAGCCGTGGAGGAAAGATCTCAAG 765
DB	844	ATCGCGAGGCTCGTGTGTACAGAGGGGTACGAGCAGCCGTGGAGGAAAGATCTCAAG 903
QY	766	AGAGTTACACAGACATGGCAGTTAGAGAAGAAAGAGAGGAGAACTGACATGCCCTTC 825
DB	904	AGAGTTACACAGACATGGCAGTTAGAGAAGAAAGAGAGGAGAACTGACATGCCCTTC 963
QY	826	CGTCAGATCACAGAGATGACATCTTAACAGTGCAGCTTATTTGTAGAATTTCGCAAGGGA 885
DB	964	CGTCAGATCACAGAGATGACATCTTAACAGTGCAGCTTATTTGTAGAATTTCGCAAGGGA 1023
QY	886	CTACCGGGATTCTCCAAGATATCTCAGTCCGATCAAAATTACATTTAAAGGCGTCATCA 945
DB	1024	CTACCGGGATTCTCCAAGATATCTCAGTCCGATCAAAATTACATTTAAAGGCGTCATCA 1083
QY	946	AGCGAAGTGATGATGCTGCGAGTGGCGCAGCGGTACGACGCGCGCAGCAGCGTGTG 1005

DB	1084	AGCGAAGTGATGATGCTGCGAGTGGCGCGACGGTACGACCGCGCAGCAGCAGCGTGTG 1143
QY	1006	TTGCGGAACAACCGAGCGTACACGCGGACAACTACCGCAAGCGCGGATGCTTACGTC 1065
DB	1144	TTGCGGAACAACCGAGCGTACACGCGGACAACTACCGCAAGCGCGGATGCTTACGTC 1203
QY	1066	ATCGAGGACTGCTGACATTTCTGTCGGTGTATGTACTCCATGAGCATGGAACAATGTGCAC 1125
DB	1204	ATCGAGGACTGCTGACATTTCTGTCGGTGTATGTACTCCATGAGCATGGAACAATGTGCAC 1263
QY	1126	TACGCGCTGCTCACCGCCATCGTTATTTATTTCTGACGCGCGGAGCCCTCGAGCAACCCCTT 1185
DB	1264	TACGCGCTGCTCACCGCCATCGTTATTTATTTCTGACGCGCGGAGCCCTCGAGCAACCCCTT 1323
QY	1186	TTAGTGGAGGAATCCAGAGATACCTTTGAAGACGCTGCGGTTTACATTTTAAATCAG 1245
DB	1324	TTAGTGGAGGAATCCAGAGATACCTTTGAAGACGCTGCGGTTTACATTTTAAATCAG 1383
QY	1246	CACAGCGCTGCGCTCGCTCGCGCGTGTGTTTTCGCAAGATCCTCGCGTGTGCTGACGGAA 1305
DB	1384	CACAGCGCTGCGCTCGCTCGCGCGTGTGTTTTCGCAAGATCCTCGCGTGTGCTGACGGAA 1443
QY	1306	CTCGCAGCGTCCGCGACGAGAACTCCAAATGTCATCTCGCTGAAGCTGGAAGACAGG 1365
DB	1444	CTCGCAGCGTCCGCGACGAGAACTCCAAATGTCATCTCGCTGAAGCTGGAAGACAGG 1503
QY	1366	AAACTTCCGCGCATTTCTCGAGGAGATCTGGGAGCTGGCGAAGTGTGACGAGCAAGCTT 1425
DB	1504	AAACTTCCGCGCATTTCTCGAGGAGATCTGGGAGCTGGCGAAGTGTGACGAGCAAGCTT 1563
QY	1426	GCCTCCCGCAGCGATGTGAGCTGGGGACGAGCTCCATTAGACGCGCGAGGACGTGGCG 1485
DB	1564	GCCTCCCGCAGCGATGTGAGCTGGGGACGAGCTCCATTAGACGCGCGAGGACGTGGCG 1623
QY	1486	ATGCGCGATGCCAGCGCTAGACGATTTGATCTGACATGTTGGGGACGCGGATTC 1545
DB	1624	ATGCGCGATGCCAGCGCTAGACGATTTGATCTGACATGTTGGGGACGCGGATTC 1683
QY	1546	CCGGTCCGGGATTTACCCCGCAGCTCCCGCCCTTACGCGCTCTTGGATATGGCCGAC 1605
DB	1684	CCGGTCCGGGATTTACCCCGCAGCTCCCGCCCTTACGCGCTCTTGGATATGGCCGAC 1743
QY	1606	TTGAGTTTTCAGCAGATGTTTACCGATGCCCTTGGAAATTCAGAGTACGCTGGGTAG 1662
DB	1744	TTGAGTTTTCAGCAGATGTTTACCGATGCCCTTGGAAATTCAGAGTACGCTGGGTAG 1800
RESULT 7		
ID	ABT07366	standard; DNA; 1776 BP.
XX	ABT07366;	
AC	AC	
XX	AC	
DT	29-AUG-2003 (revised)	
DT	07-NOV-2002 (first entry)	
XX	Chimeric ecdysone receptor coding sequence SEQ ID NO: 118.	
XX	Plant; gene expression control; insect; hormone receptor; fertility;	
XX	ecdysone receptor; gene; ds.	
XX	Manduca sexta.	
OS	Agrotis ipsilon.	
OS	Chimeric.	
XX	WO200261102-A2.	
PN	08-AUG-2002.	
XX	24-OCT-2001; 2001WO-US051417.	
PD	24-OCT-2000; 2000US-0242969P.	
XX	XX	

PA	(SYGN) SYNGENTA PARTICIPATIONS AG.
XX	Pascal EU, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX	WPI; 2002-619259/66.
DR	P-PSDB; ABJ05372.
XX	New receptor cassette encoding a chimeric receptor polypeptide, useful in
PT	regulating expression of target polypeptides in plants in the presence of
PT	appropriate ligands that may be used in controlling plant fertility.
XX	Example 23; Page 265-267; 319pp; English.
XX	The present invention relates to a receptor cassette encoding a chimeric
CC	receptor polypeptide comprising at least one DNA binding domain, a hinge
CC	domain of an ecadherin receptor (ECR) of an insect, a ligand binding
CC	domain of an insect ECR, where the ligand binding domain is heterologous
CC	with respect to the hinge domain and an activation domain. The chimeric
CC	insect hormone receptors and receptor cassettes are useful in regulating
CC	expression of target polypeptides in plants in the presence of
CC	appropriate ligands that may be used in controlling plant fertility. The
CC	method is useful for decreasing or increasing plant gene expression. The
CC	present sequence is a coding sequence described in the exemplification of
CC	the invention. (Updated on 29-AUG-2003 to standardise OS field)
XX	Sequence 1776 BP; 466 A; 444 C; 481 G; 385 T; 0 U; 0 Other;
QY	Query Match 86.7%; Score 1441.6; DB 6; Length 1776;
DB	Best Local Similarity 92.6%; Pred. No. 0;
DB	Matches 1539; Conservative 0; Mismatches 114; Indels 9; Gaps 2
QY	1 ATGAAGCTACTGTTCTTATCGAACACGATGCGATATTGGCGACTTAAAAAGCTCAAG 60
DB	124 ATGAAGCTACTGTTCTTATCGAACACGATGCGATATTGGCGACTTAAAAAGCTCAAG 183
QY	61 TGCTCCAAAGAAAACCAGAGTGCCGCCAAGTGTCTGAGAACAACATGGGAGTGTGCCTAC 120
DB	184 TGCTCCAAAGAAAACCAGAGTGCCGCCAAGTGTCTGAGAACAACATGGGAGTGTGCCTAC 243
QY	121 TCTCCCAAACCAAAGGTCCTCGTAGTGGGCACATCTCACAGAAAGTGAATCAAGG 180
DB	244 TCTCCCAAACCAAAGGTCCTCGTAGTGGGCACATCTCACAGAAAGTGAATCAAGG 303
QY	181 CTAGAAAGACTGGAAACAGCATTTTCTACTGATTTTTTCTCGAAGAACCTTGCACATGAT 240
DB	304 CTAGAAAGACTGGAAACAGCATTTTCTACTGATTTTTTCTCGAAGAACCTTGCACATGAT 363
QY	241 TTGAATAATGGATTCTTTTACAGATATAAAGCATTGTTTAACAGGATATTCTTCTACAAGAT 300
DB	364 TTGAATAATGGATTCTTTTACAGATATAAAGCATTGTTTAACAGGATATTCTTCTACAAGAT 423
QY	301 AATGTGAATAAGATGCGGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCCTCTTA 360
DB	424 AATGTGAATAAGATGCGGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCCTCTTA 483
QY	361 ACATTGAGACAGCATAGATAAAGTGCACATCATCATATCGGAAGAGAGTAGTAAACAAGGT 420
DB	484 ACATTGAGACAGCATAGATAAAGTGCACATCATCATATCGGAAGAGAGTAGTAAACAAGGT 543
QY	421 CAAGACAGTTCAGTCTATCGACGGGTATGAGSCCGGAGTGGGTCTGCTCCAGAGTCCACG 480
DB	544 CAAGACAGTTCAGTCTATCGACGGGTATGAGSCCGGAGTGGGTCTGCTCCAGAGTCCACG 603
QY	481 TCACAAGAAACAAAGAGAGAGAAAAGGACACAGAGAGAGAAAAGACAAAACCTGCCAGTCAGT 540
DB	604 TCACAAGAAACAAAGAGAGAGAAAAGGACACAGAGAGAGAAAAGACAAAACCTGCCAGTCAGT 663
QY	541 ACAGACAGTGGACGATCATATGCTGCGATTAATGCATGTGACCCCTCGCCCCCCCAGAG 600
DB	664 ACAGACAGTGGACGATCATATGCTGCGATTAATGCATGTGACCCCTCGCCCCCCCAGAG 723
QY	601 GCGGCAAGGATTACCAAGTGGTCCCGAGGTTCTTCAACGAGAGAGGCTAATGGAGACAGAC 660

Qy 901 AAGATATCTAGTCCGATCAAAATTACATTTAAAGGGGTCTATCAAGGAAGTCAATG 960
 Db 1024 AAGATATCTAGTCCGATCAAAATTACATTTAAAGGGGTCTATCAAGGAAGTCAATG 1083
 Qy 961 CTGCGAGTGGCGGACGGTACGACGCGGACGACAGCGTGTCTGGGAAACACGAG 1020
 Db 1084 CTGCGAGTGGCGGACGGTACGACGCGGACGACAGCGTGTCTGGGAAACACGAG 1143
 Qy 1021 GCGTACAGCGCGGACAACTACCGCAAGCGCGGACGATGCTTACGTCATCGAGGACCTCGTG 1080
 Db 1144 GCGTACAGCGCGGACAACTACCGCAAGCGCGGACGATGCTTACGTCATCGAGGACCTCGTG 1203
 Qy 1081 CACTTCTGCGGTGTATGTACTCCATGAGCATGACAAATGTGCACTAGCGGCTGCTCAC 1140
 Db 1204 CACTTCTGCGGTGTATGTACTCCATGAGCATGACAAATGTGCACTAGCGGCTGCTCAC 1263
 Qy 1141 GCCATCGTTATTTCTCAGACGCGGCGGCTCGAGCAACCCCTTTTAGTGGAGGAATC 1200
 Db 1264 GCCATCGTTATTTCTCAGACGCGGCGGCTCGAGCAACCCCTTTTAGTGGAGGAATC 1323
 Qy 1201 CAGAGATACTACTTGAAGACGCTCGGCTTTACATTTTAAATCAGCAGCGCTCGCCT 1260
 Db 1324 CAGAGATACTACTTGAAGACGCTCGGCTTTACATTTTAAATCAGCAGCGCTCGCCT 1383
 Qy 1261 CGCTCGCGCTGCTGTTCCGGAAGATCTCGGCGTGTGACGGAACCTCGCACGCTCGGC 1320
 Db 1384 CGCTCGCGCTGCTGTTCCGGAAGATCTCGGCGTGTGACGGAACCTCGCACGCTCGGC 1443
 Qy 1321 ACGCAGAACTCCAACTGTGATCTCGCTGAAGCTGGAAGACAGGAACTTCCGCCATTC 1380
 Db 1444 ACGCAGAACTCCAACTGTGATCTCGCTGAAGCTGGAAGACAGGAACTTCCGCCATTC 1503
 Qy 1381 CTCGAGGAGATCTGGGACGTGGCGAAGTGTGACGACGAAAGCTTGGCCCCCGACCGAT 1440
 Db 1504 CTCGAGGAGATCTGGGACGTGGCGAAGTGTGACGACGAAAGCTTGGCCCCCGACCGG 1563
 Qy 1441 CTCACGCTGGG 1451
 Db 1564 GCCGACCCAGG 1574
 RESULT 10
 ADF49208
 ID ADF49208 standard; DNA; 1863 BP.
 XX AC ADF49208;
 DT
 XX 12-FEB-2004 (first entry)
 DE Ecdysone receptor/Dof1 transactivation domain DNA seq id 136.
 XX receptor cassette; chimeric receptor polypeptide; DNA binding domain;
 KW hinge domain; ecdysone receptor; Ecr; ligand binding domain;
 KW activation domain; transgenic seed; transgenic plant; plant line;
 KW herbicide; pesticide; chimeric ecdysone receptor; Ecr;
 KW yeast GAL4 DNA binding domain; Dof1 transactivation domain; ds; gene.
 XX Synthetic.
 OS Manduca sexta.
 OS Aecomycota.
 OS Zea mays.
 XX US2003154509-A1.
 PN 14-AUG-2003.
 XX 24-OCT-2001; 2001US-00087167.
 XX 24-OCT-2001; 2001US-00087167.
 XX (PASC/) PASCAL E J.
 PA (VALE/) VALENTINE S A.

PA (BROW/) BROWN J A.
 PA (COCK/) COCKRELL A S.
 PA (JOHN/) JOHNSON B D.
 XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 PI WPI; 2003-897756/82.
 XX
 XX New receptor cassette encoding a chimeric receptor polypeptide, useful
 PT for regulating the expression of target polypeptides in plants in the
 PT presence of appropriate chemical ligands.
 XX Example 25; SEQ ID NO 136; 186pp; English.
 XX The invention describes a receptor cassette encoding a chimeric receptor
 CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
 CC (D) domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
 CC (E) domain that is heterologous with respect to the D domain, and an
 CC activation domain. The receptor cassette and method are useful in
 CC regulating the expression of target polypeptides in plants in the
 CC presence of appropriate chemical ligands. The transgenic seeds and plants
 CC can be used for the breeding of improved plant lines that, for e.g.,
 CC increase the effectiveness of conventional methods such as herbicide or
 CC pesticide treatment. This sequence encodes an ecdysone receptor-Dof1
 CC transactivation domain fusion protein.
 XX Sequence 1863 BP; 487 A; 489 C; 510 G; 377 T; 0 U; 0 Other;
 SQ
 Query Match 86.1%; Score 1431.8; DB 10; Length 1863;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 1439; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 Qy 1 ATGAGCTACTGCTCTTCTATCGAACAGCATGCGATATTTGCCGACTTAAAAAGCTCAAG 60
 Db 124 ATGAGCTACTGCTCTTCTATCGAACAGCATGCGATATTTGCCGACTTAAAAAGCTCAAG 183
 Qy 61 TGTCTCCAAAGAAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTGCTAC 120
 Db 184 TGTCTCCAAAGAAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTGCTAC 243
 Qy 121 TCTCCCAAAACCAAAAGGTCTCGCTGACTAGGCGACATCTGACAGAAAGTGGAAATCAAG 180
 Db 244 TCTCCCAAAACCAAAAGGTCTCGCTGACTAGGCGACATCTGACAGAAAGTGGAAATCAAG 303
 Qy 181 CTAGAAGACTGGAAACAGCTATTTTCTACTGATTTTCTCTCGAGAAGACCTTGACATGATT 240
 Db 304 CTAGAAGACTGGAAACAGCTATTTTCTACTGATTTTCTCTCGAGAAGACCTTGACATGATT 363
 Qy 241 TTGAAAATGGATTTCTTACAGGATATAAAGCATTTGTTAAACAGGATTTTGTACAAAGAT 300
 Db 364 TTGAAAATGGATTTCTTACAGGATATAAAGCATTTGTTAAACAGGATTTTGTACAAAGAT 423
 Qy 301 AATGTGAATAAAGATGCGGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTTA 360
 Db 424 AATGTGAATAAAGATGCGGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTTA 483
 Qy 361 ACATTGACAGACGATAGAATAAGTTCGACATCATCTCGGAAGAGAGTAGTAAACAAAGGT 420
 Db 484 ACATTGACAGACGATAGAATAAGTTCGACATCATCTCGGAAGAGAGTAGTAAACAAAGGT 543
 Qy 421 CAAAGACAGTTGACTGTATCGACCGGTATGAGGCGCGAGTGCCTGCCAGAGTCCACG 480
 Db 544 CAAAGACAGTTGACTGTATCGACCGGTATGAGGCGCGAGTGCCTGCCAGAGTCCACG 603
 Qy 481 TGCAAGAACAAAAGAGAGAAAAGGAAGACAGAGAGAAAAGAACAACTCCCAAGTCAGT 540
 Db 604 TGCAGAAACAAAAGAGAGAAAAGGAAGACAGAGAGAAAAGAACAACTCCCAAGTCAGT 663
 Qy 541 ACGACGACAGTGGACGATCATATGCTGCCATAATGCAATGTGACCTCCGCCCCACGAG 600
 Db 664 ACGACGACAGTGGACGATCATATGCTGCCATAATGCAATGTGACCTCCGCCCCACGAG 723
 Qy 601 CGCGCAAGGATTACGAAGTGGTGGTCCCGAGGTTCTCTACGGGAGAGCTAAATGGAGCAGAAC 660

Db 724 GCGGCAAGATTACAGAGTGGTCCGAGGTTCTTAACGGAGAGCTAATGGAGCAAC 783
Qy 661 AGACTGAAGAATGTGACCCGCTGTGCGCGAACAAGAGTCCCTGATCGCAGGCTCGTG 720
Db 784 AGACTGAAGAATGTGACCCGCTGTGCGCGAACAAGAGTCCCTGATCGCAGGCTCGTG 843
Qy 721 TGGTACCAAGAGGGGTACGACGCGCTCGGAGGAAGATCTCAAGAGAGTTACACAGACA 780
Db 844 TGGTACCAAGAGGGGTACGACGCGCTCGGAGGAAGATCTCAAGAGAGTTACACAGACA 903
Qy 781 TGGCAGTTAGAGAGAGAGAGAGAGGAGAACTGACATGCCCTTCCGTTCAGATCACAGAG 840
Db 904 TGGCAGTTAGAGAGAGAGAGAGGAGGAGAACTGACATGCCCTTCCGTTCAGATCACAGAG 963
Qy 841 ATGACGATCTTAAAGTGCAGCTTATTGTAGAAATTCGCAAAAGGAGTACCCGGATTCTCC 900
Db 964 ATGACGATCTTAAAGTGCAGCTTATTGTAGAAATTCGCAAAAGGAGTACCCGGATTCTCC 1023
Qy 901 AAGATATCTAGTCCGATCAATTAATTAATTAAGGCGTCAATCAAGGAAAGTATGATG 960
Db 1024 AAGATATCTAGTCCGATCAATTAATTAATTAAGGCGTCAATCAAGGAAAGTATGATG 1083
Qy 961 CTGCGAGTGGCGGACGCTACGACGCGCGACGAGCGGTCTGTTCCGCAACCAACAG 1020
Db 1084 CTGCGAGTGGCGGACGCTACGACGCGCGCGACGAGCGGTCTGTTCCGCAACCAACAG 1143
Qy 1021 GCGTACACGCGGACAACTACCGCAAGGCGGCGATGCTTACGTCAATCGAGGACCTGCTG 1080
Db 1144 GCGTACACGCGGACAACTACCGCAAGGCGGCGATGCTTACGTCAATCGAGGACCTGCTG 1203
Qy 1081 CACTTCTGTCGCTGATGCTACTCCATGACGATGGCAATGTGCATCGCGTGTCTCACC 1140
Db 1204 CACTTCTGTCGCTGATGCTACTCCATGACGATGGCAATGTGCATCGCGTGTCTCACC 1263
Qy 1141 GCATCGTTATATCTCAGACGCGCGCAGGCTCGAGCAACCCCTTTTATGTGAGGAAATC 1200
Db 1264 GCATCGTTATATCTCAGACGCGCGCAGGCTCGAGCAACCCCTTTTATGTGAGGAAATC 1323
Qy 1201 CAGAGATACTACTGAAGACGCTGGCGGTTTACATTTTAATCAGACGCGCTCGCT 1260
Db 1324 CAGAGATACTACTGAAGACGCTGGCGGTTTACATTTTAAATCAGACGCGCTCGCT 1383
Qy 1261 CGCTGGCGCTGCTGTTCCGCAAGATCTCGCGGCTGTCAGCGAACTGCGCACGCTCGGC 1320
Db 1384 CGCTGGCGCTGCTGTTCCGCAAGATCTCGCGGCTGTCAGCGAACTGCGCACGCTCGGC 1443
Qy 1321 ACGCAGAACTCCAAACATGTGCATCTCGCTGAAGCTGAAGAACAGGAAACTTCGCGCATTC 1380
Db 1444 ACGCAGAACTCCAAACATGTGCATCTCGCTGAAGCTGAAGAACAGGAAACTTCGCGCATTC 1503
Qy 1381 CTGAGGAGATCTGGACGCTGGCGAAGTGTGACGACGAAAGCTGGCCCCCGGACCGAT 1440
Db 1504 CTGAGGAGATCTGGACGCTGGCGAAGTGTGACGACGAAAGCTGGAGCTCGCCACCGCG 1563
Qy 1441 CTCAGCCTGGG 1451
Db 1564 GCCGACCCAGG 1574

RESULT 11
ABT07376
ID ABT07376 standard; DNA; 1848 BP.
XX
AC
XX
XX
DT 29-AUG-2003 (revised)
DT 07-NOV-2002 (first entry)
XX
XX
KW Chimeric ecdysone receptor coding sequence SEQ ID NO: 134.
KW plant; gene expression control; insect; hormone receptor; fertility;
KW ecdysone receptor; gene; ds.

XX Manduca sexta.
OS Manduca sexta.
OS Chimeric.
FN WO200261102-A2.
XX
PD 08-AUG-2002.
XX
PP 24-OCT-2001; 2001WO-US051417.
XX
PR 24-OCT-2000; 2000US-0242969P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
DR WPI; 2002-619259/66.
DR P-FSDB; ABJ05378.
XX
PT New receptor cassette encoding a chimeric receptor polypeptide, useful in
PT regulating expression of target polypeptides in plants in the presence of
PT appropriate ligands that may be used in controlling plant fertility.
XX
PS Example 25; Page 296-298; 319pp; English.
XX
CC The present invention relates to a receptor cassette encoding a chimeric
CC receptor polypeptide comprising at least one DNA binding domain, a hinge
CC domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
CC domain of an insect Ecr, where the ligand binding domain is heterologous
CC with respect to the hinge domain and an activation domain. The chimeric
CC insect hormone receptors and receptor cassettes are useful in regulating
CC expression of target polypeptides in plants in the presence of
CC appropriate ligands that may be used in controlling plant fertility. The
CC method is useful for decreasing or increasing plant gene expression. The
CC present invention is a coding sequence described in the exemplification of
CC the invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 1848 BP; 488 A; 456 C; 523 G; 381 T; 0 U; 0 Other;
Query Match 85.8%; Score 1426.6; DB 6; Length 1848;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 1463; Conservative 0; Mismatches 34; Indels 6; Gaps 1;
Qy 1 ATGAGCTACTGTCTTCTATCGAACAAAGCTGCGATATTTGCGGACTTAAAGAGCTCAAG 60
Db 124 ATGAGCTACTGTCTTCTATCGAACAAAGCTGCGATATTTGCGGACTTAAAGAGCTCAAG 183
Qy 61 TGCTCCAAAGAAAAACCGAAGTGCAGGCTGTTCTGAAGAAACAACTGGGAGTGTGCTAC 120
Db 184 TGCTCCAAAGAAAAACCGAAGTGCAGGCTGTTCTGAAGAAACAACTGGGAGTGTGCTAC 243
Qy 121 TCTCCAAAAACCAAGAGTCTCCGCTGATAGGCGACATCTCAGAGAGAGACCTTCACATGATT 180
Db 244 TCTCCAAAAACCAAGAGTCTCCGCTGATAGGCGACATCTCAGAGAGAGACCTTCACATGATT 303
Qy 181 CTAGAAAGACTGGAACAGCTATTTCTACTGATTTTTCTCGAGAGAGACCTTCACATGATT 240
Db 304 CTAGAAAGACTGGAACAGCTATTTCTACTGATTTTTCTCGAGAGAGACCTTCACATGATT 363
Qy 241 TTGAAAATGGATTCTTTTACAGGATATAAAGCATTTGTTAAACAGGATTTTGTACAGAT 300
Db 364 TTGAAAATGGATTCTTTTACAGGATATAAAGCATTTGTTAAACAGGATTTTGTACAGAT 423
Qy 301 AATGTGAATAAGATCCGCTCAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTA 360
Db 424 AATGTGAATAAGATCCGCTCAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTA 483
Qy 361 ACATTTGAGACGACATAGATAAGTCCGACATCATCTCGAAGAGAGAGTAGTAACAAGT 420
Db 484 ACATTTGAGACGACATAGATAAGTCCGACATCATCTCGAAGAGAGAGTAGTAACAAGT 543
Qy 421 CAAAGACAGTTGACTGTATTCGACGCGGTATGAGGCCGAGTGTGCTGCCAGAGTCCACG 480

Db	544	CAAGACAGTTGACTGTATCGACGCGTATGAGGCCGAGTGGTCTGCTCCAGAGTCACG	603	Db	1618	GAG 1620
Qy	481	TGCAAGAAACAAAGAGAAAGAAAGACAGAGAGAAAGAAAGAAACAACTGCCAGTCAGT	540	RESULT 12		
Db	604	TGCAAGAAACAAAGAGAAAGAAAGACAGAGAGAAAGAAAGAAACAACTGCCAGTCAGT	663	ID ADF49206		
Qy	541	ACGACGACAGTGGACGATCATATGCTGCCATATATGCAATGTGACCTCCGCCCCACAG	600	XX ADF49206;		
Db	664	ACGACGACAGTGGACGATCATATGCTGCCATATATGCAATGTGACCTCCGCCCCACAG	723	XX AC ADF49206;		
Qy	601	CGGCAAGATTACAGAGTGTCCGAGGTTCTTAACGAGAGAACTTAATGGACAGAAC	660	XX AC ADF49206;		
Db	724	CGGCAAGATTACAGAGTGTCCGAGGTTCTTAACGAGAGAACTTAATGGACAGAAC	783	DT 12-FEB-2004 (first entry)		
Qy	661	AGACTGAAGAAATGTGACGCCCTGTGCGCGAACAGAGTCCCTGATGCGAGGCTCGTG	720	XX Ecdysone receptor/C1 transactivation domain DNA seq id 134.		
Db	784	AGACTGAAGAAATGTGACGCCCTGTGCGCGAACAGAGTCCCTGATGCGAGGCTCGTG	843	XX receptor cassette; chimeric receptor polypeptide; DNA binding domain;		
Qy	721	TGGTACCAAGGGGTACGACGAGCCGTGGAGGAGATCTCAAGAGAGTTACACAGACA	780	XX hinge domain; ecdysone receptor; ECR; ligand binding domain;		
Db	844	TGGTACCAAGGGGTACGACGAGCCGTGGAGGAGATCTCAAGAGAGTTACACAGACA	903	XX activation domain; transgenic seed; transgenic plant; plant line;		
Qy	781	TGGCAGTTAGAGAGAGAGAGAGAGGAGAACTGACATGCCCTTCCGTCAGATCACAGAG	840	XX herbicide; pesticide; chimeric ecdysone receptor; ECR; gene.		
Db	904	TGGCAGTTAGAGAGAGAGAGAGGAGAACTGACATGCCCTTCCGTCAGATCACAGAG	963	XX yeast GAL4 DNA binding domain; C1 transactivation domain; ds; gene.		
Qy	841	ATGACGATCTTAACAGTCAGCTTATGTAGAAATTCGCAAGGGGACTACCGGATTTCTCC	900	OS Synthetic.		
Db	964	ATGACGATCTTAACAGTCAGCTTATGTAGAAATTCGCAAGGGGACTACCGGATTTCTCC	1023	OS Manduca sexta.		
Qy	901	AGATATCTCAGTCGATCAATTAATTAAGGGGTATCAAGGAGTGTGATGATG	960	OS Ascomycota.		
Db	1024	AGATATCTCAGTCGATCAATTAATTAAGGGGTATCAAGGAGTGTGATGATG	1083	OS Zea mays.		
Qy	961	CTGCCAGTGGCGGAGGTACGACCGCGCGAGCAGCGTCTGTTCCGCAACCAACAG	1020	XX US2003154509-A1.		
Db	1084	CTGCCAGTGGCGGAGGTACGACCGCGCGAGCAGCGTCTGTTCCGCAACCAACAG	1143	XX 14-AUG-2003.		
Qy	1021	GGGTACACGCGCAACATACCGCAAGCGGCGATGTCTAGTCATCGAGGACTGTGTG	1080	XX 24-OCT-2001; 2001US-00087167.		
Db	1144	GGGTACACGCGCAACATACCGCAAGCGGCGATGTCTAGTCATCGAGGACTGTGTG	1203	XX 24-OCT-2001; 2001US-00087167.		
Qy	1081	CACTTCTGTCGCTGTATGTCATGACATGACATGACATGTCATGTCATGTCATGTC	1140	XX (PASC/) PASCAL E J.		
Db	1204	CACTTCTGTCGCTGTATGTCATGACATGACATGTCATGTCATGTCATGTCATGTC	1263	XX (VALE/) VALENTINE S A.		
Qy	1141	GCATCGTTATATCTCAGACCGGCGAGCCCTCGAGCAACCCCTTTTATGGAGGAATC	1200	XX (BROW/) BROWN J A.		
Db	1264	GCATCGTTATATCTCAGACCGGCGAGCCCTCGAGCAACCCCTTTTATGGAGGAATC	1323	XX (COCK/) COCKRELL A S.		
Qy	1201	CAGAGATCTACTTGAAGACGTGCGGGTTTACATTTTAAATCAGACAGCGCTCGGCT	1260	XX (JOHN/) JOHNSON B D.		
Db	1324	CAGAGATCTACTTGAAGACGTGCGGGTTTACATTTTAAATCAGACAGCGCTCGGCT	1383	PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;		
Qy	1261	CGCTGCGCGCTGCTGTCGCGAGATCTCGCGGTGTCGACGAACTGCGACGCTCGGC	1320	XX WPI; 2003-897756/82.		
Db	1384	CGCTGCGCGCTGCTGTCGCGAGATCTCGCGGTGTCGACGAACTGCGACGCTCGGC	1443	DR New receptor cassette encoding a chimeric receptor polypeptide, useful		
Qy	1321	ACGCAAGTCCAAATGTGATCTCGCTGAAGCTGAAGAACAGGAAACTTCCGCAATTC	1380	XX for regulating the expression of target polypeptides in plants in the		
Db	1444	ACGCAAGTCCAAATGTGATCTCGCTGAAGCTGAAGAACAGGAAACTTCCGCAATTC	1503	XX presence of appropriate chemical ligands.		
Qy	1381	CTCGAGGATCTGGGAGCTGGCGGAGTGTGACGAGAACTGGCCCCCGGACCGAT	1440	XX Example 25; SEQ ID NO 134; 186pp; English.		
Db	1504	CTCGAGGATCTGGGAGCTGGCGGAGTGTGACGAGAACTGGCCCCCGGACCGAT	1557	XX The invention describes a receptor cassette encoding a chimeric receptor		
Qy	1441	GTGAGCTGGGAGCAGCTCCACTTTAGACGCGGAGGAGTGGCGATGGCGATCGGAC	1500	XX polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge		
Db	1558	GTGAGCTGGGAGCAGCTCCACTTTAGACGCGGAGGAGTGGCGATGGCGATCGGAC	1617	XX (D) domain of an ecdysone receptor (ECR) of an insect, a ligand binding		
Qy	1501	GGG 1503		XX (E) domain that is heterologous with respect to the D domain, and an		
				XX activation domain. The receptor cassette and method are useful in		
				XX regulating the expression of target polypeptides in plants in the		
				XX presence of appropriate chemical ligands. The transgenic seeds and plants		
				XX can be used for the breeding of improved plant lines that, for e.g.		
				XX increase the effectiveness of conventional methods such as herbicide or		
				XX pesticide treatment. This sequence encodes an ecdysone receptor-C1		
				XX transactivation domain fusion protein.		
				XX Sequence 1848 BP; 488 A; 456 C; 523 G; 381 T; 0 U; 0 Other;		
				XX Query Match 85.8%; Score 1426.6; DB 10; Length 1848;		
				XX Best Local Similarity 97.3%; Pred. No. 0;		
				XX Matches 1463; Conservative 0; Mismatches 34; Indels 6; Gaps 1;		
				Qy 1 ATGAAGTACTGTCTTCTATCGAAACAGCATGCGATATTTCCGACTTAAAGCTCAAG 60		
				Db 124 ATGAAGTACTGTCTTCTATCGAAACAGCATGCGATATTTCCGACTTAAAGCTCAAG 183		
				Qy 61 TGCTCCAAAGAAACCGAGTGGCGCAAGTGTCTGAAGAAACAACTGGGAGTGTGCTTAC 120		
				Db 184 TGCTCCAAAGAAACCGAGTGGCGCAAGTGTCTGAAGAAACAACTGGGAGTGTGCTTAC 243		

QY 121 TCTCCAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAGTGGAAATCAAGG 180
Db 244 TCTCCAAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAGTGGAAATCAAGG 303
QY 181 CTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTCTCCTCGAGAAGACCTTTGACATGATT 240
Db 304 CTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTCTCCTCGAGAAGACCTTTGACATGATT 363
QY 241 TTGAAAATGGATTCCTTTACAGATATAAAAGCATTTGTTAAACAGGATTTATTTGTACAAGAT 300
Db 364 TTGAAAATGGATTCCTTTACAGATATAAAAGCATTTGTTAAACAGGATTTATTTGTACAAGAT 423
QY 301 AATGTGAATTAAGATGCGCTGACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTTA 360
Db 424 AATGTGAATTAAGATGCGCTGACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTTA 483
QY 361 ACATTTGAGACAGCATAGAAATAGTTCGCACATCATCATCGGAAGAGAGTAGTAACAAGGT 420
Db 484 ACATTTGAGACAGCATAGAAATAGTTCGCACATCATCATCGGAAGAGAGTAGTAACAAGGT 543
QY 421 CAAAGACAGTTGACTGTATCGACGGGTATAGGCCCGGAGTGGCTGCTCCAGAGTCCACG 480
Db 544 CAAAGACAGTTGACTGTATCGACGGGTATAGGCCCGGAGTGGCTGCTCCAGAGTCCACG 603
QY 481 TGCAGAACCAAAAGAGAAAGCAAGCAACAGACAGAGAGAAAGCAAACTGCCAGTCAGT 540
Db 604 TGCAGAACCAAAAGAGAAAGCAAGCAACAGACAGAGAGAAAGCAAACTGCCAGTCAGT 563
QY 541 ACGACGACAGTGGACGATCATATGCTTCGCTAATGCAATGTGACCCCTCCGCCCCACAG 600
Db 564 ACGACGACAGTGGACGATCATATGCTTCGCTAATGCAATGTGACCCCTCCGCCCCACAG 723
QY 601 GCGGCAAGGATTCACGAAGTGTCCGAGGTTCTTAACGGAAGAGCTTAATGGAGCAGAAC 660
Db 724 GCGGCAAGGATTCACGAAGTGTCCGAGGTTCTTAACGGAAGAGCTTAATGGAGCAGAAC 783
QY 661 AGACTGAAGAAATGTACGCGCTGTGCGCAACCAAGAGTCCCTGATCGCAGGCTCGTG 720
Db 784 AGACTGAAGAAATGTACGCGCTGTGCGCAACCAAGAGTCCCTGATCGCAGGCTCGTG 843
QY 721 TGGTACCAGAGGGGTACAGCAGCGCTCGGAGGAGATCTCAAGAGAGTTACACAGACA 780
Db 844 TGGTACCAGAGGGGTACAGCAGCGCTCGGAGGAGATCTCAAGAGAGTTACACAGACA 903
QY 781 TGGCAGTTAGAAAGAAAGAAAGAGAGGAGAAACCTGACATGCCCTTCGTCAGATCAACAG 840
Db 904 TGGCAGTTAGAAAGAAAGAAAGAGAGGAGAAACCTGACATGCCCTTCGTCAGATCAACAG 963
QY 841 ATGACGATCTTAACAGTGCAGCTTATTTAGAAATTCGCAAGGGACTACCGGATTCCTCC 900
Db 964 ATGACGATCTTAACAGTGCAGCTTATTTAGAAATTCGCAAGGGACTACCGGATTCCTCC 1023
QY 901 AAGATATCTCAGTCCGATCAAAATTTACATTTAAGGCGTTCATCAAGCGAAGTGTATG 960
Db 1024 AAGATATCTCAGTCCGATCAAAATTTACATTTAAGGCGTTCATCAAGCGAAGTGTATG 1083
QY 961 CTGCGAGTGGCGCAGCGGTACGACGCGCGACGGAAGAGTGTGTTTCGCGAACAACAG 1020
Db 1084 CTGCGAGTGGCGCAGCGGTACGACGCGCGACGGAAGAGTGTGTTTCGCGAACAACAG 1143
QY 1021 GCGTACCGCGGACAACTACCCAGGGGGGATGCTCTACGTCATCGAGGACCTGCTG 1080
Db 1144 GCGTACCGCGGACAACTACCCAGGGGGGATGCTCTACGTCATCGAGGACCTGCTG 1203
QY 1081 CACTTCTGCGGTATGTACTCATGAGCATGGACAATGTGCACTACGCGTGTCTCACC 1140
Db 1204 CACTTCTGCGGTATGTACTCATGAGCATGGACAATGTGCACTACGCGTGTCTCACC 1263
QY 1141 GCCATCGTTATATTTCTCAGACCGGCCAGGCTTCGAGCAACCCCTTTTAGTGGAGGAAATC 1200
Db 1264 GCCATCGTTATATTTCTCAGACCGGCCAGGCTTCGAGCAACCCCTTTTAGTGGAGGAAATC 1323

QY 1201 CAGAGATACCTACTGAAGACGCTGCGGGTTTACATTTTAAATCAGACAGCGCGTCCGCT 1260
Db 1324 CAGAGATACCTACTGAAGACGCTGCGGGTTTACATTTTAAATCAGACAGCGCGTCCGCT 1383
QY 1261 CGCTGCGCGCTGCTGTTTCGGCAGATCCTCGGCGTCTGACGGAACCTGCGCACCTCGGC 1320
Db 1384 CGCTGCGCGCTGCTGTTTCGGCAGATCCTCGGCGTCTGACGGAACCTGCGCACCTCGGC 1443
QY 1321 ACGCAGAACTCCAACTATGTGCTGCTGAAGCTGAAGAACAGGAAACTTCCGCCATTTC 1380
Db 1444 ACGCAGAACTCCAACTATGTGCTGCTGAAGCTGAAGAACAGGAAACTTCCGCCATTTC 1503
QY 1381 CTCGAGAGATCTCGGACGCTGCGGCGAAGTGTGCGAGAGAGCTTGCCTCCCGCCGAT 1440
Db 1504 CTCGAGAGATCTCGGACGCTGCGGCGAAGTGTGCGAGAGAGCTT-----CCCAAGGCC 1557
QY 1441 GTACGCTTGGGGGACGAGCTTACCTAGACGCGGAGGACGTGGCGATGGCGCATGCCGCGAC 1500
Db 1558 GTGCGGTGCACGCGGGGAGACTCTTCTTCCACCGGACACAGCCGCGCACGCGGCGC 1617
QY 1501 GCG 1503
Db 1618 GAG 1620

RESULT 13
ABT07371
ID ABT07371 standard; DNA; 1428 BP.
XX AC ABT07371;
XX DT 07-NOV-2002 (first entry)
XX DE Chimeric ecdysone receptor coding sequence SEQ ID NO: 128.
XX KW Plant; gene expression control; insect; hormone receptor; fertility;
XX OS ecdysone receptor; gene; ds.
XX OS Manduca sexta.
XX OS Unidentified.
XX OS Chimeric.
XX WO200261102-A2.
XX PD 08-AUG-2002.
XX PF 24-OCT-2001; 2001WO-US051417.
XX PR 24-OCT-2000; 2000US-0242969P.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PA Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX PI WPI; 2002-619259/66.
XX DR P-PSDB; ABJ05377.
XX PT New receptor cassette encoding a chimeric receptor polypeptide, useful in
XX PT regulating expression of target polypeptides in plants in the presence of
XX PT appropriate ligands that may be used in controlling plant fertility.
XX PS Example 25; Page 291-293; 319pp; English.
XX CC The present invention relates to a receptor cassette encoding a chimeric
XX CC receptor polypeptide comprising at least one DNA binding domain, a hinge
XX CC domain of an ecdysone receptor (EcR) of an insect, a ligand binding
XX CC domain of an insect EcR, where the ligand binding domain is heterologous
XX CC with respect to the hinge domain and an activation domain. The chimeric
XX CC insect hormone receptors and receptor cassettes are useful in regulating
XX CC expression of target polypeptides in plants in the presence of
XX CC appropriate ligands that may be used in controlling plant fertility. The
XX CC method is useful for decreasing or increasing plant gene expression. The
XX CC present sequence is a coding sequence described in the exemplification of

CC		the invention	
XX			
SQ	Sequence	1428 BP; 423 A; 338 C; 379 G; 288 T; 0 U; 0 Other;	
	Query Match	85.7%; Score 1425; DB 6; Length 1428;	
	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 1425; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	ATGAAGCTACTGTCCTTATCGAACCAAGCATGGCATAATTGCCGCATTTAAAAAGCTCAAG	60
Dd	1		
Qy	61	TGCTCCAACAAAAAACCGAAGTGCGCCAAAGTGTCTGAAGAACAACCTGGGAGTGTCTGCTAC	120
Dd	61	TGCTCCNAAGNANAACCGAAGTGTGCCCNAAGTGTCTGNAGNACNACTGGGAGTGTGCTGTAC	120
Qy	121	TCTCCCCAAACC AAAAGGTC TC CGCTG CAT CT GA AGG CA CAT CT GA CAGA GT GG NA AT CA AGG	180
Dd	121	TCTCCCCAAACC AAAAGGTC TC CGCTG CAT CT GA AGG CA CAT CT GA CAGA GT GG NA AT CA AGG	180
Qy	181	CTAAGAAAGCTGGAAACAGCTATTTCTACTGATTTTTCTCTGAGAAGACCTTGACATGATTT	240
Dd	181		
Qy	241	TTGAAAAATGGATTTCTTTTACAGGATATAAAAAGCATTTGTTAAACAGGATTAATTTGTACAAGAT	300
Dd	241	TTGAAAAATGGATTTCTTTTACAGGATATAAAAAGCATTTGTTAAACAGGATTAATTTGTACAAGAT	300
Qy	301	AATGTGAATAAAGATGCGGTACAGATAGATTTGGCTTCAGTGCAGACTGATATGCCTCTTA	360
Dd	301	AATGTGAATAAAGATGCGGTACAGATAGATTTGGCTTCAGTGCAGACTGATATGCCTCTTA	360
Qy	361	ACATTGAGACAGCATAGAATAAAGTGCACATCATCATCGGAAGAGAGTAGTAAACAAGGT	420
Dd	361	ACATTGAGACAGCATAGANNTAAGTGCACATCATCATCGGAAGAGAGTAGTAAACAAGGT	420
Qy	421	CAAAGA CAG TTGA CTGTAT CGA CCG GTAT CAG GCC CG AG TG CG GT CC GC AG AG TCC AC G	480
Dd	421	CAAAGA CAG TTGA CTGTAT CGA CCG GTAT CAG GCC CG AG TG CG GT CC GC AG AG TCC AC G	480
Qy	481	TGCAAGAACAAACAGAGAGAAAAGGAAGCACAGAGAGAAAAAGACAACATGCCACAGTCAGT	540
Dd	481	TGCAAGAACAAACAGAGAGAAAAGGAAGCACAGAGAGAAAAGCNAAAATGCCACAGTCAGT	540
Qy	541	ACGACGACAGTGGACGATCATATGCCCTGCCAATAATGCAATGTGACCTCCGCCCCCAGAG	600
Dd	541	ACGACGACAGTGGACGATCATATGCCCTGCCAATAATGCAATGTGACCTCCGCCCCCAGAG	600
Qy	601	GCGGCNAGGATTCACGAGTGGTCCCGAGGTTCCTAAACGGAGAAAGCTAAATGGAGACAGAAC	660
Dd	601	GCGGCNAGGATTCACGAGTGGTCCCGAGGTTCCTAAACGGAGAAAGCTAAATGGAGACAGAAC	660
Qy	661	AGACTGAAGAAATGTGACGCCCTCTCGGCCGAAC CAGAAGTCCCTGATCGCGAGGCTCGTG	720
Dd	661	AGACTGAAGAAATGTGACGCCCTCTCGGCCGAAC CAGAAGTCCCTGATCGCGAGGCTCGTG	720
Qy	721	TGGTACCAAGGAGGGTACGACACCGCTCGGAGAGAATCTCTAAGAGAGTTACACAGACA	780
Dd	721	TGGTACCAAGGAGGGTACGACACCGCTCGGAGAGAATCTCTAAGAGAGTTACACAGACA	780
Qy	781	TGGCAGTTAGAAAGAAGAGAGAGAGGAAACTGCACATGCCCCCTTCCTCGATCAGATCACAGAG	840
Dd	781	TGGCAGTTAGAAAGAAGAGAGAGAGGAAACTGCACATGCCCCCTTCCTCGATCAGATCACAGAG	840
Qy	841	ATGACGATCTTAAACNGTCAGCTTATTTGTAGAAATTCGCAAGGSACTACCGGGATTTCTCC	900
Dd	841	ATGACGATCTTAAACNGTCAGCTTATTTGTAGAAATTCGCAAGGSACTACCGGGATTTCTCC	900
Qy	901	AAGATATCTCAGTCCGATCAAAATACATTTATTAAGGCGGTATCAACGCGAAGTGAATGATG	960
Dd	901	AAGATATCTCAGTCCGATCAAAATACATTTATTAAGGCGGTATCAACGCGAAGTGAATGATG	960
Qy	961	CTGCGAGTGGCGCAGCGVTA CGA CCG CGCG CAG CGG CAG CAG TGT GTT CTC CGA ACA ACC AG	1020

for regulating the expression of target polypeptides in plants in the presence of appropriate chemical ligands.

Example 25; SEQ ID NO 128; 186pp; English.

The invention describes a receptor cassette encoding a chimeric receptor polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge (D) domain of an ecdysone receptor (EcR) of an insect, a ligand binding (E) domain that is heterologous with respect to the D domain, and an activation domain. The receptor cassette and method are useful in regulating the expression of target polypeptides in plants in the presence of appropriate chemical ligands. The transgenic seeds and plants can be used for the breeding of improved plant lines that, for e.g. increase the effectiveness of conventional methods such as herbicide or pesticide treatment. This sequence encodes an ecdysone receptor-VP16 transactivation domain fusion protein.

Sequence 1428 BP; 423 A; 338 C; 379 G; 288 T; 0 U; 0 Other;

Query Match 85.7%; Score 1425; DB 10; Length 1428;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGAAGCTACTCTCTTCTATCGAACAAGCATCGGATATTGCGGACTTAAAGAGCTCAAG	60
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QY	61	TGCTCCAAAGAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTGGTAC	120
DB	61	TGCTCCAAAGAAAACCGAAGTGGCGCAAGTGTCTGAAGAACAACTGGGAGTGTGGTAC	120
QY	121	TTCTCCAAAACCAAAGGTTCTCGCTAGTGGGACATCTCAGAGAGTGAATCAAGG	180
DB	121	TTCTCCAAAACCAAAGGTTCTCGCTAGTGGGACATCTCAGAGAGTGAATCAAGG	180
QY	181	CTAGAAGACTCGAAGGCTATTTCTACTGATTTTCTCGAAGAGACCTTCGACATGATT	240
DB	181	CTAGAAGACTCGAAGGCTATTTCTACTGATTTTCTCGAAGAGACCTTCGACATGATT	240
QY	241	TTGAAAATCGATTTCTTACAGATATAAAGCATTTGTTAAAGGATTTTGTACAGAT	300
DB	241	TTGAAAATCGATTTCTTACAGATATAAAGCATTTGTTAAAGGATTTTGTACAGAT	300
QY	301	ATGTGNAATAGATCCCTCAGATAGATTGGCTTCAGTGGAGACTATATGCTCTTA	360
DB	301	ATGTGNAATAGATCCCTCAGATAGATTGGCTTCAGTGGAGACTATATGCTCTTA	360
QY	361	ACATTGAGACAGCATAGATAAGTGGACATCATCATCGAAGAGAGTAGTAACAAGGT	420
DB	361	ACATTGAGACAGCATAGATAAGTGGACATCATCATCGAAGAGAGTAGTAACAAGGT	420
QY	421	CAAAGACAGTTGATGTATCGACGGCTATAGGCGCGAGTGGCTGCTCCAGAGTCCAG	480
DB	421	CAAAGACAGTTGATGTATCGACGGCTATAGGCGCGAGTGGCTGCTCCAGAGTCCAG	480
QY	481	TGCAAGAACAAAGAGAGAAAGGAGACACAGAGAGAAAGACAACTGCCAGTCACT	540
DB	481	TGCAAGAACAAAGAGAGAAAGGAGACACAGAGAGAAAGACAACTGCCAGTCACT	540
QY	541	ACGACGACAGTGGACCATCATATGCTTGCATATGCAATGTGACCTCCGCCCCCAGAG	600
DB	541	ACGACGACAGTGGACCATCATATGCTTGCATATGCAATGTGACCTCCGCCCCCAGAG	600
QY	601	CGCGCAAGGATTCACGAAGTGGTCCGAGGTTCTTAACCGAGAGAGTAAATGGAGCAG	660
DB	601	CGCGCAAGGATTCACGAAGTGGTCCGAGGTTCTTAACCGAGAGAGTAAATGGAGCAG	660
QY	661	AGACTGAAGATGTGACCGCTGTGCGGCAACAGAGAGTCCCTGATCGGAGGCTCGTG	720
DB	661	AGACTGAAGATGTGACCGCTGTGCGGCAACAGAGAGTCCCTGATCGGAGGCTCGTG	720
QY	721	TGCTACCAAGGGGTACGAGAGCGGTTCGAGAGAGATCTCAAGAGAGTTACACAGACA	780

Db	721	TGCTACCAAGGGGTACGAGAGCGGTTCGAGAGAGATCTCAAGAGAGTTACACAGACA	780
QY	781	TGGCAGTTAGAAAGAAAGAGAGAGGAAACTGACATGCCCTTCCGTGACATCACAGAG	840
Db	781	TGGCAGTTAGAAAGAAAGAGAGAGGAAACTGACATGCCCTTCCGTGACATCACAGAG	840
QY	841	ATGACGATCTTAAACAGTGCAGCTTATTGTAGAAATTCGAAAGGGAGTACCGGGATTCTCC	900
Db	841	ATGACGATCTTAAACAGTGCAGCTTATTGTAGAAATTCGAAAGGGAGTACCGGGATTCTCC	900
QY	901	AAGATATCTCAGTCCGATCAAAATTTACATTTAAAGGGCTCATCAAGGCAAGTGTATG	960
Db	901	AAGATATCTCAGTCCGATCAAAATTTACATTTAAAGGGCTCATCAAGGCAAGTGTATG	960
QY	961	CTGCGAGTGGCGCGACGGTACGACGGCGGACGAGCGTGTCTTCGCGAAACCAACGAG	1020
Db	961	CTGCGAGTGGCGCGACGGTACGACGGCGGACGAGCGTGTCTTCGCGAAACCAACGAG	1020
QY	1021	CGGTACACGGCGGACAACTACCGCAAGCGGGGCGATGCTCTAGTTCATCGAGGACCTGCTG	1080
Db	1021	CGGTACACGGCGGACAACTACCGCAAGCGGGGCGATGCTCTAGTTCATCGAGGACCTGCTG	1080
QY	1081	CACCTCTGTCGGTGTATGCTTCCATGAGCATGGACATGTGCACTACGCGTGTCTCACC	1140
Db	1081	CACCTCTGTCGGTGTATGCTTCCATGAGCATGGACATGTGCACTACGCGTGTCTCACC	1140
QY	1141	GCCATCGTTATATCTCAGACGGCGGCGGCTTCGAGCAACCCCTTTTGTAGTGAGGAAATC	1200
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QY	1201	CAGAGATACTTCTGAAGACGCTCGGGTTTACATTTTAAATCAGACACGCGCGTGGCT	1260
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QY	1321	ACGAGAACTCCAAACATGTGCACTCTGCTGAGCTGAAAGAACAGGAAACTTCCGCCATTTC	1380
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QY	1381	CTGCGAGGATCTGGGAGTGGCCGAAAGTGTGACGACGAGAGCTT 1425	
Db	1381	CTGCGAGGATCTGGGAGTGGCCGAAAGTGTGACGACGAGAGCTT 1425	

RESULT 15

ABT07367

ID ABT07367 standard; DNA; 1767 BP.

XX AC ABT07367;

XX DT 29-AUG-2003 (revised)

XX DT 07-NOV-2002 (first entry)

XX XX Chimeric ecdysone receptor coding sequence SEQ ID NO: 120.

XX KW Plant; gene expression control; insect; hormone receptor; fertility;

XX KW ecdysone receptor; gene; ds.

XX OS *Manduca sexta*.

XX OS *Oestrinia nubilalis*.

XX OS Chimeric.

XX XX WO200261102-A2.

XX XX 08-AUG-2002.

XX XX 24-OCT-2001; 2001WO-US051417.

XX XX 24-OCT-2000; 2000US-0242969P.

XX XX

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 11:02:48 ; Search time 5669.37 Seconds
(without alignments)
11158.701 Million cell updates/sec

Title: US-10-087-167-104_COPY_2007_3668
Perfect score: 1662
Sequence: 1 atgaagctactgtctcttat.....ttgacgagtagtggtggtag 1662

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: gb_est1:*
 - 2: gb_est2:*
 - 3: gb_hc1:*
 - 4: gb_est3:*
 - 5: gb_est4:*
 - 6: gb_est5:*
 - 7: gb_est6:*
 - 8: gb_g881:*
 - 9: gb_g882:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	%	DB ID	Description
1	306.8	18.5	963	CNS0905M	BX067382 Single re
2	224	13.5	728	BM650826	BM650826 17006873
3	220.4	13.3	851	CNS011ME	AL100448 Drosophila
4	214.4	12.9	271	CG918549	CG918549 OIS0458-0
5	189	11.4	470	AA538642	AA538642 LD18219.5
6	183.6	11.0	607	AA664510	AA664510 ESTF52-
7	151.6	9.1	574	AI258616	AI258616 LP01848.5
8	144.8	8.7	197	CG706271	CG706271 O2S2032.0
9	143.2	8.6	1050	CNS016YX	AL107379 Drosophila
10	135.6	8.2	1031	BQ058428	BQ058428 AGENCOURT
11	134.6	8.1	918	BQ214241	BQ214241 AGENCOURT
12	134.4	8.1	867	BQ222200	BQ222200 AGENCOURT
13	134.2	8.1	667	CD673041	CD673041 fs1905.y
14	134.2	8.1	1685	CR614375	CR614375 full-leng
15	134.2	8.1	1763	CR610600	CR610600 full-leng
16	134.2	8.1	1828	CR617823	CR617823 full-leng
17	134.2	8.1	1922	CR604070	CR604070 full-leng
18	134.2	8.1	1924	CR609885	CR609885 full-leng
19	134.2	8.1	1965	CR598124	CR598124 full-leng
20	134.2	8.1	1978	CR598123	CR598123 full-leng
21	134.2	8.1	2041	BC033500	BC033500 Homo sapi
22	133	8.0	842	CNS06JUC	AL401698 T7 end of
23	132.8	8.0	721	BE382387	BE382387 601298693
24	131.8	7.9	651	CN309352	CN309352 170005999

C 25	128.8	7.7	1088	5	BX463524	BX463524
C 26	123.4	7.4	1062	5	BX367164	BX367164
C 27	123.2	7.4	1963	3	AK077620	Mus muscu
C 28	122	7.3	866	4	BG675073	BG675073
C 29	121.2	7.3	649	6	CD304821	CD304821
C 30	121	7.3	622	5	BQ636916	BQ636916
C 31	121	7.3	1026	5	BQ052341	BQ052341
C 32	119.8	7.2	957	2	BE878950	601492653
C 33	119.6	7.2	1003	5	BX344136	BX344136
C 34	119.6	7.2	1135	5	BX365740	BX365740
C 35	119.4	7.2	1138	5	BM912640	BM912640
C 36	119	7.2	965	1	AL582953	AL582953
C 37	118.4	7.1	618	6	CD309514	CD309514
C 38	117.8	7.1	986	5	BQ877581	BQ877581
C 39	117.8	7.1	2035	3	CR749648	Homo sapi
C 40	115.6	7.0	920	1	AL522738	AL522738
C 41	115	6.9	972	1	AL522399	AL522399
C 42	114	6.9	1158	4	BM554635	BM554635
C 43	113.6	6.8	444	9	AG215235	AG215235
C 44	113.2	6.8	919	4	BI654278	BI654278
C 45	113	6.8	1085	5	BX406790	BX406790

ALIGNMENTS

RESULT 1
CNS0905M
LOCUS
DEFINITION
Single read from an extremity of a full-length cDNA clone made from Anopheles gambiae total females. 5-PRIME end of clone
FK0AAC51AC03 of strain 6-9 of Anopheles gambiae (African malaria mosquito).
ACCESSION
BX067382
VERSION
BX067382.1
KEYWORDS
HTC.
SOURCE
Anopheles gambiae (African malaria mosquito)
ORGANISM
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
REFERENCE
1 (bases 1 to 963)
AUTHORS
Direct Submission
TITLE
Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :
JOURNAL
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
FEATURES
- Web : www.genoscope.cns.fr
Location/Qualifiers
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/strain="6-9"
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/note="end : 5-PRIME"

ORIGIN
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Best Local Similarity 70.8%; Pred. No. 2.8e-72;
Matches 436; Conservative 0; Mismatches 177; Indels 3; Gaps 2;
QY 814 GACATGCCCTTCGTCAGATCACAGATGACGATCTTAAACAGTCGAGCTTATTGTAGAA 873
DB 9 GAAATCCATTCCTCCGGCACATAACGGAATCCATCTCCACAGTACAATACTGTCGAG 68
QY 874 TTCCGAAAGGGACTACCGGATTCCTCAAGATATCTCAGTCCGATCAATATTATTATTA 933
DB 69 TTTCGGAGGGACTCCAGATTCACCAAGATCCCGCAG-AGGATCAGATAAGTTACTTA 127
QY 934 AAGGCGTATCAAGCGAAAGTATGATGTGCGAGTGGCGGACGGTACGACCGGGGAGC 993
DB 128 AAGGCGTGTCTCCAGTGAGTGATGATGTTTCCGAATGGCCCGCGGTACGACCGCAACC 187

QY 994 GACACGCGTGTGTTGCGAACAACAGCGCTACACGCGCGAACAATCCGCAAGCGCGGC 1053
 Db 188 GACTCCATCTCTTTGCCAACAACCGATCGTACACGCGCGAATCGTACAAGATGCGCGGC 247
 QY 1054 ATGTCCTACGTCATCAGGAGCTCTGTCACCTCTGTCGGTGTATCTCCATCAGCATG 1113
 Db 248 ATGCGGACACGATCGAGGACCTGCTGCACCTTCGCCGGCAGATGTACACGCTCACCGTG 307
 QY 1114 GACAATGTGCACTACGCGCTGCTCACCGCCATCGTTATATCTCAGACCGCGCGGCTC 1173
 Db 308 GACAACGTCGATAGCGCTGCTGACCGGATCGTCACTTCTCCGACCGCGCGGCTC 367
 QY 1174 GAGCAACCCCTTTAGTGGAGAAATCCAGAGATCTACTTTGAAGAGCTCGCGGTTTAC 1233
 Db 368 GAGAAGCGGAGCTGCTGGAACGATCCAGAGCTACTACATCGACACGCTCGCGGCTTAC 427
 QY 1234 ATTTTAATACGACAGCGCTGCGCTGCTGCGCGCTGCTGTTTCGGCAAGATCCTCGGC 1293
 Db 428 ATCTTGAACCGGACGCGGCGGACCGAAGTGTAGC--GTACGTTTCGGGAATCTGCTCG 485
 QY 1294 GTGCTGACGGAATCTCGCACGCTCGGCACGAGAACTCCAAATGTGTCATCTCCTGAAAG 1353
 Db 486 ATCTGACCGAGCTCGGACGCTCGGCAACGAGAACTCGGAGATGTGCTTCTCGCTCAAG 545
 QY 1354 CTGAAGAACAGGAACTTCGCGCATCTCTCGAGGAGATCTGGGAGTGGCGGAAGTGTG 1413
 Db 546 CTGAAGAACCGTAAGCTCGCGCTTCTCGTGGAGGAGATATGGGACGTGCGAGCATACCG 605
 QY 1414 AGCAGAAAGCTTGCCC 1429
 Db 606 CCGGTGGCTGGCTC 621

RESULT 2
 BM650826
 LOCUS 728 bp mRNA linear EST 26-FEB-2002
 DEFINITION 1700687372602 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
 19600449637314 5', mRNA sequence.

ACCESSION BM650826
 VERSION BM650826.1 GI:18950337
 KEYWORDS EST.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoides;
 Anopheles.

REFERENCE 1 (bases 1 to 728)
 AUTHORS Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
 Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
 TITLE Celera Anopheles gambiae EST project
 JOURNAL Unpublished (2002)
 COMMENT Contact: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 240453151
 Fax: 2404534580
 Email: HoltR@celera.com
 Plate: NU01004AYT row: E column: 24
 Seq primer: M13 Reverse.

FEATURES
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 /mol_type="mRNA"
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 /db_xref="taxon:7165"
 /clone="19600449637314"
 /dev_stage="Adult"
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 /clone_lib="A.Gam.ad.cDNA1"
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
 adult mosquitoes (mixed sex) frozen on liquid nitrogen.

cDNA inserts >500 bp cloned directionally into pSport 1.
 Not 1 site is 3'. Clones available through the Malaria
 Research and Reference Reagent Resource Center
 (www.malaria.mr4.org)."

ORIGIN

Query Match 13.5%; Score 224; DB 4; Length 728;
 Best Local Similarity 61.4%; Pred. No. 1.1e-49;
 Matches 403; Conservative 0; Mismatches 235; Indels 18; Gaps 2;
 QY 428 AGTTGACTGTATCGACGCGTATGAGCCCGAGTGCCTGTCGAGTCCACGTGCAAGA 487
 Db 79 AGAAGTGTCTCGCGTCCGATCGCGCGAGTGCCTGTCGCGGAGAATCAGTGCCTCA 138
 QY 488 ACAAAGAGAGAAAAGGAAGCACAGAGAGAAAACAACTGCCAGTCAAGTACGACGA 547
 Db 139 TCAAGCGGAGAGAGAGAGGCGCAAGAGAGAGAAAGGTGCGCGCGAACCCTGCGA 198
 QY 548 CAGTGACCATCATATGCTTGCCTAATGCAATGTGACCTCCCGCCCCCAGAGCGCGCA 607
 Db 199 CCACCACCGTGTAGTACAACGACAGCAGCTACAAGTCGGAGCTCTGCCGCTGCTGA 258
 QY 608 GGATTCAAGAGTGTGTCGAG-----GTTCTTAACGAGAGAACTAATGAGC 655
 Db 259 TGAAGTGTGAATCACCGCCCGCGATACCGCTACTGCCGAGAAAGCTGTGTAACG 318
 QY 656 AGAACAGACTGAAGATGTGACCGCTGTGCGGGAACCAAGTCCCTGATCCGAGGC 715
 Db 319 AAAACGCAACAAAGAAACATACCTCTGCTGACGGCGAACAGATGGCGCTCATCTACAAC 378
 QY 716 TCGTGTGTACACGAGGGGTACGACGCGCTCGGAGGAAGATCTCAAGAGAGTTACAC 775
 Db 379 TGATCTGTACCAAGTGTGCTACGACACCGTTCGGAGGAATCTCAAGAGGATAATGA 438
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 QY 836 CAGAGTACGATCTTAACAGTGCAGCTTATTGTAGAATTGCAAAAGGGACTACCGGGAT 895
 Db 493 CGGAATACCATCTCCACAGTACAATACTGTCGAGTTCCGAGAGGACTGCCAGCAT 552
 QY 896 TCTCCAAGATATCTCAGTCCGATCAAAATTACATTATTAAGGGCTCATCAAGCGAAGTGA 955
 Db 553 TTACCAAGATCCCGCAGGAGGATCAGATAACGTTACTTAAAGGCTGTCTCCAGTGAGTGA 612
 QY 956 TGATGTGCGAGTGGCGGACGCTGACGCGCGGACGAGCAGGTGCTCTTCGCGACA 1015
 Db 613 TGATGTGCGAATGGCGCGCGGTACGACCGCAAAACCGACTCCATCTCTTTGCCAACA 672
 QY 1016 ACCAGGCGTACGCGCGCAACTACCGCAAGCGGCGATGTCTTACGTATCGAG 1071
 Db 673 ACCGATCGTACGCGGACTCTGTACAGATGGGGGATGGCGGACACCATCGAG 728

RESULT 3

CNS011ME 851 bp DNA linear GSS 26-JUL-1999
 LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC
 DEFINITION BACN06K02 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.

ACCESSION AL100448
 VERSION AL100448.1 GI:5612059
 KEYWORDS GSS.
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 851)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

FEATURES	Location/Qualifiers
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ORIGIN

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Query Match      13.3%; Score 220.4; DB 9; Length 851;
Best Local Similarity 64.7%; Pred. No. 1.1e-48;
Matches 343; Conservative 0; Mismatches 186; Indels 1; Gaps 1;
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995	ACAGCGTGTGTTCCGCGAACCAACGAGCGGTACACGCGCGCAAACTACCGAAGCGCGGCA	1054
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1055	TGTTCTACGTATCAGAGACCTGTGCACTTCTGTGCGTGATCTACTCTCATAGAGCATGG	1114
386	TGGCTGATAACATTGAAGACCTGTGCAATTTCTGCCGCAAAATGTTCTTCGATGAAGTGG	445
1115	ACAAATGTGCACATACGCGTGTCTACCGGCATCGTTATATTCTCAGACCGCGCCAGGCGCTCG	1174
446	ACAAAGTCGNAATACGGGCTTCTCACTGCAATGTGATCTTCTCGGACCGCGCGGCGCTGG	505
1175	AGCAACCCCTTTTAGTGAGAGAAATCCAGAGATACTTCTGAAGACGCTGCGGGTTTACA	1234
506	AGAAGGCCCAACTAGTCTGAAGCGATCCAGAGCTACTACATCGACACGCTACGCAATTTATA	565
1235	TTTTAAATCAGACACAGCGCTCGCTCGTGGCGCGTGCTGTTCGGCAAGATCTCTCGCG	1294
566	TACTCAACCGCACTGCGGCACTCAATG-AGCTCGTCTTCTACGCAAAAGCTGCTCTCGA	624
1295	TGCTGACGGAACTGCGACGCTCGGACGCGAGAACTCCAAACATGTCATCTCGCTGAAGC	1354
625	TCCTCACCGAGCTGCGTACGCTGGGCAACGAGACGGCGAGATGTGTTTCTCACTAAAGC	684
1355	TGNAGAACAGGAACTTCCGCCATTCTCTCGAGGAGATCTGGGACGTGGCCGAAGTGTGGA	1414
685	TCAAAACCGCAAACTGCCAAAGTTCTCTCGAGGAGATCTGGGACGTTCTATGCCATCCGC	744
1415	CGACGAAGCTTGCCCCCGCGACGATGTGTCAGCTCTGGGGACGAGCTCCAC	1464
745	CATCGCTCAGTTCGCACTTTCAGATTACCCAGGAGGAGAAACGAGCGTCTC	794

RESULT 4	CG918549	271 bp	DNA	linear	GSS 16-DEC-2003
OCUS	CG918549/c				
DEFINITION	O1S0458-03C1-G10 UniformMu MutAIL Library Zea mays genomic clone O1S0458-03C1-G10, genomic survey sequence.				
ACCESSION	CG918549				
VERSION	CG918549.1	GI:39778232			
KEYWORDS	GSS.				
ORGANISM	Zea mays				
	Zea mays				
	Eukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta;				

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 271)
Latschew, S., Tan, B.-C., Settles, A.M. and McCarty, D.R.
Sequence tagged transposon insertions from the UniformMu maize
population
Unpublished (2003)
Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322

FEATURES

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1. .271
/organism="Zea mays"
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/strain="W22 (ACR, bz1-m9)"
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ORIGIN

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Matches 221	Conservative 0	Mismatches 11	Indels 0	Gaps 0
1413	GACGACGAAGCTTCGCCCGCCCGACCGATGTCAGCGCTCGGGGACGAGCTCCACTTAGACGG	1472		
234	GAAGCTAAAGTCGCCCGCCCGACCGATGTCAGCGCTCGGGGACGAGCTCCACTTAGACGG	175		
1473	CGAGACGTGCGGATGGGGCATGCCGACGCGCTAGACGATTCGATCTGACATGTTGGG	1532		
174	CGAGACGCTGGCGATGGCGCATGCCGACGCGCTAGACGATTCGATCTGACATGTTGGG	115		
1533	GGACGGGGATTTCCCGGGGTCCGGGATTTACCCGCCAGACTCCGCCCGCTCTACGGCGCTCT	1592		
114	GGACGGGGATTTCCCGGGGTCCGGGATTTACCCGCCAGACTCCGCCCGCTCTACGGCGCTCT	55		
1593	GGATATGCCGACTTCGAGTTTGGACAGATGTTTACCGATGCCCTTGGAAAT	1644		
54	GGATATGCCGACTTCGAGTTTGGACAGATGTTTACCGATGCCCTTGGAAAT	3		

RESULT 5

AA538642	470 bp	linear	EST 19-APR-2001
LD18219.5	prime LD	<i>Drosophila melanogaster</i>	embryo BlueScript
M74078	<i>Drosophila melanogaster</i>	cDNA clone LD18219	5 prime similar to
	<i>Drosophila melanogaster</i>	ecdysone receptor (Scr) mRNA,	
	complete cds,	mRNA sequence.	
AA538642			
AA538642.1	GI:2285158		
EST.		<i>Drosophila melanogaster</i>	(fruit fly)
KEYWORDS		<i>Drosophila melanogaster</i>	
SOURCE		Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;	
ORGANISM		Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
		Ephydroidea; Drosophilidae; Drosophila.	
		1 (bases 1 to 470)	
REFERENCE		Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,	
AUTHORS		Lewis,S. and Rubin,G.M.	

TITLE BDGP/HMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: <http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu>
Plate: 182 row: B column: 7
High quality sequence stop: 343.
Location/Qualifiers
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/note="Organ: embryo; Vector: BlueScript SK; Site_1:
EcoRI; Site 2: XhoI; Constructed using Stratagene ZAP-cDNA
Synthesis kit. Oligo dT-primed and directionally cloned at
EcoRI and XhoI in BlueScript SK(+/-)"
ORIGIN
Query Match 11.4%; Score 189; DB 1; Length 470;
Best Local Similarity 63.6%; Pred. No. 3.7e-40;
Matches 288; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

Qy 1012 AACACACGGCTACACGGGACAACTACCGAGGGCGCATGCTCTACGTATCGAG 1071
Db 1 AATAATAGATCATATACCGGGATTTCTACAAAATGGCCGAATGGCTGATAAATTGAA 60
Qy 1072 GACCTGTGCACTTCTGTGGTGTATGTACTCCATGACATGGACAATGTGCATACGCG 1131
Db 61 GACCTGTGCACTTCTGGCGCAATGTTCTCGATGAGGTGGACAAGCTCGAATACGCG 120
Qy 1132 CTGCTACCGCATCGTTATATTTCTACAGCGGCGGCTCGAGCAACCCCTTTTAGTG 1191
Db 121 CTTCCTACCTGATGTATCTTCTCGAGCGGCGGCTCGAGAGGCGCTAACTAGTC 180
Qy 1192 GAGGAATCCAGAGATCTACTTGAAGACGCTGCGGTTTACATTTAAATCAGACAGC 1251
Db 181 GAAGCGATCCAGAGCTACTACATCGACAGCTACGCATTTATATCTCAACCGCCTGC 240
Qy 1252 GCGTGGCTCTGCTGGCGGCTGCTTTCGGCAAGATCCTCGGCTGCTGACGGAATGCGC 1311
Db 241 GCGGACTCAATGAGCTCTGCTTCTACGAAAGCTGCTCTCGATCTCACCGAGCTGGT 300
Qy 1312 AGCTCGGACGACGAACTCCAAATGTGATCTCGCTGAAGCTGAAGAACAGGAACCTT 1371
Db 301 AGCTGGGCAACAGAACGCGGAGATGTTTCTCACTAAAGCTCAAAAACCGCAAACTG 360
Qy 1372 CGGCCATCTCTGAGGAGATCTGGGACGCTGGCGGAAGTGTGACGACGAAGCTTGCCTCC 1431
Db 361 CCCAAGTCTCTGAGGAGATCTGGGACGCTGATGCCATCCCGCCATCGTCCAGTCGCAC 420
Qy 1432 CCGACCGATGTGAGCTGCGGGACGAGCTCCAC 1464
Db 421 CTTTCAGATTACCCAGGAGGAGAACGAGCGTCTC 453

RESULT 6
LOCUS AA664510/c
DEFINITION ESTFrg2- Human Brain, Clontech Homo sapiens cDNA clone pUC19-Frg2
3', mRNA sequence.
ACCESSION AA664510
VERSION AA664510.1 GI:2619123
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 607)
Ming, H. and Huang, B.R.
TITLE Research on mechanism of p75NTR induced apoptosis
JOURNAL Unpublished (1997)
COMMENT Other ESTs: ESTFrg2+
Contact: Ming Hong
National Laboratory of Medical Molecular Biology
Chinese Academy of Medical Sciences & PUMC
5 Dongdan Santiao, Beijing 100005, P.R.China
Tel: 86-10-65296406
Email: huangbr@dm.imicams.ac.cn
Seq primer: M13 Reverse
High quality sequence stop: 607.
Location/Qualifiers
FEATURES
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1. 607
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Query Match 11.0%; Score 183.6; DB 1; Length 607;
Best Local Similarity 87.1%; Pred. No. 1.2e-38;
Matches 243; Conservative 0; Mismatches 31; Indels 5; Gaps 4;
Qy 171 GGAATCAAGCTAGAAAGCTGGAACAGCTATTTCTACTGATTTTCTCGAAGACCT 230
Db 566 GNGATCCAGGCTGAAAGCTGGAAGCGCTTTTCNACGGATTTTCCCGCGAAGCCCT 507
Qy 231 TGACATGATTTTG--AAATGGATTTCTTACAGATATAAAGCATT-GTTAAGAGATT 287
Db 506 TGACCGAGATTTTGGAAAANGGGATTTCTTTACNGGATTTAAACCAATGGTTTACAGATT 447
Qy 288 ATTTGTA-CAAGATAATGTGAATAAGATCGCTCGACAGATAGATTGGCTT-CAGTGGAG 345
Db 446 ATTTGTACCAAGATAATGTGAATAAGATCGCTCGACAGATAGATTGGCTTCCAGTGGAG 387
Qy 346 ACTGATATGCTCTTAACATTTGAGACAGCATAGATAAGTCGACATCATCATCGGAAGAG 405
Db 386 ACTGATATGCTCTTAACATTTGAGACAGCATAGATAAGTCGACATCATCATCGGAAGAG 327
Qy 406 AGTAGTAACAAGGTCAAGACAGCTTGACTGTATCGACG 444
Db 326 AGTAGTAACAAGGTCAAGACAGCTTGACTGTATCGCGC 288

RESULT 7
LOCUS AI258616
DEFINITION LP01848:5prime LP Drosophila melanogaster larval-early pupal pOT2
Drosophila melanogaster cDNA clone LP01848 5prime similar to
M74078: Ecr FBgn0000546 PID:g157318 SWISS-PROT:P34021, mRNA
sequence.
ACCESSION AI258616
VERSION AI258616.1 GI:3866141
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 574)
AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,

Lewis, S. and Rubin, G. M.
 BDGP/HMI Drosophila EST Project
 Unpublished (2001)
 Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: http://www.fruitfly.org/EST_estfruitfly.berkeley.edu
 hit genomic sequence DS05325
 Plate: 18 row: D column: 12
 High quality sequence stop: 533.
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 pOT2"
 /note="Organ: whole body; Vector: pOT2; Site 1: EcoRI;
 Site 2: XhoI; Sized fractionated cDNAs were directly
 ligated into pOT2. Plasmid cDNA library."
 "

TITLE
 JOURNAL
 COMMENT

KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE

JOURNAL
 COMMENT

FEATURES
 source

1..574
 /organism="Drosophila melanogaster"
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 pOT2"
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 Site 2: XhoI; Sized fractionated cDNAs were directly
 ligated into pOT2. Plasmid cDNA library."
 "

Query Match 9.1%; Score 151.6; DB 1; Length 574;
 Best Local Similarity 60.0%; Pred. No. 6.7e-30;
 Matches 275; Conservative 0; Mismatches 174; Indels 9; Gaps 1;

QY 630 GTTCTTAACCGAGAACTAATGAGCAGACAGACTGAAGATGTGACCCGCTGTCCGC 689
 DB 126 GCTACTACCTGATGAATATTGGCCAAGTGTCAAGCGCGCAATATACCTTCTCTTAACGTA 185

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QY 750 GGAGGAAGATCTCAAGAGAGTTACACAGACATCGCATGCTAGAGAGAGAGAGAGGAGGA 809
 DB 246 TGAAGAGGATCTCAGCGGTATAT- - - - -GAGTCAACCGATGAGACAGAGAGCCA 296

QY 810 AACTGCATCGCCCTTCGTCAGATCAGAGATGACGATCTTAAACAGTCAGCTTATGTT 869
 DB 297 AACGGAGCTCAGCTTTCGGCATATACCGAGATAACCATACTCACGGTCCAGTTGATTGT 356

QY 870 AGAATTCGCAAGGAGTACCGGATCTCCAGATATCTCAGTCCGATCAATTAACATT 929
 DB 357 TGAGTTTGTAAAGGCTACACAGCGTTTAAAGATACCCAGGAGGACAGATCACGTT 416

QY 930 ATTAAGGGCTCATCAAGCGAGTGTATGCTGCGAGTGGCGCGGATACGACGCGC 989
 DB 417 ACTAAAGGCTGCTGTCGAGGTGATGATGCTGCGTATGCGACGAGCTATGACACAG 476

QY 990 GACGGACAGCGTCTGTTTCGCAACCAACAGGCGGTACACGCGGACAACTACCGCAAGGC 1049
 DB 477 CTCGGACTCAATTTCTTCGCAATATAGATCATATACGCGGATCTTTACAAATGGC 536

QY 1050 GGGATGCTCATGCTATCAGGACCTGCTGCATTCT 1087
 DB 537 CGGAATGGCTGATAACATTGAAGACCTGCTGCATTCT 574

RESULT 8
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 LOCUS
 DEFINITION
 02S2032-03C1-D09 UniformMu MutTail Library zea mays genomic clone
 02S2032-03C1-D09, genomic survey sequence.
 ACCESSION
 CG706271
 VERSION
 CG706271.1 GI:37696881

Lewis, S. and Rubin, G. M.
 BDGP/HMI Drosophila EST Project
 Unpublished (2001)
 Contact: Stapleton, M.
 BDGP
 Lawrence Berkeley National Lab
 One Cyclotron Rd, Berkeley, CA 94720, USA
 Fax: 510 486 6798
 Email: [http://www.fruitfly.berkeley.edu](http://www.fruitfly.org/EST_estfruitfly.berkeley.edu)
 hit genomic sequence DS05325
 Plate: 18 row: D column: 12
 High quality sequence stop: 533.
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 /organism="Drosophila melanogaster"
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 Site 2: XhoI; Sized fractionated cDNAs were directly
 ligated into pOT2. Plasmid cDNA library."
 "

TITLE
 JOURNAL
 COMMENT

KEYWORDS
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 ORGANISM

REFERENCE
 AUTHORS
 TITLE

JOURNAL
 COMMENT

FEATURES
 source

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 pOT2"
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 Site 2: XhoI; Sized fractionated cDNAs were directly
 ligated into pOT2. Plasmid cDNA library."
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Query Match 9.1%; Score 151.6; DB 1; Length 574;
 Best Local Similarity 60.0%; Pred. No. 6.7e-30;
 Matches 275; Conservative 0; Mismatches 174; Indels 9; Gaps 1;

QY 630 GTTCTTAACCGAGAACTAATGAGCAGACAGACTGAAGATGTGACCCGCTGTCCGC 689
 DB 126 GCTACTACCTGATGAATATTGGCCAAGTGTCAAGCGCGCAATATACCTTCTCTTAACGTA 185

QY 690 GAACAGAGAGTCCCTGATCGGAGGCTCGTGTGTACAGGAGGGGTACGAGCGGTC 749
 DB 186 CAATCAGTTGGCGGTTATATACAAAGTAAATTTGGTACAGGATGGCTATGAGCAGGCATC 245

QY 750 GGAGGAAGATCTCAAGAGAGTTACACAGACATCGCATGCTAGAGAGAGAGAGGAGGA 809
 DB 246 TGAAGAGGATCTCAGCGGTATAT- - - - -GAGTCAACCGATGAGACAGAGAGCCA 296

QY 810 AACTGCATCGCCCTTCGTCAGATCAGAGATGACGATCTTAAACAGTCAGCTTATGTT 869
 DB 297 AACGGAGCTCAGCTTTCGGCATATACCGAGATAACCATACTCACGGTCCAGTTGATTGT 356

QY 870 AGAATTCGCAAGGAGTACCGGATCTCCAGATATCTCAGTCCGATCAATTAACATT 929
 DB 357 TGAGTTTGTAAAGGCTACACAGCGTTTAAAGATACCCAGGAGGACAGATCACGTT 416

QY 930 ATTAAGGGCTCATCAAGCGAGTGTATGCTGCGAGTGGCGCGGATACGACGCGC 989
 DB 417 ACTAAAGGCTGCTGTCGAGGTGATGATGCTGCGTATGCGACGAGCTATGACACAG 476

QY 990 GACGGACAGCGTCTGTTTCGCAACCAACAGGCGGTACACGCGGACAACTACCGCAAGGC 1049
 DB 477 CTCGGACTCAATTTCTTCGCAATATAGATCATATACGCGGATCTTTACAAATGGC 536

QY 1050 GGGATGCTCATGCTATCAGGACCTGCTGCATTCT 1087
 DB 537 CGGAATGGCTGATAACATTGAAGACCTGCTGCATTCT 574

RESULT 8
 CG706271
 LOCUS
 DEFINITION
 02S2032-03C1-D09 UniformMu MutTail Library zea mays genomic clone
 02S2032-03C1-D09, genomic survey sequence.
 ACCESSION
 CG706271
 VERSION
 CG706271.1 GI:37696881

GSS.
 Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 197)
 Latchaw, S., Tan, B.-C., Settles, A.M. and McCarty, D.R.
 Sequence tagged transposon insertions from the UniformMu maize
 population
 Unpublished (2003)
 Contact: Donald R. McCarty
 Plant Molecular and Cellular Biology Program
 University of Florida
 PO 110690 Gainesville, FL 32611-0690, USA
 Tel: 352-392-1928 x322
 Email: drm@ufl.edu
 Sequence flanking probable Mu insertion site in UniformMu line:
 02S2032-03, Primer set: C
 Class: transposon insertion site.
 Location/Qualifiers
 1..197
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 /mol_type="Genomic DNA"
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 /cultivar="UniformMu"
 /db_xref="taxon:4577"
 /clone="02S2032-03C1-D09"
 /clone_lib="UniformMu MutTail Library"
 /note="Vector: TOPO-PCR4; DNA flanking Mu transposon
 insertions in Mu inactive lines were extracted from the
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 interlaced PCR (TAIL) protocol using primers specific for
 the Mu terminal inverted repeat and a set of 16 arbitrary
 primers. Amplicons were size enriched using Sepharose 400
 spin columns and cloned into the TOPO PCR4 vector."
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Query Match 8.7%; Score 144.8; DB 9; Length 197;
 Best Local Similarity 95.5%; Pred. No. 3.6e-28;
 Matches 149; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1413 GACGACGAGCTTGGCCCCCGACCGATGTCTAGCTGGGGGACGAGCTCCACTTAGACGG 1472
 DB 38 GAAGCGTAAAGTCGCCCCCGACCGATGTCTAGCTGGGGGACGAGCTCCACTTAGACGG 97

QY 1473 CAGACAGCTGGCGATGGCGCATGCCGCGCTAGACGATTTCGATCTGCACATGTTGGG 1532
 DB 98 CGAGGACGTGGCGATGGCGCATGCCGCGCTAGACGATTTCGATCTGCACATGTTGGG 157

QY 1533 GCACGGGGATTCCCGGGTCCGGGATTTACCCCCCA 1568
 DB 158 GGACGGGGATTCCCGGGTCCGGGATTTACCCCCCA 193

RESULT 9
 CDS016YX
 LOCUS
 DEFINITION
 Drosophila melanogaster genome survey sequence SP6 end of BAC
 BACN17G18 of DrosBAC library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 AL107379
 AL107379.1 GI:5627062
 GSS.
 Drosophila melanogaster (fruit fly)
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1050)
 Genoscope.
 Direct Submission
 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)

COMMENT
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (BDGP) - <http://www.edgp.ebi.ac.uk> - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelOAC11.

FEATURES

Location/Qualifiers
source

1. 1050
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
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/plasmid="pBelOAC11"
/note="end : SP6"

ORIGIN

Query Match 8.6%; Score 143.2; DB 9; Length 1050;
Best Local Similarity 51.1%; Pred. No. 1.6e-27;
Matches 246; Conservative 1; Mismatches 231; Indels 3; Gaps 2;

QY 935 AGGCGTCATCAAGCAAGTATGATGCTGCGAGTGGCGGACGGTACGACCGCGGACGG 994
DB 388 AGGCGTGTCTGTCGGAGGTGNTGCTGCGTNTGGCAGCAGCTATGCCACAGCTCGG 447
QY 995 ACAGCGTGTCTGTCGGAACACACAGGCGGTACACGCGGACAACTACCGCAAGCGGGCA 1054
DB 448 ACTCNNTTCTTCGCGNTNATAGTCTNTNCGCGGNTTCTTNCANATGCCGGAA 507
QY 1055 TGCTCTACGTATCGAGGACCTGTGCACTTCTGTCGGTGTATGTACTTCCATGAGCATGG 1114
DB 508 TGGCTGNTAACTTGNAGACCTGTGCTNTTCTGCGCCNNNTGTTCTCGTNGNGTGG 567
QY 1115 ACATGTGCACTACCGGTGTCTACCGCATCTGTATATCTCAGACCGGCGGCGCTCG 1174
DB 568 NCCNCGTCGNATNCCGCTTCTCNCCTGCACTGTGNTCTTCGCGGCGGCGGCGCTCG 627
QY 1175 AGCAACCCCTTTTGTAGTGAGGAAATCCAGAGATACCTTGAAGACGCTGCGGGTTTACA 1234
DB 628 NGNNGCCNNNTGTCGNGCGTCCNGAGCTNCTNCACTGNNACGNTNNGNATTTTWA 687
QY 1235 TTTTAAATCAGACAGCGGTGCGCTCGCTGCGCGCTGTGTCGGCAAGATCCTCGCG 1294
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QY 1295 TGCTAGCGAACTGCGCAGCTGCGCAGCAGCAACTCCAAATGTCATCTCGCTGAAGC 1354
DB 748 TCTTCCCGG-GCTGGCTNCGCTGGGCGNCCNGNANGC--GNGTGTGTTTCTACTAAGNT 804
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DB 805 NNNAGTCCGNNNCTGNCNNGTTCTCGGNGGNTTCTGGGNGTNTNNNNNCCGN 864
QY 1415 C 1415
DB 865 C 865

RESULT 10

BQ058428
LOCUS BQ058428 1031 bp mRNA linear EST 29-MAR-2002
DEFINITION AGENCOURT 6794704 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5814274
5', mRNA Sequence.
ACCESSION BQ058428
VERSION BQ058428.1 GI:19817768
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1031)
NIH-MGC <http://mgs.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLC2067 row: k column: 11
High quality sequence stop: 634.

FEATURES

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/clone="IMAGE:5814274"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 99"

/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 8.2%; Score 135.6; DB 5; Length 1031;
Best Local Similarity 55.6%; Pred. No. 1.9e-25;
Matches 330; Conservative 0; Mismatches 249; Indels 15; Gaps 3;

QY 820 CCCTTCGTCAGATCAAGAGATGACGATCTTAACAGTCAGCTTATTGATTCGCA 879
DB 191 CGCTTTCCCACTTCCAGGAGCTGGCCATCATCTCAGTCAGGAGATCGTGGACTTCGCT 250
QY 880 AAGGACTACCGGATCTCCAAGATATCTCAGTCCGATCAAAATTAATTATTAAGCGC 939
DB 251 AAGCACTGCTGTTTCTTCAGCTGGCGGAGGACCCAGATCGCCCTCTGAAGCA 310
QY 940 TCATCAAGCGAAGTATGATGCTGCGAGTCGCGCGACGCTACGACGCGCGGACGACGACG 999
DB 311 TCCACTATCGAGATCATGTGCTAGAGACAGCCAGGCGCTACAACACGACGACAGAGTGT 370
QY 1000 GTGCTGTTCCGGAACAACAGGCGGTACACGCGGACAACTACCGAAGCGGGCAT--G 1056
DB 371 ATCACTTCTTGAAGGACTTTCACACAGCAAGACACTTCCACCGTCGAGGCTCGAG 430
QY 1057 TCCTACTGTCATCGAGGACCTGCTGCATCTTCTGCTGCTGTATGTACTCCATGAGCATGGAC 1116
DB 431 GTGGAGTTTATCAACCCCATCTTCGAGTTCTCGGGGCCATCGCGGCTGGAC 490
QY 1117 AATGTGCACTACCGCTGCTCAACGCCATCGTTTATATCT--CAGACCGGCCAGGCTC 1173
DB 491 GAGCTGAGTACGCCCTGCTCATGCCATCAACATCTTCTCGCGCGACCGGCCCAACGTG 550
QY 1174 GAGCAACCCCTTTTGTAGTGGAGGAATCCAGAGATCTACTTGAAGACGCTGCGGGTTTAC 1233
DB 551 CAGGAGCGGGCGCGGTGGAGGCGTTTGACAGAGCCCTACGTGGAGGCGCTGCTCTCTAC 610
QY 1234 ATTTTAAATCAGCACAGCGGCTCGCTTCGCTCGCGCGCTGTGTTTGGCAAGATCCTCGGC 1293
DB 611 AC-----GCCATCAAGAGCGCCGACGACCTGCGCTTCCCGCGCATGCTCATG 661
QY 1294 GTGTCGCGAACTGCGCAGCTCGGCAAGCGGACGAGAACTCCAAACATGTGCATCTCGCTGAAG 1353

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|||||
662 AAGTGGTGAAGCTGCGCAGCTGAGCTCTGTGCACTCGGAGAGCTCTTCGCTTGGCG 721
|||||
1354 CTGAGAAACAGGAAGTCTCGGCATCTCCGAGGAGATCTGGAGCTGGCCCAA 1407
|||||
722 CTCAGGACAAGAAGCTGCGCTCTGCTGGTGGAGATCTGGAGCTGCCCAA 775
|||||

RESULT 11
BQ214241 918 bp mRNA linear EST 02-MAY-2002
AGENCOURT 7589981 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6070455
5', mRNA sequence.
ACCESSION BQ214241
VERSION BQ214241.1 GI:20395641
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 918)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13354 row: m column: 16
High quality sequence stop: 626.
Location/Qualifiers
1. 918
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6070455"
/tissue types="large cell carcinoma"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

FEATURES
source
Query Match 8.1%; Score 134.6; DB 5; Length 918;
Best Local Similarity 54.3%; Pred. No. 3.4e-25;
Matches 344; Conservative 0; Mismatches 274; Indels 15; Gaps 3;

ORIGIN
QY 820 CCCTTCGTCAGATACAGAGATGACATCTTAACAGTCAGCTTATTGTAGAAATCGCA 879
DB 32 CGCTTCCCACTTCACGAGCTGGCCATCATCTCAGTCAGAGATCGTGGACTTCGCT 91
QY 880 AAGGGACTACGGGATCTCCAGATATCTCAGTCGATCAATTAATTAAGGCG 939
DB 92 AAGCAAGTGTGTTCTCTGAGCTGGCGGGAGAGACAGATCGCCCTCTGAGGCA 151
QY 940 TCATCAAGCGAAGTATGATGCTGCGAGTGGCGGAGCGTACAGCGGGCGAGCGAGC 999
DB 152 TCCACTATCAGATCATGTCTGTAGACAGCAGCGGCTTACACACAGAGAGAGTGT 211
QY 1000 GTGCTGTTCGGAACACACAGCGGTACAGCGGAGCACTACCGAGCGGGCAT---G 1056
DB 212 ATCACTTCTTGAAGGACTTCACATACAGCAAGGACGACTTCCACGTCGAGGCTG 271
QY 1057 TCCTACGTCATCGAGGACCTGCTGCACTCTGTGCGGTGTATGTACTCCATGAGCATG 1116
DB 272 GTGAGGTTTCATCAACCCCATCTTCGAGTTCTCGCGGGCCATGCGGCGCTGGAC 331

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QY 1117 AATGTGACTACGGCTGCTCACCGCCATCGTTATATTCT---CAGACCGCGCAGGCCTC 1173
DB 332 GAGCGTGAGTACGCCCTCTCATCGCCATCAACATCTTCTCGGCGGACCGGCCAACGTG 391
QY 1174 GAGCAACCCCTTTAGTGGAGGAATCCAGAGATCTACTTTGAGACGCTGGGGTTTAC 1233
DB 392 CAGGAGCGGGCGCGTGGAGGCGTTGACAGAGCCCTACGTGGAGGCGCTGCTGTCTTAC 451
QY 1234 ATTTTAAATACAGACAGCGCTGCGCTCGCTGCGCGCTGCTTTCGCGCAAGATCTCGGC 1293
DB 452 A-----CGCGATCAAGAGCGCGAGCAGCTGCGCTTCCCGGCATGCTCATG 502
QY 1294 GTGCTGACGGAACCTGCGCAGCTCGGACGAGTCTCAACATGTGATCTTCGCTGAAG 1353
DB 503 AAGCTGTGTGAGCTGCGCAGCTGAGCTCTGTGCACTCGGAGAGGTCTTCGCTTGGCG 562
QY 1354 CTGAAGAACAGGAATCTTCGCCATCTCTCGAGGAGATCTGGAGCTGGCGCAAGTGTG 1413
DB 563 CTCCAGGACAAGAAGCTGCGCTCTGCTGCGAGATCTGGGACGTCCACGAGTGAGGG 622
QY 1414 AGGACGAAGCTTGGCCCCCGGACCGATGTTCAGC 1446
DB 623 GCTGCCACCCAGCCCGCCACAGCCTTGCCTGAGC 655

RESULT 12
BQ222200 867 bp mRNA linear EST 02-MAY-2002
LOCUS AGENCOURT 7503312 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6018964
DEFINITION 5', mRNA sequence.
ACCESSION BQ222200
VERSION BQ222200.1 GI:20403609
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 867)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13220 row: 1 column: 05
High quality sequence stop: 674.
Location/Qualifiers
1. 867
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6018964"
/tissue type="epithelioid carcinoma"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_70"
/notes="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.1 Kb. Library constructed by Life
Technologies."

FEATURES
source
Query Match 8.1%; Score 134.4; DB 5; Length 867;
Best Local Similarity 55.3%; Pred. No. 3.8e-25;
Matches 330; Conservative 0; Mismatches 252; Indels 15; Gaps 3;

ORIGIN
QY 820 CCCTTCGTCAGATACAGAGATGACATCTTAACAGTCAGCTTATTGTAGAAATCGCA 879

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Db 96 CGCTTTGCCCACTTCACGAGACTGCCCATCATCTCAGTCCAGGAGATCGTGACTTCGCT 155
Qy 880 AAGGAGCTACCGGATTCCTCAAGATATCTCAGTCCGATCAAAATACATTATTAAGGCG 939
Db 156 AAGCAAGTGCCTGGTTCTCTCAGCTGGGCGGAGGACAGATCGCCCTCTCTGAAGGCA 215
Qy 940 TCATCAAGCAAGTGAATGATGCTGGAGTGGCGGACGAGTACGAGCGGCGGACGAGC 999
Db 216 TCCACTATCGAGATCATCTGCTAGAGACAGCCAGGCGCTACAAACGAGACAGAGTGT 275
Qy 1000 GTGCTGTTTCGCGAACAACAGCGGTACACGCGCGACAACTACCGCAAGCGGGGCAT--G 1056
Db 276 ATCACTTCTTGAAGGACTTCACCTACAGCAAGACAGACTTCACCGTGCAGGCTGCAG 335
Qy 1057 TCCTACGTCATCAGGAGCTCTGCGACTTCTGTGCGGTGTATGTACTCCATGAGATGGAC 1116
Db 336 GTGGAGTTTCATCAACCCCATCTTCGAGTTCTCGCGGGCCATGCGCGGCTGGGCTGGAC 395
Qy 1117 AATGTGCTACTAGCGCTGCTCAGCCCATCGTTATATCTCT--CAGACCGGCGAGGCTC 1173
Db 396 GACGCTGAGTACGCCCTCTCATCGCCATCAACATCTTCTCGCGCGACCGGCGCCAAAGTG 455
Qy 1174 GAGCAACCCCTTTAGTGGAGGAAATCCAGAGATACACTTTGAAGAGCGCTCGCGGTTTAC 1233
Db 456 CAGGAGCGCGCGCTGGAGCGTTGCAGCAGCCCTACGTGGAGGCGCTGCTGCTCTAC 515
Qy 1234 ATTTTAAATAGCACAGCGCTGCGCTCGCTGCGCGCGTGTGTTGCGGCAAGATCCTCGGC 1293
Db 516 AC-----GCGCATCAAGAGGCGCGAGACAGCTGCGCTTCCGCGCATGCTCATG 566
Qy 1294 GTGCTGACGGAACCTTCGCGCACTCGGACGCGAGACTCCACATGTGCATCTCGCTGAAG 1353
Db 567 AAGCTGTGTAGCGCTGCGCACGCTGAGCTCTGTGCACCTCGGAGCGAGTCTTCGCTTGGCG 626
Qy 1354 CTGAAGAACAGGAACTTCGCGCATCTCCTCGAGAGATCTGGGACGTGGCGCAAGTG 1410
Db 627 CTCAGGACAGAGCTGCGCGCTCTGCTGTGCGGATCTGGGAGCTCCACGAGNTG 683
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RESULT 13

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LOCUS CD673041 667 bp mRNA linear EST 24-JUN-2003
DEFINITION fg19905.v1 Human Iris cDNA (Normalized): fg Homo sapiens cDNA clone
fg19905.5, mRNA sequence.
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ACCESSION CD673041
```

```
VERSION CD673041.1 GI:32174772
```

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KEYWORDS EST.
```

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SOURCE Homo sapiens (human)
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```
ORGANISM Homo sapiens
```

```
EuKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 667)
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```
Wistow,G., Bernstein,S.L., Ray,S., Wyatt,M.K., Behal,A.,
```

```
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
```

```
Expressed sequence tag analysis of adult human iris for the NEIBank
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Project: steroid-response factors and similarities with retinal
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pigment epithelium
```

```
Mol. Vis. 8 (4), 185-195 (2002)
```

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22103462
```

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12107412
```

```
Contact: Wistow G
```

```
Section on Molecular Structure and Function
```

```
National Eye Institute
```

```
6/331, NIH, Bethesda, MD 20892-2740, USA
```

```
Tel: 301 402 3452
```

```
Fax: 301 496 0078
```

```
Email: graeme@helix.nih.gov
```

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Plate: 19 row: G column: 05
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Seq primer: M13RP1 reverse primer (ABI).
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```
Location/Qualifiers
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1..667
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/organism="Homo sapiens"
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FEATURES

```
source
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RESULT 14

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mol_type="mRNA"
db_xref="taxon:9606"
clone="fg19905"
tissue_type="iris"
dev_stage="Adult"
lab_host="EMDH10B"
clone_lib="Human Iris cDNA (Normalized): fg"
notes="Organ: Eye; Vector: pCMVSPORT6; A human iris
library (bx) was normalized by self-subtraction. One
portion of double stranded plasmid DNA representing the
library was linearized by NotI. This NotI digested library
was used as a template for biotinylated RNA synthesis
using SP6 RNA polymerase. Another portion of the double
stranded plasmid library was converted to single-stranded
circles in vitro using Gene II and Exonuclease III (Life
Technologies). Single-stranded DNA (1 mg) was hybridized
(Cot 500) with 41 mg of Bio-RNA and vector blocking
oligonucleotides. The hybridized Bio-RNA/ss-circles were
removed by streptavidin:phenol extraction. EST analysis
was performed on the library at the NIH Intramural
Sequencing Center (NISC)."
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ORIGIN

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Query Match 8.1%; Score 134.2; DB 6; Length 667;
Best Local Similarity 54.6%; Pred. No. 4e-25;
Matches 340; Conservative 0; Mismatches 268; Indels 15; Gaps 3;
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Qy 820 CCCTTCGTCAGATCAAGAGATGACGATCTTAACAGTCAGCTTATTGTAGATTCCGCA 879
Db 10 CGCTTTGCCCACTTCAGGAGCTGGCCATCATCTCAGTCCAGGAGATCGTGGAGCTTCGCT 69
Qy 880 AAGGAGCTACCGGATTTCTCAAGATATCTCAGTCCGATCAAAATTAATATTAAAGCGC 939
Db 70 AAGCAAGTGCCTGGTTCTCTGAGCTGGGCGGAGAGCCAGATCGCCCTCTCTGAAGGCA 129
Qy 940 TCATCAAGCGAAGTGAATGATGCTGCGAGTGGCGGACGCGTACGACGGGCGGACGAGCAGC 999
Db 130 TCCACTATCGAGATCATGCTGTAGAGACAGACCGAGCGCTACAACCAACGAGACAGAGTGT 189
Qy 1000 GTGCTGTTTCGGAACACACAGGCGGTACACGCGGACAACTACCGCAAGGCGGGCAT--G 1056
Db 190 ATCACTTTTGAAGGACTTTCACCTACGACGAGACGACTTCCACCGTGAGGCGCTGCAG 249
Qy 1057 TCCTACGTCATCGAGGACCTGCTGCACATCTCTGCGGTGTATGTACTCCATGAGCATGGAC 1116
Db 250 GTGGAGTTTCATCAACCCCATCTTCGAGTTCTCGCGGSCCATGCGGCGGCTGGGCTGGAC 309
Qy 1117 AATGTGCACTACGCGCTGCTCACCGCCATCGTTATATTTCT--CAGACCGGCGGAGGCTC 1173
Db 310 GACGCTGAGTACGCGCTGCTCATCGCCATCAACATCTTCTCGGCGGACCGGCGGCAACGTG 369
Qy 1174 GAGCAACCCCTTTTAGTGGAGGAAATCCAGAGATACCTTGAAGACGCTGCGGGTTTAC 1233
Db 370 CAGGAGCGGGCGCGCTGGAGGCGGTTGACAGAGCCCTACGTGAGGCGGCTGCTGCTCTAC 429
Qy 1234 ATTTTAAATCAGACACAGCGGCTGCGCTCGCTGCGGCGCTGCTGTTTGGCAAGATCCTCGGC 1293
Db 430 AC-----GCGCATCAAGAGGCGGACGAGCTGCGCTTCCCGCGCATGCTCATG 480
Qy 1294 GTGCTGACGGAACTGCGCACGCTCGGCGCAGAGAACTCCAAACATGTGCAATCTCGCTGAG 1353
Db 481 AAGCTGTGAGCGCTGCGCACGCTGAGCTCTGTGCACCTCGGAGCAGGCTTTCGCGCTTCGGG 540
Qy 1354 CTGAAGAACAGGAACTTCGCGCAATTCCTCGAGGAGATCTGGGACGTGGCGGCAAGTGTGCG 1413
Db 541 CTCAGGACAAAGAGCTGCGCGCTCTCTCTGTGCGAGATCTGGGACGCTCCACGAGTAGGGG 600
Qy 1414 ACGACGAAGCTTGCCCCCCCCGAC 1436
Db 601 GCTGCCACCCAGCCCCCAGGCC 623
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CR614375      1685 bp      mRNA      linear      HTC 21-JUL-2004
LOCUS      full-length cDNA clone CS0DM011YB14 of Petal liver of Homo sapiens
DEFINITION      (human).
ACCESSION      CR614375.1 GI:50495182
VERSION      HTC; CnSLT_cDNA.
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1685)
AUTHORS      Li W.B., Gruber C., Jessee J. and Polayes D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL      Unpublished
REMARK      Contact : Feng Liang Email : fliang@lifetech.com URL :
              http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
              Paraday Avenue
              2 (bases 1 to 1685)
REFERENCE      Genoscope.
AUTHORS      Direct Submission
TITLE      Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL      BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
              - Web : www.genoscope.cns.fr)
COMMENT      1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
              end enriched, double-strand cDNA was digested with Not I and cloned
              into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
              was normalized. Library was constructed by Life Technologies, a
              division of Invitrogen.
FEATURES      Location/Qualifiers
              source
              1..1685
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="CS0DM011YB14"
              /tissue_type="Petal liver"
              /plasmid="pCMVSPORT_6"

ORIGIN
Query Match      8.1%; Score 134.2; DB 3; Length 1685;
Best Local Similarity 54.6%; Pred. No. 5.2e-25;
Matches 340; Conservative 0; Mismatches 268; Indels 15; Gaps 3;

QY      820 CCCTCCGTCAGATACAGAGATGAGCATCTTAACAGTCGACGTATTGTAGAAATCGCA 879
DB      731 CGCTTTGCCCACTTACGAGAGCTGGCCATCATCTCAGTCCAGAGATCGTGACTTCGCT 790
QY      880 AAGGGAATACCGGATTTCTCCAAGATATCTCAGTCGATCAAAATTAATTAAGGCG 939
DB      791 AAGCAAGTCGCTGGTTCTCGAGCTGGCGCGGAGGACAGATCGCCCTCTCGAAGCA 850
QY      940 TCATCAAGCGAAGTGATGATGCTGCGAGTGGCGCAGCGTACGACCGCGGCGACGAC 999
DB      851 TCCACTATCGAGATCATGCTGCTAGAGACAGCGCGGCTACAAACAGCAGACAGAGTGT 910
QY      1000 GTGCTGTCGGAACAAACAGGCGGTACGCGCGCAACTACCGAAGGGGGCAT---G 1056
DB      911 ATCACCTTCTTGAAGGACTTCACTACAGCAAGGACGACTTCCACCGTCGAGCCCTGCAG 970
QY      1057 TCCTAGCTCATCAGGACCTGCTGCACCTCTGTCGGTGATGTAATTAATTAAGTGGAC 1116
DB      971 GTGGAGTTTCATCAACCCCATCTTCGAGTTCTCGGGCCATGCGGGCTGGGCTGGAC 1030
QY      1117 AATGTGCATACACGCGTGTCTCACCGCATCGTTATATTTCT---CAGACCGGCGAGGCTC 1173
DB      1031 GACGCTGAGTACGCGCTGCTCATCGCCATCAACATCTTCTCGGCGGACCGCCACGCTG 1090
QY      1174 GAGCAACCCCTTTAGTGGAGGAATCCAGAGATATCTATTAAGACGCTGCGGGTTTAC 1233
DB      1091 CAGGAGCGGCGCGCTGGAGGGGTTTGACGACGACCCCTTACGTGGAGGCGCTGCTCTCTAC 1150
QY      1234 ATTTTAATCAGCACAGCGGCTCGCTCGCTGCGCGCTGCTGTTTCGGCAAGATCTTCGGC 1293

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Db      1151 AC-----GGCATCAAGAGCGCCAGACAGAGCTGGCGCTTCCCGCGCATCTCATG 1201
QY      1294 GTGCTGACGGAATGCGCAGCGCTCGCAACGAGAAATCCAAATGTGCAATCTCGCTGAAG 1353
DB      1202 AAGCTGTGAGCCTGCGCAGCGCTGAGCTCTGTGCACTCGGAGCAGGTCTTCGCTTGGCG 1261
QY      1354 CTGAAGAACAGGAATCTTCGCGCCATTCCTCGAGAGAGATCTCGGACGTCGGCGAAGTGTG 1413
DB      1262 CTCAGGACAAGAGCTGCGCGCTCTGCTGTGCGAGATCTGGGACGCTCCACGAGTGAGGG 1321
QY      1414 ACGACGAGCTTGGCCCGCCGAC 1436
DB      1322 GCTGCCACCGACGCCCCACAGCC 1344

RESULT 15
LOCUS      CR610600      1763 bp      mRNA      linear      HTC 21-JUL-2004
DEFINITION      full-length cDNA clone CS0DJ010YB16 of T cells (Jurkat cell line)
              Cot 10-normalized of Homo sapiens (human).
ACCESSION      CR610600
VERSION      CR610600.1 GI:50491407
KEYWORDS      HTC; CnSLT_cDNA.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1763)
AUTHORS      Li W.B., Gruber C., Jessee J. and Polayes D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL      Unpublished
REMARK      Contact : Feng Liang Email : fliang@lifetech.com URL :
              http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
              Paraday Avenue
              2 (bases 1 to 1763)
REFERENCE      Genoscope.
AUTHORS      Direct Submission
TITLE      Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL      BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
              - Web : www.genoscope.cns.fr)
COMMENT      1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
              end enriched, double-strand cDNA was digested with Not I and cloned
              into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
              was normalized. Library was constructed by Life Technologies, a
              division of Invitrogen.
FEATURES      Location/Qualifiers
              source
              1..1763
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="CS0DJ010YB16"
              /tissue_type="T cells (Jurkat cell line) Cot
              10-normalized"
              /plasmid="pCMVSPORT_6"

ORIGIN
Query Match      8.1%; Score 134.2; DB 3; Length 1763;
Best Local Similarity 54.6%; Pred. No. 5.3e-25;
Matches 340; Conservative 0; Mismatches 268; Indels 15; Gaps 3;

QY      820 CCCTTCCTCGTCAGATCAAGAGATGACGATCTTAAACAGTCGACGTATTGTAGAAATCGCA 879
DB      817 CGCTTTGCCCACTTACGAGAGCTGGCCATCATCTCAGTCGAGAGATCGTGGAATTCGCT 876
QY      880 AAGGGAATACCGGATTTCTCCAAGATATCTCAGTCGATCAAAATTAATTAAGGCG 939
DB      877 AAGCAAGTCGCTGGTTCTCGAGCTGGCGCGGAGGACAGATCCGCTCTCTGALGGCA 936
QY      940 TCATCAAGCGAAGTGATGATGCTGCGAGTGGCGCGGACGGTACGACCGCGCGACGACG 999
DB      937 TCCACTATCGAGATCATGCTGCTAGACAGCAGCGCGGCTACAAACAGCAGACAGAGTGT 996
QY      1000 GTGCTGTTCCGGAACAAACAGGCGGTACGCGCGCAAACTACCGCAAGGGGGCAT---G 1056

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Db	997	ATCACCTTCTGTAAGGACTTCACCTCAGCAAGGACGACTTCCACCGTGAGGCCCTGCAG	1056
Qy	1057	TCCTACGTCTCATCGAGGACCTGCTGCATCTTCTGTCGGTGTATGTACTCCATGAGCATGGAC	1116
Db	1057	GTGGAGTTCATCAACCCCATCTTCGAGTCTTCGGGGCCATCGCGGGCTGGCCCTGGAC	1116
Qy	1117	AATGTGCATACGCGCTGCTCACCGCCATCGTTATATCT--CAGACCGGCCAGGCGCTC	1173
Db	1117	GACGCTGAGTAGGCCCTGCTCATCGCCATCAACATCTTCTCGGCGGACCGGCCCAACGTG	1176
Qy	1174	GAGCAACCCCTTTTAGTGGAGGAAATCCAGAGATACTACTTGAAGACGCTGCGGGTTTAC	1233
Db	1177	CAGGAGCCGGCCGCTGGAGGCGTTTCGACGAGCCCTACGTGGAGGCGCTGCTGTCTCTAC	1236
Qy	1234	ATTTTAAATCAGACACGGCGTGCCTCGCTGCGCGCTGTGTTTCGCAAGATCCCTCGGC	1293
Db	1237	AC-----GCGCATCAAGAGGCCGAGGACGAGCTGCGCTTCCCGCGCATGCTCATG	1287
Qy	1294	GTGCTGACGGAACCTGCGCACGCGCTCGGCACGAGAACTCCAACTGTGCATCTCGCTGAAG	1353
Db	1288	AAGCTGTGAGCCTTGGGACGCTGAGCTCTGTGCACTCGGAGCAGGTCTTCGCTTGGCG	1347
Qy	1354	CTGAAGAACAGGAAACTTCGSCCATTCCTCGAGAGATCTTGGGACGTGGCCGAAGTGTG	1413
Db	1348	CTCCAGGACAAGAAGCTGCCCTCTGTGTGCGAGATCTGGGACGCTCCGACGATGAGGG	1407
Qy	1414	ACGAGGAAGCTTGGCCCCCGAC	1436
Db	1408	GCTGGCCACCCAGCCCCACAGCC	1430

Search completed: April 14, 2005, 18:41:11
Job time : 5679.37 secs

Qy	690	GAACCAAGTCCCTGATCGAGGCTCTGTGTGTACAGGAGGGTACGAGCAGCGCTC	749
Db	1240	CAACCAAGTCCCTGATCGAGGCTGTGTGTACAGGACGATACGAGCAGCGCTTC	1299
	750	GGAGGAAGTCTCAAGAGATTACACAGACATGCGAGTTAGAGAGAAAGAGGAGGA	809
Db	1300	GGAAAGAGTCTCAAAAGGGTGACGAGACTTGGCAATCAGCAGATGAAGAAGACGAGA	1359
Qy	810	AACTGACATGCCCTTCGCTCAGATCACAGAGATGACGATCTTAACAGTCAGACTTATTGT	869
Db	1360	CTCAGACATGCCATTCGCCAGATCACAGAAATGACCATCCTCACAGTCAGCTAATAGT	1419
Qy	870	AGAATTCGAAAGGACTACCGGATTCTCCAAGATATCTCAGTCCGATCAATACAAATTACATT	929
Db	1420	CGAGTTTGGCCAAAGGCTTACTCTGGTTCTCAAGATCTCAACACTCACCAGATCACATT	1479
Qy	930	ATTAAGGCGTCATCAAGCGAAGTGATGCTCCGAGTGGCGCAGCGGTACGACGCGGC	989
Db	1480	ATTAAGGCATGCTCAAGCGAAGTGATGCTCCGAGTAGCGAGGCGGTACGACGCGGT	1539
Qy	990	GACGGAAGCGTGTGTTCGGGAACAACAGGCGGTACACGGCGACAACCTACCGCAGGC	1049
Db	1540	GTCGGATAGCGTTCTGTTCGCCAACAACAGGCGGTACACTCGCGACAACCTACCGCAGGC	1599
Qy	1050	GGGCGATGTCCTACGTCATCGAGGACCTGCTGCACTTCTGTCCGTGTATGTACTCCATGAG	1109
Db	1600	GGGCAATGGCGTACGTATCGAGGACCTGCTGCACTTCTGCCGTGTCATGTACTCGATGTC	1659
Qy	1110	CATGGACAAATGTGCACTACGGCTGTCTACCGCCATCGTTATATCTTCAGACGGGCCAGG	1169
Db	1660	GATGGACAAACGTGATTAACGGCTCTCACTGCCATCGTTATATCTTCGGATCGGCCGG	1719
Qy	1170	CCTCGAGCAACCCCTTTTAGTGGAGGAAATCCAGAGATCTACTTTGAAGACGCTCGCGGT	1229
Db	1720	CCTAGACGACCAACAGCTAGTAGAAGATCCAGCGGTATTACCTGAACAGCGTCCGGT	1779
Qy	1230	TTAATTTAAATCAGACACAGCGGTGCTCGCTGCGCGGTGCTGTTTCGGCAAGATCCT	1289
Db	1780	GTACATCATGAACACAGCACAGCGGTGCGCAACGCTGCGCGCTCATCTACGCAAGATTTCT	1839
Qy	1290	CGGCGTGTGACGGAATGCGCACGCTCGGCACGACAGAACTCCAACATGTGCATCTCGCT	1349
Db	1840	GTCGGTGTCTAACGAGTTGCGGACGCTGGGACATGCAGNAATTCGAACATGTGCATCTCGCT	1899
Qy	1350	GAAGCTGAAGAACAGGAAATTCGCGCAATTCCTCAGAGAGATCTGGGACGTGGCCGGAAGT	1409
Db	1900	GAAGCTCAAGAACAGGAAGCTGCGCGCGTTCCTCGAGGAGATTTTGGGACGTGGCCGACGT	1959
Qy	1410	GTCGACGACGAAGCTTGCGCCCGCCGACCGGATGTGAGCTGCGGGACAGAGTCTCACTTAGA	1469
Db	1960	GTCGACGGCGACGGCGCTGTGTGGCGCAGCGGCGCTACGGCGCTCTAGCCCGCCACG	2019
Qy	1470	CGGCGAGGACGTGGCGATGGCGCATATGCCGACGGCGTAGACGAATTCGAT	1518
Db	2020	CGATCGCGCCGCTCTGCGCGCGCGCCGCGGGCTTGCTCTTAGCGTAGTAGAT	2068

RESULT 2

```

US-08-653-648A-2
; Sequence 2, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martineau, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9

```

QY 1260 TCGCTGCGCGTGTCTGTCGCAAGATCTCTGGCGTGTCTGACGAACTGCGCAGCTCGG 1319
 Db 1561 CCGGGCGCGCGTCTCTGCGCGAGATCTCTGGCGATCTGACGGAGATCCCGACGCTGGG 1620
 QY 1320 CACGAGAACTCCCAACATCTGTCATCTCGCTGAAAGCTGAAGAACAGAACTTCGCGCCATT 1379
 Db 1621 CATGAGAACTCCCAACATCTGTCATCTCTCTCAAGCTGAAGAACAGAAAGTTCGCGCGTT 1680
 QY 1380 CCGTGGAGATCTGGGACGTCGCGCGAAGTGTGACGACG 1419
 Db 1681 CCGTGGAGATCTGGGACGTCGCGCGAAGTGTGACGACG 1720

RESULT 3

US-09-564-418-2
 ; Sequence 2, Application US/09564418
 ; Patent No. 6610828
 ; GENERAL INFORMATION:
 ; APPLICANT: Syngenta
 ; APPLICANT: Jenson, Ian
 ; APPLICANT: Martinez, Alberto
 ; APPLICANT: Greenland, Andrew James
 ; TITLE OF INVENTION: A GENE SWITCH
 ; FILE REFERENCE: 1392/4/3
 ; CURRENT APPLICATION NUMBER: US/09/564,418
 ; CURRENT FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: US 09/564,418
 ; PRIOR FILING DATE: 2000-05-03
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 1934
 ; TYPE: DNA
 ; ORGANISM: Heliothis virescens
 US-09-564-418-2

Query Match 39.7%; Score 660.4; DB 4; Length 1934;
 Best Local Similarity 80.7%; Pred. No. 2.3e-181;
 Matches 807; Conservative 0; Mismatches 166; Indels 27; Gaps 2;

QY 435 TGTATCGACGCGTATGAGCGCGAGTGTCTGCTCCGAGAGTCCAGTGAAGAACAAAG 494
 Db 733 TCTTGGCGTGGCATGAGCGCGAGTGTCTGCTCCGAGAACCACTGTGCAATGAACG 792
 QY 495 AAGAGAAAGGAGCAACAGAGAAAGAAAGCAAACTGCGAGTGTGACGACAGTGA 554
 Db 793 GAAAGAGAAAGGCGCAGAGGAAAGAAAGCAAAATGCGCGTGTGACGACGACGATGA 852
 QY 555 CGATCATATGCTGCGCATATGCAATGTCACCTCCGCGCGCGCGCGCGCGCGCGCGCG 612
 Db 853 CGATCATATGCTGCGCATATGCAATGTCACCTCCGCGCGCGCGCGCGCGCGCGCGCG 912
 QY 613 -----CAGCAAGTGTCTCCGAGTGTCTTAACGAGAGTCTAATGAGAGCAAA 659
 Db 913 GGNATGTGTCACGACGAGTGTGCGCACGATCTCTGAATGAGAACTAATGAGCAAG 972
 QY 660 CAGACTGAAGATGTGACGCGCTGTGCGGGAACAGAGTCTCCATGCGAGGCTGT 719
 Db 973 CAGATTGAAGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1032
 QY 720 GTGGTACAGAGGCGGTACGAGCAGCGCTGCGGAGAGATCTCAAGAGAGTTACAGAC 779
 Db 1033 GTGGTACAGAGGCGGTATGAAACAACTTCCGAGGAGACCTGAAGAGGTTACAGATC 1092
 QY 780 ATGCGAGTTAG 839
 Db 1093 -----GGACGAG 1140
 QY 840 GATGACGATCTTAACAGTGTGAGTATTTGTAGAAATTCGGAAGGAGTACCGGATCTC 899
 Db 1141 GATGACGATCTTACAGTGTGAGTATTTGTAGAAATTCGGAAGGAGTACCGGATCTC 1200
 QY 900 CAAGATATCTCAGTCCGATCAATTTAAGGCGTCTCAAGGAGTGTATGAT 959

Db 1201 CAAGATCTCGCAGTCCGACAGATCAGCTTATTAAAGCGCTGCTCAAGTGAAGTATGAT 1260
 QY 960 GCTCGAGTGGCGGACGCTGACGCGCGGACGAGCGAGTGTGTTTCGCGAAACCA 1019
 Db 1261 GCTCGAGTGGCTGCGCGGTATGACGCGGCGCACGACAGCGTACTGTTTCGCGAACCA 1320
 QY 1020 GGCGTACACGCGCGACAACTACCGCAAGCGCGGCGATGTCTTACGTATCGAGGACCTGCT 1079
 Db 1321 GGCGTACACTCGCGACAACTACCGCAAGCGGACGATGGCGTACGTATCGAGGACCTGCT 1380
 QY 1080 GCATTTCTGTCGCTGTATGTACTCTCATGAGCATGGAATGTGACTACGCGCTGCTCAC 1139
 Db 1381 GCATTTCTGTCGCTGTATGTACTCTCATGAGTATGATGATGATGATGATGATGATGAT 1440
 QY 1140 CGCCATGTTATATTTCTCAGACCGCGCGGCGCTGAGCAACCCCTTTTGTAGTGAAGAAAT 1199
 Db 1441 AGCCATTTGTCATCTCTCAGACCGCGCGGCGCTGAGCAACCCCTTTTGTAGTGAAGAAAT 1500
 QY 1200 CCAGAGATCTACTTTGAAGACGCTGCGGGTTTACATTTTAAATCAGCAGCGCTGCGC 1259
 Db 1501 CCAGAGATTTACTCTGAACACGCTACGGGTGTACATCTGAACAGACAGCGCTGCGC 1560
 QY 1260 TCGTGGCGCGTGTGTTTCGCAAGATCTCTGCGCGTGTGACGGAATCTGCGCAGCTCGG 1319
 Db 1561 CCGCGCGCGCTCATCTTCTGCGCGAGATCTCTGCGCATACTGACGAGATCTCGCAGCTGG 1620
 QY 1320 CACGAGAACTCCCAACATCTGCTCTGAGCTGAGAGAACAGAACTTTCGCGCAAT 1379
 Db 1621 CATGAGAACTCCCAACATCTGCTCTGAGCTGAGAGAACAGAACTTTCGCGCAAT 1680
 QY 1380 CCGTGGAGATCTGGGACGTCGCGCGAAGTGTGACGACG 1419
 Db 1681 CCGTGGAGATCTGGGACGTCGCGCGAAGTGTGACGACG 1720

RESULT 4

US-09-564-418-61/c
 ; Sequence 61, Application US/09564418
 ; Patent No. 6610828
 ; GENERAL INFORMATION:
 ; APPLICANT: Syngenta
 ; APPLICANT: Jenson, Ian
 ; APPLICANT: Martinez, Alberto
 ; APPLICANT: Greenland, Andrew James
 ; TITLE OF INVENTION: A GENE SWITCH
 ; FILE REFERENCE: 1392/4/3
 ; CURRENT APPLICATION NUMBER: US/09/564,418
 ; CURRENT FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: US 09/564,418
 ; PRIOR FILING DATE: 2000-05-03
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 61
 ; LENGTH: 1934
 ; TYPE: DNA
 ; ORGANISM: Heliothis virescens
 US-09-564-418-61

Query Match 39.7%; Score 660.4; DB 4; Length 1934;
 Best Local Similarity 80.7%; Pred. No. 2.3e-181;
 Matches 807; Conservative 0; Mismatches 166; Indels 27; Gaps 2;
 QY 435 TGTATCGACGCGTATGAGCGCGAGTGTCTGCTCCGAGAGTCCAGTGAAGAACAAAG 494
 Db 1202 TCTTGGCGTGGCATGAGCGCGGCGTGTGCTCCGAGAACCACTGTGCAATGAACG 1143
 QY 495 AAGAGAAAGGAGCAACAGAGAAAGAAAGCAAACTGCGAGTGTGACGACAGTGA 554
 Db 1142 GAAAGAGAAAGGCGCAGAGGAAAGAAAGCAAAATGCGCGTGTGACGACGACGATGA 1083
 QY 555 CGATCATATGCTGCGCATATGCAATGTCACCTCCGCGCGCGCGCGCGCGCGCGCG 612

Db 1082 CGATCAGATGCTCCCATCATGCAATGTGACCCCTCGCCCCAGGAGCGCGTGAATTC 1023
Qy 613 -----CACGAAGTGGTCCGAGGTTCTTAACGGAGAGCTAATGAGACAGAA 659
Db 1022 GGAATGTGTGACGACGAGGTGGTCCACGATTCCTGAATGAGAAGCTAATGGAACAGAA 963
Qy 660 CAGACTGAGAAATGTGACGCGCTGTGGCGAACCAGAGTCCCTGATCGGAGGCTCGT 719
Db 962 CAGATTGAAGAACGTGCCCCCTCACTGCGCAATCAGAAATGCTGATCGCAAGGCTCGT 903
Qy 720 GTGGTACCAGAGGGGTACGAGCGAGCTTATTTGTAAGATTGCAAAAGGAGATCTCAAGAGAGTTACACAGAC 779
Db 902 GTGGTACCAGAGGCTATGAACACCTTCGAGGAGACCTGAAGAGGGTTACACAGTC 843
Qy 780 ATGGCAGTTAGAAAGAGAGAGAGGAGAACTGACATGCGCTTCGTCAGATCAGACA 839
Db 842 -----GGACGAGGACGACGAAAGACTCGGATATGCGCTTCCGTCAGATTACCGA 795
Qy 840 GATGACGATCTTAACAGTGCAGCTTATTTGTAAGATTGCAAAAGGAGCTACCGGATTC 899
Db 794 GATGACGATCTTCAAGTGCAGCTCATCTGTAAGATTGCTAAGGCGCTCCCGGCTTCG 735
Qy 900 CAAGATATCTCAGTCCGATCAAAATPACATTTAAAGCGCTCATCAAGCGAAGTGATGAT 959
Db 734 CAAGATCTCGAGTCGGACAGATCACGTTATTTAAAGCGCTGCTCAAGTGAGGTGATGAT 675
Qy 960 GCTGAGTGGCGGACCGGTACGAGCGGCGACGAGCGTGTGTTCCGCGAACAACCA 1019
Db 674 GCTCGAGTGGCTCGCGGCTATGACGCGGCGCACCGACAGCGTACTGTTCCGCGAACAACCA 615
Qy 1020 GCGGTACACGCGCGCAACTACCGCAAGCGGCGATGCTTACGTACGTACGAGGACCTGCT 1079
Db 614 GCGGTACACTCGCAAACTACCGCAAGCGGCGATGCGGTACGTACGTACGAGGACCTGCT 555
Qy 1080 GCATCTTGTGCGGTATGTACTCATCAGCATGAGCAATGTGCACTACGCGCTGCTCAC 1139
Db 554 GCATCTTGTGCGGTGATGTACTCCATGATGATGATTAACGTGCTGATTTGCGCTGCTTAC 495
Qy 1140 CGCCATCGTTATTTCTCAGACCGCGGAGGCTCGAGCAACCCCTTTTGTGAGGAGAAAT 1199
Db 494 AGCCATTTGCTATCTTCTCAGACCGCGCGGCTTGAAGCAACCCCTGTTGGTGGAGGACAT 435
Qy 1200 CCAGAGATACTACTTGAAGACGCTCGGGTTTACATTTTAAATCAGCACAGCGGCTCGCC 1259
Db 434 CCAGAGATATTAACCTGACACGCTACGGGTGTACATCTGAAACAGACAGCGGCTCGCC 375
Qy 1260 TCGCTCGCGCGTGTGTCGCAAGATCTCGCGCTGTGACGGAATCGCGACGCTCGG 1319
Db 374 CCGCGCGCGCTCATCTTCCGCGAGATCTTGGGACATCTGAGGAGATCCGACGCTGGG 315
Qy 1320 CACGAGAACTCCAACTGTGATCTCGCTGAAGCTGAAGAACAGAACTTCGCGCAAT 1379
Db 314 CATGAGAACTCCAACTGTGATCTCCCTCAAGCTGAAGAACAGAAAGCTTCGCGCGTT 255
Qy 1380 CCTCGAGGAGATCTGGGAGTGGCGAGTGTGCGAGCG 1419
Db 254 CCTCGAGGAGATCTGGGAGTGGCGAGCTGGCGAGCG 215

RESULT 5

US-08-653-648A-3

; Sequence 3, Application US/08653648A

; Patent No. 6379945

; GENERAL INFORMATION:

; APPLICANT: Jepson, Ian

; APPLICANT: Greenland, Andrew

; APPLICANT: Martinez, Alberto

; TITLE OF INVENTION: A Gene Switch

; FILE REFERENCE: PPD50047/US

; CURRENT APPLICATION NUMBER: US/08/653,648A

; CURRENT FILING DATE: 1996-05-24

; PRIOR APPLICATION NUMBER: GB 9510759.5

; PRIOR FILING DATE: 1995-05-26

; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 2464
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (2241)..(2241)
; OTHER INFORMATION: Unsure
; US-08-653-648A-3

Query Match 39.7%; Score 660.4; DB 3; Length 2464;
Best Local Similarity 80.7%; Pred. No. 2.7e-181;
Matches 807; Conservative 0; Mismatches 166; Indels 27; Gaps 2;

Qy 435 TGTATGACGCGTATGAGGCGCGAGTCCGTCGTCACAGATCCACGTGCAAGACAAAG 494
Db 612 TCTTGGCTGGGATGAGCGCGAGTGGTGGCGGAGAACGAGTGTCAATGAAACG 671
Qy 495 AAGAGAAAAGGAGACAGAGAGAAAAGAACTGCCAGTCCAGTACGACGACAGTGA 554
Db 672 GAAAGAGAAAAGCGCAGAGGAGAAAAGCAATTTGCCGTCAGTACGACGACAGTAGA 731
Qy 555 CGATCATATGCTCCCATTAATGCAATGTGACCCCTCGCGCCCCAGAGGCGCAAGGATT-- 612
Db 732 CGATCATGCTCCCATCATGCAATGTGACCCCTCGCGCCCCAGAGGCGCTAGAAATTC 791
Qy 613 -----CAGCAAGTGTCCGAGGTTCTTAACGAGAAAGCTAATGAGACAGAA 659
Db 792 GGAATGTGTGACGACGAGGTGGTCCACGATTTCTGTAATGAGAGGCTAATGAGACAGAA 851
Qy 660 CAGATGAAGAAATGTGACGCGCTGTGCGGCAACCAAGTCCCTGTATCGCGAGGCTCGT 719
Db 852 CAGATTGAAGAACTGTCGCCCTCTACTGCAATCAGAACTGTTGATCGCAAGGCTCGT 911
Qy 720 GTGTATCAGAGGGGTACAGACGCGCTCGGAGGAAGATCTCAAGAGAGTTACACAGAC 779
Db 912 GTGTATCAGAGAGGCTATGAACAACTTCGAGGAAGACCTGAAGAGGGTTACACAGTC 971
Qy 780 ATGCGCTTAGAAGAAAGAGAGGAGAACTGACATGCCCTTCGCTCAGATCAGACA 839
Db 972 -----GGACGAGGACGACGAGACTCGGATATGCCGTTCCGTCAGATTACCGA 1019
Qy 840 GATGACGATCTTAACAGTGCAGCTTATTTAGAAATTCGCAAAAGGACTACCGGATTC 899
Db 1020 GATGACGATCTCAGCTCAGCTCATCGTAGAATTCGTTAAGGGCTTCGCGGCTTCGC 1079
Qy 900 CAAGATATCTCAGTCCGATCAATTTACATTTTAAAGCGCTCATCAAGCGAAGTGTGAT 959
Db 1080 CAAGATCTCGAGTCGGACCAATCAGCTTATTTAAAGCGCTGCTCAAGTGAAGTGTGAT 1139
Qy 960 GCTCGAGTGGCGGAGTACGACGCGGAGCGGACGAGCAGCGGTGTGTTCCGCGAACAACCA 1019
Db 1140 GCTCCGAGTGGCTCGGCGGTATGACGCGGCGCACCGACAGGCTACTGTTCCGCAACAACCA 1199
Qy 1020 GCGGTACACGCGGACAACTACCGCAAGGCGGCGATGTCTTACGTCATCGAGGACCTGCT 1079
Db 1200 GCGGTACACTCGCGCAAACTACCGCAAGGCGGCGATGCGCTACGTCATCGAGGACCTGCT 1259
Qy 1080 GCATCTTGTGCGGTATGATCTCCATGAGCATCGAATGTGCACTACGCGCTGCTCAC 1139
Db 1260 GCATCTTGTGCGGTGATGATCTCCATGATGATGAATGATGATGATGATGATGATGAT 1319
Qy 1140 CGCCATCGTTATTTCTCAGACCGCGCGGCTTCGAGCAACCCCTTTTGTGAGGAGAAAT 1199
Db 1320 AGCCATTTGTCATCTTCTCAGACCGCGCGGCTTGAAGCAACCCCTGTTGTTGGTGGAGACAT 1379

QY 1200 CCAGAGATCTTGAAGACGCTCGCGTTTACATTTTAATCAGCACACGCGTCCG 1259
 DB 1380 CCAGAGATTTTACCTGAAACACGCTACGCGGTGTACATCTGAAACAGAAACACGCGTCCG 1439
 QY 1260 TCGCTGCGCCGCTGCTTTCGCGCAAGATCTCGCGGTGTGACGGAATTCGCGACGCTCGG 1319
 DB 1440 CCGCGCGCGCTCATCTTCGCGGAGATCTCGGCGATCTGACGAGATCCGACGCTGG 1499
 QY 1320 CACGAGAACTCCAAATGTCATCTCGCTGAAGTGAAGAACAGGAACTTCGCGCAAT 1379
 DB 1500 CATGCAGAACTCCAAATGTCATCTCGCTGAAGTGAAGAACAGGAACTTCGCGCCGT 1559
 QY 1380 CCTCAGAGATCTCGGACGTGCGCGAAGTGTGCGACGAG 1419
 DB 1560 CCTCAGAGATCTCGGACGTGCGCGAAGTGTGCGACGAG 1599

RESULT 6

US-09-564-418-3

; Sequence 3, Application US/09564418

; Patent No. 6610828

; GENERAL INFORMATION:

; APPLICANT: Syngenta

; APPLICANT: Jepson, Ian

; APPLICANT: Martinez, Alberto

; APPLICANT: Greenland, Andrew James

; TITLE OF INVENTION: A GENE SWITCH

; FILE REFERENCE: 1392/4/3

; CURRENT APPLICATION NUMBER: US/09/564,418

; CURRENT FILING DATE: 2000-05-03

; PRIOR APPLICATION NUMBER: US 09/564,418

; PRIOR FILING DATE: 2000-05-03

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 2464

; TYPE: DNA

; ORGANISM: Heliothis virescens

; FEATURE:

; NAME/KEY: misc

; LOCATION: (2241)..(2241)

; OTHER INFORMATION: n is a, c, g, or t

US-09-564-418-3

Query Match 39.7%; Score 660.4; DB 4; Length 2464;

Best Local Similarity 80.7%; Pred. No. 2.7e-181;

Matches 807; Conservative 0; Mismatches 166; Indels 27; Gaps 2;

QY 435 TGTATCGACGCGTATGAGCCCGAGTGGTGTGTCCTCCAGAGTCCACGTGCAAGAACAAAG 494
 DB 612 TCTTGGGTGGGATGAGCCCGAGTGGTGTGTCCTCCAGAGTCCACGTGCAAGAACAAAG 671
 QY 495 AAGAGAAAGGAGACAGAGAGAAAGACAAATTCGCGTACGACGACAGTGA 554
 DB 672 GAAAGAGAAAGGAGAGAGAAAGACAAATTCGCGTACGACGACAGTGA 731
 QY 555 CGATCATATGCTTCCATATGCAATGTGACCTCCGCGCCCGAGCGCGCAAGGATT-- 612
 DB 732 CGATCATATGCTTCCATATGCAATGTGACCTCCGCGCCCGAGCGCGTGAATTTCT 791
 QY 613 -----CAGCAAGTGTCCGAGGTTCTTAAACGAGAACCTAATGAGCAGAA 659
 DB 792 GGAATGTGTGACGACGAGGTGTGCGGACGATTTCTGAAATGAGAACCTAATGAGCAGAA 851
 QY 660 CAGACTGAAGATGTGACGCGGTGTGCGGACGACGAGAGTCTGATCGAGGCTCGT 719
 DB 852 CAGATTGAAGAGCTGCGCCCTCTCACTGCAATCAGAGTCTGATCCGAGGCTCGT 911
 QY 720 GTGCTACGAGAGGGGTACGAGCAGCGGTGCGGAGGAGATCTCAAGAGAGTTACACAGAC 779
 DB 912 GTGCTACGAGAGGGGTATGCAACACCTTCGAGGAGACCTGAGAGGGTTACACAGTC 971

QY 780 ATGCGAGTTAGAAGAGAGAGAGAGAGAAATGACATGCCCTTCCGTTCAGATCACAGA 839
 DB 972 -----GGACGAGGAGCAGGAAGACTCGGATATGCGTTCCGTTCAGATTCACGA 1019
 QY 840 GATGACGATCTTAACAGTGCAGCTTATGTAGAAATTCGCAAGAGGACTACCGGATTCCTC 899
 DB 1020 GATGACGATCTTAACAGTGCAGCTTATGTAGAAATTCGCAAGAGGACTACCGGATTCCTC 1079
 QY 900 CAAGATATCTCAGTCCGATCAAAATTAATTAAGGCGCTCATCAAGCGAAGTGTGATGAT 959
 DB 1080 CAAGATCTCGAGTTCGAGCAGATCACTTATTAAGGCGTCTCAAGTGAAGTGTGATGAT 1139
 QY 960 GCTCGAGTGGCGGACGCGTACGACGCGGCGACGAGCGTGTGTTTCGCGAACAAACA 1019
 DB 1140 GCTCGAGTGGCTCGGCGGTATGACGCGGCGACCGACAGCGTACTGTTTCGCGAACAAACA 1199
 QY 1020 GCGGTACACGCGGCGACAACTACCGCAAGGCGGCGATGCTTACCTACGTCAGGAGCTGCT 1079
 DB 1200 GCGGTACACTCGGACAACTACCGCAAGGCGGCGATGCGGTACGTCAGGAGCTGCT 1259
 QY 1080 GCATCTCTGTCGCGTGTATGATCTCATGAGCATGGACAATGTGCACTACGCGCTGCTCAC 1139
 DB 1260 GCATCTCTGTCGCGTGTATGATCTCATGATGATGATGATGATGATGATGATGATGATGAT 1319
 QY 1140 CGCATCTGTTATTTCTCAGACCGGCGGCTCGAGCAACCCCTTTTATGAGGAGAAAT 1199
 DB 1320 AGCCATTGTCATCTTCTCAGACCGGCGGCGGCTTGGAGCAACCCCTGTTGGTGGAGGACAT 1379
 QY 1200 CCAGAGATCTTGAAGAGCGTGGCGGTTTACATTTTAAATCAGCACAGCGCGTCCG 1259
 DB 1380 CCAGAGATCTTGAAGAGCGTGGCGGTTTACATTTTAAATCAGCACAGCGCGTCCG 1439
 QY 1260 TCGTGGCGCGGCTGTTTCGCAAGATCTCGGCGTGTGACGGAATTCGCGACGCTCGG 1319
 DB 1440 CCGCGCGCGGCTGTCATCTTCGCGGAGATCTTCGCGGATCTGCGGAGATCCGACGCTGG 1499
 QY 1320 CACGAGAACTCCAAATGTCATCTCGCTGAAGCTGAAGAACAGGAAATTTCCGCAATT 1379
 DB 1500 CATGCAGAACTCCAAATGTCATCTCGCTGAAGCTGAAGAACAGGAAATTTCCGCGGTT 1559
 QY 1380 CCTCAGAGATCTCGGACGTGCGCGAAGTGTGCGACGAG 1419
 DB 1560 CCTCAGAGATCTCGGACGTGCGCGAAGTGTGCGACGAG 1599

RESULT 7

US-09-564-418-62/c

; Sequence 62, Application US/09564418

; Patent No. 6610828

; GENERAL INFORMATION:

; APPLICANT: Syngenta

; APPLICANT: Jepson, Ian

; APPLICANT: Martinez, Alberto

; APPLICANT: Greenland, Andrew James

; TITLE OF INVENTION: A GENE SWITCH

; FILE REFERENCE: 1392/4/3

; CURRENT APPLICATION NUMBER: US/09/564,418

; CURRENT FILING DATE: 2000-05-03

; PRIOR APPLICATION NUMBER: US 09/564,418

; PRIOR FILING DATE: 2000-05-03

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 62

; LENGTH: 2464

; TYPE: DNA

; ORGANISM: Heliothis virescens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (2241)..(2241)

; OTHER INFORMATION: n = a, c, g, or t, or i

US-09-564-418-62

Query Match 39.7%; Score 660.4; DB 4; Length 2464;

Best Local Similarity 80.7%; Pred. No. 2.7e-181; Matches 807; Conservative 0; Mismatches 166; Indels 27; Gaps 2;	
Qy	435 TGTATCGACCGGTATAGCGCCGAGTGGTCCGTCAGAGTCCACGTCGCAAGAACAAAAG 494
Db	1853 TCTTGGGTGGCATAGGCCCGAGTGGTGGTCCGGAGAACCAAGTGCATGAAACG 1794
Qy	495 AAGAGAAAGAAAGACAGAGAGAGAAAGAAACAACTGCCAGTCAAGTACGACGAGTGGGA 554
Db	1793 GAAAGAGAAAAGGCGCAGAGGAGAAAGAAACAAATTCGCCGTACAGTACGACGACAGTAGA 1734
Qy	555 CGATCATATGCTGCCATTAATGCAATGTGACCCCTCCGCCCCAGAGGGGCAAGGATT-- 612
Db	1733 CGATCATATGCTCCCATCATGCAATGTGACCCCTCCGCCCCAGAGGGCGGTAGAAATCT 1674
Qy	613 -----CACGAAGTGGTCCCGAGGTTCCTAACGGAGAGAGCTTAATGGAGCAGAA 659
Db	1673 GGAATGTGTGACGACGAGGTGGTCCACAGATTCTCTGAATGAGAAGCTTAATGGAAACAGAA 1614
Qy	660 CAGACTGAAGAAATGTGACCGCGTGTCCGCGAAACAGAAAGTCCCTGTATCGCGAGGCTCGT 719
Db	1613 CAGATTGAAGAACGTGCCGCCCTCACTGCCAATCAGAAGTCTGTTGATCGCAAGGCTCGT 1554
Qy	720 GTGTACAGAGGGGTACGAGCAGCGCTCGAGGAAGATCTCAAGAGAGTTACACAGAC 779
Db	1553 GTGTACAGAGAGGCTATGAACAACTTCGAGGAAGACTGAAGAGGTTACACAGTC 1494
Qy	780 ATGGCAGTTAGAAGAGAGAGAGAGGAAACCTGACATGCCCTTCCGTCCAGATCAGAGA 839
Db	1493 -----GGACGAGGACGACGAAGACTCGGATATGCCGTTCCTCCAGATTACCGA 1446
Qy	840 GATGACGATCTTAACAGTGCAGCTTATTTGTAGAATTCGCAAGGAGCTACCGGATCTC 899
Db	1445 GATGACGATCTTACAGTGCAGCTCATCGTGAATTCGTAAGGGCCCTCCCGGGCTTCGC 1386
Qy	900 CAAGATATCTCAGTCCGATCAAAATTTACATTTATTAAGGCGTCACTCAAGCGAAGTGATGAT 959
Db	1385 CAAGATCTCGAGTCCGACCAAGTCACTGTTATTAAGGCGTCTCAAGTGAAGTGATGAT 1326
Qy	960 GCTGCGAGTGGCGCAACGGTACGACGCGCGCAGACGAGTGTGTTCCGGCAACACCA 1019
Db	1325 GCTCGAGTGGCTCGCGGTATGACGCGGCCACCCGACAGCGTACTGTTTCGGGAAACACCA 1266
Qy	1020 GCGGTACAGCGCGACACTACCGCAAGCGGCGATGCTTACGTCATCGAGGACCTGCT 1079
Db	1265 GCGGTACACTCGCGACAACTACCGCAAGCGAGCGATGGCGTACGTCATCGAGGACCTGCT 1206
Qy	1080 GCACATCTCTCGGTATGTACTTCCATGAGCATGGACAAATGTGCACTACGCGCTGCTCAC 1139
Db	1205 GCACATCTCTCGGTGATGTACTTCCATGATGATGATTAACGTGCAATATGCGCTGCTTAC 1146
Qy	1140 CGCCATCGTTATATTCTACAGCGGCGAGGCTTCAGACAAACCCCTTTTAGTGGAGGAAT 1199
Db	1145 AGCCATTGTCTCTCAGACCGGCGCGGCTTGAGCAACCCCTGTTGGTGGAGGACAT 1086
Qy	1200 CCAGAGATCTACTTGAAGACGCTCGGGTTTACATTTTAATACAGCAGCGCTCGCC 1259
Db	1085 CCAGAGATATTACTTGAACACGCTACGGGTGTACATCTTGAAACCAAGACGCGCTCGCC 1026
Qy	1260 TCGCTCGCGCGTGTCTCGGCAAGATCTCGCGCTGTGTGACGGAACCTGCGCACGCTCGG 1319
Db	1025 CGCGCGCGGTCATCTTCGGCGAGATCTTCGGGCATCTGACGAGATCCCGCACGCTGGG 966
Qy	1320 CACGCAAGATCTCAACATGTGATCTCGCTGAAGCTGAAGAACAGGAACCTTCGCGCAT 1379
Db	965 CATGCAAGATCTCAACATGTGATCTTCCCTCAAGCTGAAGAACAGGAAGCTCCGCGGTT 906
Qy	1380 CCTCGAGGAGATCTGGGACGTGGCGAAGTGTGACGACG 1419
Db	905 CCTCGAGGAGATCTGGGACGTGGCGACGCTGGCGACGACG 866

US-08-653-648A-4 ; Sequence 4, Application US/08653648A ; Patent No. 6379945 ; GENERAL INFORMATION: ; APPLICANT: Jepson, Ian ; APPLICANT: Greenland, Andrew ; APPLICANT: Martinez, Alberto ; TITLE OF INVENTION: A Gene Switch ; FILE REFERENCE: PPD50047/US ; CURRENT APPLICATION NUMBER: US/08/653,648A ; CURRENT FILING DATE: 1996-05-24 ; PRIOR APPLICATION NUMBER: GB 9510759.5 ; PRIOR FILING DATE: 1995-05-26 ; PRIOR APPLICATION NUMBER: GB 9605656.9 ; PRIOR FILING DATE: 1996-03-18 ; PRIOR APPLICATION NUMBER: GB 9513882.2 ; PRIOR FILING DATE: 1995-07-07 ; PRIOR APPLICATION NUMBER: GB 9517316.7 ; PRIOR FILING DATE: 1995-08-24 ; NUMBER OF SEQ ID NOS: 65 ; SOFTWARE: PatentIn version 3.0 ; SEQ ID NO 4 ; LENGTH: 2745 ; TYPE: DNA ; ORGANISM: Heliothis virescens ; FEATURE: ; NAME/KEY: Unsure ; LOCATION: (2522)..(2522) ; OTHER INFORMATION: Unsure ; US-08-653-648A-4	
Query Match 39.7%; Score 660.4; DB 3; Length 2745; Best Local Similarity 80.7%; Pred. No. 2.9e-181; Matches 807; Conservative 0; Mismatches 166; Indels 27; Gaps 2;	
Qy	435 TGTATCGACCGGTATAGCGCCGAGTGGTCCGTCAGAGTCCACGTCGCAAGAACAAAAG 494
Db	893 TCTTGGGTGGCATAGGCCCGAGTGGTGGTCCGGAGAACCAAGTGTCAATGAAACG 952
Qy	495 AAGAGAAAGAAAGACAGAGAGAAAGAAACAACTGCCAGTCAAGTACGACGACAGTGGGA 554
Db	953 GAAAGAGAAAAGCGCAGAGGAGAAAGAAATTCGCCGTCAAGTACGACGACAGTAGA 1012
Qy	555 CGATCATATGCTGCCATAATGCAATGTGACCCCTCCGCCCCAGAGGGGCAAGGATT-- 612
Db	1013 CGATCATATGCTCCCATCATGCAATGTGACCCCTCCGCCCCAGAGGGCGGTAGAAATCT 1072
Qy	613 -----CACGAAGTGGTCCCGAGGTTCCTAACCGAGAGAGCTTAATGGAGCAGAA 659
Db	1073 GGAATGTGTGACGACGAGGTGGTCCACAGATTCTCTGAATGAGAAGCTTAATGGAAACAGAA 1132
Qy	660 CAGACTCAAGAAATGTGACGCGCTGTCCGGCAACAGAAAGTCCCTGTATCGCGAGGCTCGT 719
Db	1133 CAGATTGAAGAACTGCGCCGCCCTCACTGCAATCAAGAGTCTGTTGATCGCAAGGCTCGT 1192
Qy	720 GTGTACAGAGGGGTACGAGCAGCGCTCGAGGAAGATCTCAAGAGAGTTACACAGAC 779
Db	1193 GTGTACAGAGAGGCTATGAACAACTTCGAGGAAGACCTGAAAGGGGTTACACAGTC 1252
Qy	780 ATGCGAGTTAGAGAGAGAGAGAGGAGAACTGACATGCCCTTCGCTCAGATCAGAGA 839
Db	1253 -----GGACGAGGACGACGAAGACTCGGATATGCCGTTCGCTCAGATTACCGA 1300
Qy	840 GATCAGCATCTTAACAGTGCAGCTTATTTGTAGAATTCGCAAGGAGGACTTACCGGATCTTC 899
Db	1301 GATGACGATCTCAGAGTGCAGCTCATCGTAGAATTCGTAAGGGCCCTCCCGGGCTTCGC 1360
Qy	900 CAAGATATCTCAGTCCGATCAAAATTAATTATTAAGCGCTCATCAAGCGAGTGTGAT 959
Db	1361 CAAGATCTCGAGTCCGACGAGATCAGCTTATTAAGCGCGTGTCTCAAGTGAAGTGTGAT 1420
Qy	960 GCTCGAGTGGCGGACGCTACGACGCGGCGACGACGAGCTGTCTGTTCCGCAACAAACA 1019

1421	Db	GTCCGAGTGGCTCGCGGGTATGACGCGGCCACCGACAGGTACTGTTTCGGCAACAA	1480
1020	Qy	GGCGTACACGCGCAACAATCTACCGAAGCGGGCATGTCTCTACGTCATCGAGCACTGCT	1079
1481	Db	GGCGTACACTCGCGCAACAATCTACCGAAGCGAGCATGGCGTACGTCATCGAGCACTGCT	1540
1080	Qy	GCACCTTCTGTCGGTGTATGTATCTCAATGACATGAGCAATGTGCATACGCGCTGCTCAC	1139
1541	Db	GCACCTTCTGTCGGTGTATGTATCTCAATGATGATGGATTAACGTGCATTTATGCGCTGCTTAC	1600
1140	Qy	CGGCATCGTTATATTTCTCAGACCGCGCAGCGCTTCGAGCAACCCCTTTTATGTCAGGAAAT	1199
1601	Db	AGCCATGTGCATCTTCTCAGACCGCGCGGGCTTGAGCAACCCCTGTTGTCGAGGAGAT	1660
1200	Qy	CCAGAGATACTACTGAAAGACGTCGCGGGTTTACATTTTAAATCAGCACAGCGCTCGCC	1259
1661	Db	CCAGAGATATTACTGAAACAACGCTACGCGGTGTATCATCTCTGAACAGAAACAGCGCTCGC	1720
1260	Qy	TCCCTCGCGCTGCTGTTTCGGCAAGATCCTTCGCGGTGCTGACGGAATCGCGACGCTCGG	1319
1721	Db	CCGCGGCGCGCTCATCTTTCGGCGAGATCCTTGGGCATACTGACGGAGATCGCACGCTGGG	1780
1320	Qy	CAGCGAAACTCCAAACATGTGCATCTCGCTGAAAGCTGAAGAACAGGAACTTTCGCGCAT	1379
1781	Db	CATGCAACAATCCAAACATGTGCATCTCCCTCAAGCTGAAGAACAGGAACTGCGCGCTT	1840
1380	Qy	CCTCGAGGAGATCTGGGACGTGCGCGGAAGTGTTCGACGACG	1419
1841	Db	CCTCGAGGAGATCTGGGACGTGCGGACGTGCGGACGTGCGGACGACG	1880

RESULT 9

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US-09-564-418--4
; Sequence 4, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jepson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 2745
; TYPE: DNA
; ORGANISM: Heliothis virescens
; FEATURE:
; NAME/KEY: misc
; LOCATION: (2522)..(2522)
; OTHER INFORMATION: n=a, c, g, or t
; US-09-564-418--4

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	Query Match	39.7%	Score 560.4	DB 4	Length 2745
	Best Local Similarity	80.7%	Pred. No. 2.9e-181		
	Matches 807	Conservative	0	Mismatches 166	Indels 27
	Gaps				
Qy	435	TGTTATCGACGGTATGAGGCCGCGAGTGCCTGCCAGAGTCCACAGTGCAGAACAAAAG	494		
Db	893	TC TTGCGGTGGCATATGAGGCCGCGAGTGCCTGCTCCGAGAACACAGTGTGCMATGAAACG	952		
Qy	495	AAGAGAAAAGCAAGCACAGAGAGAAAAAGACAAATCTGCAGTCTAGTACGACACAGTGGGA	554		
Db	953	GAAGAGAAAAGGCCAGAGGGNAAGAACAATTTGCCGCTAGTACGACGACAGTAGA	1012		
Qy	555	CGATCATATGCTGCCATAATGCAATGTGACCTTCCGCCCCCCAGAGGGCGCAAGGNT--	612		
Db	1013	CGATCACATGCTCCCATCTGCAATGTGACCTTCCGCCCCCCAGAGGGCGGTAGAAATCT	1072		

Qy	613	-----CACGAAGTCGTC	CGAGTTCCTTA	CGGAGACGCTAATCGACAGAA	659		
Db	1073	GGAAATGTGTGCACAC	CGAGGTGGTGC	CAGATCTCTGAA	TGAAGAGCTTAATCGAACAGAA	1132	
Qy	660	CACACTGAAGAAATGT	GACGCCGCTGT	CGCGCAACCAAGTCCCT	GATCGCAGGCTCGT	719	
Db	1133	CAGATTGAAGACGTG	CCCCCCTC	ACTGCCAATCAGAAGT	CGTTGATCGCAAGGCTCGT	1192	
Qy	720	GTGGTACGAGGAGGT	ACGAGCCGTCG	GAGGAGAGATCTCA	GAGAGATTACACAGAC	779	
Db	1193	GTGGTACCGGAGGCT	TATGAACAACCTT	CCGAGGAGACCTG	AAGAGGGTTACACAGTC	1252	
Qy	780	ATGGCAGTTAGAGAA	GAGAGAGGAAACT	GTGACATCGCTCCCT	TCAGATCACAGA	839	
Db	1253	-----GGACGAGGA	CGACGAGACTCG	GATATGCCGTTCCGT	TCAGATTACCGA	1300	
Qy	840	GATGACGATCTTAAC	AGTCAGCTTATT	GTAGAAATTCG	CAAAAGGAGACTAC	CGGGATTCCTC	899
Db	1301	GATGACGATTCTCAC	AGTGCAGCTCAT	CTGTAGAAATTCG	TAAAGGGCTCTCC	CGGGCTTCGC	1360
Qy	900	CAAGATATCTCAGT	CCGATCAAAATTA	TACATTTAAAGGCGT	CATCAAGCGAGTGA	TGATGAT	959
Db	1361	CAAGATCTCCAGT	CCGACCAATCA	CGTTATTAAAGGCGT	GTCTAAGTGA	TGATGAT	1420
Qy	960	GCTCGCAGTGGCG	ACGCGTACGACGCG	CGGACAGCGTCTCT	GTTCGCGAAACAACCA	1019	
Db	1421	GCTCGAGTGGCTCG	GGCGGTATGACGGG	CCACCGAGGTACTGT	TCGGAACAACCA	1480	
Qy	1020	GGGCTACACGCGG	CAACAATPACCG	AAAGCGGCGATGT	CTTACGTCA	TACGAGACCTGCT	1079
Db	1481	GGCGTACACTCGC	GACAACTPACCG	AAAGCGGCGATGG	CGGTACGTCA	TACGAGACCTGCT	1540
Qy	1080	GCACCTTCGTGGT	GTATGTACTCCAT	GATGAGCATGGACA	TGTGCACTACG	CGCTGCTCAC	1139
Db	1541	GCACCTTCGTGGT	GTACTTCCAT	GTATGATGGATAC	GTGCATTTAT	CGCTGCTTAC	1500
Qy	1140	CGCCATCGTTATATT	CTCAGACCGCG	CAGGCCCTCG	AGCAACCCCTTT	TAGTGAGGAAAT	1199
Db	1601	AGCAATGTGTATCT	TTCAGACCGCG	CCCGGCTTGAG	CAACCCCTTGT	TGTGAGGAGAT	1660
Qy	1200	CCAGAGATACTTGT	GAAGACGTGCGGG	TTTATATTT	AAATACGACAG	CGCGTCCG	1259
Db	1661	CCAGAGATATTA	CTGAAACGCTAC	CGGTGTACATCCT	GAACAGAAACAG	CGCGTCCG	1720
Qy	1260	TCGCTGGCGGTGT	GTTCGGCAAGAT	TCCTCGCGTCT	GCAGCACTGCG	CGACGCTCGG	1319
Db	1721	CCGCGGCGCGGT	GTATCTTCGG	CGAGATTCCTGGG	CACTACTGACGAG	ATCCGACGCTGG	1780
Qy	1320	CACGCAGAACTCCA	CAATGTGTGATCT	CGCTGAAGCTGA	AGAACAGGAACTT	TCGCGCAT	1379
Db	1781	CATCGAAGATCC	CAACATGTGTGAT	CTCTCCCTCA	AGTGAACAGG	AAAGCTGCGCGCGTT	1840
Qy	1380	CCTCGAGGAGAT	CTGGGACGTGG	CCGAAAGTGTG	ACGACG	1419	
Db	1841	CCTCGAGGAGAT	CTGGGACGTGG	CCGACGTGGG	ACGACG	1880	

RESIT.T 10

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RESULT 10
US-08-653-648A-10/c
; Sequence 10, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9

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; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 10
; LENGTH: 2463
; TYPE: DNA
; ORGANISM: Heliothis virescens
; NAME/KEY: modified base
; LOCATION: (224)..(224)
; OTHER INFORMATION: 1
US-08-653-648A-10

Query Match 39.6%; Score 657.6; DB 3; Length 2463;
Best Local Similarity 80.4%; Pred. No. 1.8e-180;
Matches 806; Conservative 0; Mismatches 169; Indels 27; Gaps 2;

QY 435 TGTATCGACGGCTATGAGCGCCGAGTGGTGTCTCCAGAGTCCAGTGTCAAGAAACAAAG 494
DB 1852 TCTTCGGGTGGCATGAGCGCCGAGTGGTGTGCGGAGAACCAAGTGTCAATGAACG 1793
QY 495 AAGAGAAAGGAAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 554
DB 1792 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1733
QY 555 GCATCATATGCTGCTCAATGATGACCTCCGCGCCCGAGAGGGGCAAGGATT-- 612
DB 1732 CGATCACATGCTCCCATCATGCAATGATGACCTCCGCGCCCGAGAGGGGCGGTAGATTCT 1673
QY 613 -----CACGAAGTGGTCCCGAGGTTCTTAACGGAGAGAGTAAATGGAGCAGAA 659
DB 1672 GGAATGTGTGACAGCAGAGGTGTGCGACGATTCTCTGAATGAGAGAGTAAATGGAGCAGAA 1613
QY 660 CAGACTGAAGATGTGACCGCCCTGTGCGGAGAACAGAGTCCCTGATCGCGAGGCTGT 719
DB 1612 CAGATTGAAGAACGTGCGCCCTCACTGCCAATCAGAGTGGTTGATCGCAAGGCTGT 1553
QY 720 GTGTACAGAGAGGGGTACGACGCGTGGAGGAGATCTCAAGAGAGTTACACAGAC 779
DB 1552 GTGGTACAGAGAGGGGTATGAACACCTTCCGAGAGAGACCTGAGAGGGTTACACATC 1493
QY 780 ATGGCAGTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 839
DB 1492 -----GGACGAGGAGCAGAGAGACTCGGATATGCGGTTCCGTCAGATTACCGA 1445
QY 840 GATGACGATCTTAACAGTGCAGCTTATTGTAGAAATTCGCAAGGAGCTACCGGATTCTC 899
DB 1444 GATGACGATCTTACAGTGCAGCTCATGCTAGAAATTCGTAAGGGCTCCCGGGGTTCCG 1385
QY 900 CAAGATATCTCAGTCCGATCAAAATTACATTTATTAAGGGCTCATCAAGCGAGTGTATGAT 959
DB 1384 CAAGATCTCGAGTCCGACAGATCACGTTATTAAAGGGCTCTCAAGTGAAGTGTATGAT 1325
QY 960 GCTGCGAGTGGCGCAGCGTACGACGCGCGAGCAGAGCGTGTGTTGCGGAAACAACA 1019
DB 1324 GCTCCGAGTGGCTCGCGGTATGACGCGGCCACCGACAGCGTACTGTTCCGCAACAACA 1265
QY 1020 GGGTACACGCGGACAACTACCGCAAGGGGCGATGCTCTACGTCATCGAGGACTGCT 1079
DB 1264 GCGGTACATCGCGCAAACTACCGCAAGGGGAGGAGCATGGCGTACGTCATCGAGGACTGCT 1205
QY 1080 GCATTTCTGTCGGTGTATGTACTTCCATGAGCATGGAGCAATGTGCACTACGCGCTGCTAC 1139
DB 1204 GCATTTCTGTCGGTGTATGTACTTCCATGATGATGATGATGATGATGATGATGATGATGAT 1145
QY 1140 CGCATCTGTTATTTCTCAGACCGCGGAGGCGCTCGAGCAACCCCTTTAGTGAGGAGAT 1199
DB 1144 AGCCATTGTCATTTCTCAGACCGCGGCTTGAGCAACCCCTTTGTTGGTGGAGACAT 1085

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QY 1200 CCAGAGATACTACTTGAAGACGCTGGGCTTTTACATTTTAAATCAGACAGCGCGTCGCC 1259
DB 1084 CCAGAGATATTACTTGAACACGCTACGCTACGCTGTATCATCTCTGAACCAAGACAGCGCGTCGCC 1025
QY 1260 TCGCTGCGCGCTGCTGTTTCGGCAAGATCTTCGGCGTGTGCTGAGCGAACTGCGCACGCTCGG 1319
DB 1024 CCGCGCGCGCTCATCTTCGGCGAGATCTTCGGGCATCTGCGGAGATCCGACGAGATCCGACGCTGGG 965
QY 1320 CAGCGAGAACTCCAAACATGTGCTGCTGCTGAGCTGAGAGCTGAAGACAGGAACTTCCGCGCAT 1379
DB 964 CATCGAGAACTCCAAACATGTGCTGCTGCTGAGCTGAGAGCTGAAGACAGGAACTTCCGCGCAT 905
QY 1380 CTTCTGAGGAGATCTGGGAGCTGGCGGAGTGGCGGAGTGTGCTGAGCGAGAA 1421
DB 904 CTTCTGAGGAGATCTGGGAGCTGGCGGAGTGGCGGAGTGTGCTGAGCGAGAA 863

RESULT 11
US-08-891-298-2
; Sequence 2, Application US/08891298
; Patent No. 630488
; GENERAL INFORMATION:
; APPLICANT: Gage, Frederick H.
; APPLICANT: Suhr, Steven T.
; TITLE OF INVENTION: Modified Lepidopteran Receptors
; TITLE OF INVENTION: and Hybrid Multi-Functional Proteins for Use in Transcription
; TITLE OF INVENTION: and Transgene Expression Regulation
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows DEMONSTRATION Version 2.0D
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,298
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 185..2002
; OTHER INFORMATION:
US-08-891-298-2

Query Match 39.2%; Score 652.2; DB 3; Length 2711;
Best Local Similarity 77.7%; Pred. No. 7e-179;
Matches 815; Conservative 0; Mismatches 228; Indels 6; Gaps 2;

QY 405 GAGTAGTAAAGAGTCAAGACAGATTGACTGTATCGAGCGGTATGAGCGCGGAGTGGT 464

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955 GAAATGTCAGAGTTCGATTAAGAAATGCTAGCGGTAGGAATGAGCGCTGTAATGTGT 1014
465 COTCCAGAGTCCAGTCAAGAAACAAAGAGAGAAAGGAGACACAGAGGAAAGA 524
1015 CATACAGAGCCAGTAAATAAAGACAGGCAAGAAAGAAAGAAAGGAATA-- 1072
525 CAAACTGCCAGTCAGTACGACACAGTGGACCATCATATGCTGCTGCATATCAATGTGA 584
1073 -TTATTACCTGTGTAGTACACACAGTTCGAAGACCATGCCCCGATCATCATCATGTGA 1131
585 CCTCCGCCCCAGAGCGGCAAGGATTCACGAAGTGTGTCGAGGTCTTCAACGAGAA 644
1132 TCACCTCCGCCGAGCGCCAGGATTCACGAAGTGTGTCGAGGTATCTTTTCGAGAA 1191
645 GCTAATGGAGACAGACACTGAAGATGTGACGCGCTGTGCGGGAACAGAAATCCCT 704
1192 GCTGATGGAGACAGACAGGCAAGAAACATACCACCATTTGTGCGGCAATCAGAAGTCTCT 1251
705 GATCGGAGCTCGTGTGTACAGGAGGCTACGAGCAGCGCTCGAGGAAAGATCTCAA 764
1252 GATCGGAGCTCGTGTGTACAGGAGGATATGAGCAGCGCTCGACGAGATCTCAA 1311
765 GAGAGTTACACAGATCGCAGTTAGAAAGAGAGAGGAGAACTGACATGCCCTT 824
1312 AAGAGTTACGAGACTTGGCAGT---CGATGAGAGGACGAGGAATCCGATCTACCTTT 1368
825 CCGTCAGATCACAGAGATGACGATCTTAAAGTGCAGCTTATTGTAGAAATTCGCAAGGG 884
1369 CCGCCAGATCACGAGATGACGATCTTAAAGTGCAGCTTATTGTAGAAATTCGCAAGGG 1428
885 ACTACCGGATCTCAAGATATCTCAGTCCGATCAAAATTAATTAAGCGCTCATC 944
1429 TCTACCGGCTTTTCAAGATATCACAGTCTGATCAAAATTAATTAAGCGCTCATC 1488
945 AAGCGAAGTATGATGCTCGAGTGGCGGACCGGTACGACGCGCGGACGAGCGTGCT 1004
1489 CAGCGAGTGTATGATGCTCGGCTGGGAGGCGATACGACGCGCGCTCCGACAGCGTGCT 1548
1005 GTTCCGAAACAAACGAGCTTACAGCGCGGAACTACCGGAGCGGCGATGCTTACGT 1064
1549 GTTCCGAAACAAACGAGCTTACAGCGCGGAACTACCGGAGCGGCGATGCTTACGT 1608
1065 CATCGAGAGCTCTGCACTTCTGCTGGTGTATGATCTCATGATGAGCAATGTGCA 1124
1609 CATCGAGAGCTCTGCACTTCTGCTGGTGTATGATCTCATGATGAGCAATGTGCA 1668
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1185 TTTAGTGGAGAAATCCAGAGATACCTATTGAAAGACGCTCGGCTTTTACATTTTAATCA 1244
1729 GCTGGTAGAGAGATCCAGAGATACCTATTGAAAGACGCTCGGCTTTTACATTTTAATCA 1788
1245 GCACAGCGCTCGCTCGCTCGGCGGCTGCTGCTGGCAAGATCTCGGCGCTGCTGAGGA 1304
1789 GAACAGCGCTCGCTCGGCGGCTGCTGCTGGCAAGATCTCGGCGGCTGCTGAGGA 1848
1305 ACTCGCAGCTCGGCGGCTGCTGCTGGCAAGATCTCGGCGGCTGCTGAGGA 1364
1849 GCTACGCGCTCGGCGGCTGCTGCTGGCAAGATCTCGGCGGCTGCTGAGGA 1908
1365 GAAACTTCGCGCATCTTCGAGGAGATCTGGAGCGTGGCGGAGTGTGCGAGGAGCT 1424
1909 GAAGCTCGCGCGCTTCTCGAGGAGATCTGGAGCGTGGCGGAGTGTGCGAGGAGCT 1968
1425 TGCCCCCGGACCGATGTACGCTGGGGG 1453
1969 CACGGTGTGCGCGGCGGCGGCGGCGGCGG 1997

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; Sequence 9, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1934
; TYPE: DNA
; ORGANISM: Heliothis virescens
; US-08-653-648A-9

Query Match 39.2%; Score 650.8; DB 3; Length 1934;
Best Local Similarity 80.1%; Pred. No. 1.5e-178;
Matches 801; Conservative 0; Mismatches 172; Indels 27; Gaps 2;

QY 435 TGTATCGAGCGCTATGAGCCCGAGTGTCTGTCAGAGTCCACGTGCAAGAAACAAAG 494
DB 1202 TCTTGGCGTGGCATGAGCCCGAGTGTGTCGCGGAGAACACAGTGTGCAATGAAACG 1143
QY 495 AAGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 554
DB 1142 GAAAGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1083
QY 555 CGATCATATGCTGCGCATATGCAATGTCACCTCGCGCCCGAGAGCGGCAAGGATTT-- 612
DB 1082 CGATCATATGCTGCGCATATGCAATGTCACCTCGCGCCCGAGAGCGGCTAGATTTCT 1023
QY 613 -----CAGCAAGTGTCTCCGAGGTTCTTAACGAGGAGGAGGAGGAGGAGGAGGAGGAG 659
DB 1022 GGAATGTGTGACGACAGAGTGTGTGCGCACAGTTCCTGATGAGAGCTAATGAAACAGAA 963
QY 660 CAGACTGAAGATGTGACGCGCTGTGCGGGAACAGAGTCCCTCATCGGAGGCTCGT 719
DB 962 CAGATTGAAGAACGTCGCGCCCTCTCACTGCCAATCAGAAAGTCTGTTGATCGCAAGGCTCGT 903
QY 720 GTGGTACGAGGAGGAGTACGAGCAGCGCTCGGAGGAGGAGTCTCAAGAGAGTTCACAGAG 779
DB 902 GTGGTACGAGGAGGAGTATGAAACACCTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 843
QY 780 ATGCGCAGTTAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 839
DB 842 -----GGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 795
QY 840 GATGAGCATCTTAACAGTGTGAGTATTTAGAAATTCGCAAGGAGGAGTACCGGAGTCTC 899
DB 794 GATGAGCATCTTCAAGTGTGAGTATTCGTTAGAAATTCGTTAAGGAGGAGGAGGAGGAGGAG 735
QY 900 CAGATATCTCAGTGTGAGTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 959
DB 734 CAAGATCTCGAGTGTGAGTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 675
QY 960 GCTCGGAGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1019
DB 674 GCTCGGAGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 615
QY 1020 GCGGTACACGCGGAGCAAACTTACCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1079
DB 614 GCGGTACACCTCGGAGCAAACTTACCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 555

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 11:19:52 ; Search time 999.495 Seconds

(without alignments)
10087.965 Million cell updates/sec

Title: US-10-087-167-104_COPY_2007_3668

Perfect score: 1662

Sequence: 1 atgagctactgtcttctat.....ttgacgagtagcgggtgtag 1662

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5622541 seqs, 303335566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1662	100.0	3972	16	US-10-087-167-104
2	1612.8	97.0	1767	16	US-10-087-167-122
3	1552.2	93.4	1800	16	US-10-087-167-126
4	1441.6	86.7	1776	16	US-10-087-167-118
5	1431.8	86.1	1863	16	US-10-087-167-136
6	1426.6	85.8	1848	16	US-10-087-167-134
7	1425	85.7	1428	16	US-10-087-167-128
8	1424	85.7	1767	16	US-10-087-167-120
9	1422	85.6	1809	16	US-10-087-167-142
10	1314.2	79.1	1782	16	US-10-087-167-124
11	1216.6	73.2	1518	16	US-10-087-167-93

12	1167.4	70.2	1500	16	US-10-087-167-69
13	1166	70.2	1800	16	US-10-087-167-147
14	1109.8	66.8	1533	16	US-10-087-167-79
15	996.2	59.9	1509	16	US-10-087-167-65
16	978.6	58.9	1500	16	US-10-087-167-67
17	976.6	58.8	1500	16	US-10-087-167-67
18	976.6	58.8	2840	15	US-10-083-842A-6
19	954.6	57.4	1551	16	US-10-087-167-1
20	954.6	57.4	1551	16	US-10-087-167-71
21	951.8	57.3	1464	16	US-10-087-167-83
22	899.4	53.5	1524	16	US-10-087-167-77
23	871.8	52.5	1515	16	US-10-087-167-75
24	831.6	50.0	838	16	US-10-087-167-7
25	799.8	48.1	1506	16	US-10-087-167-63
26	760.2	45.7	1503	16	US-10-087-167-91
27	734.2	44.2	1542	16	US-10-087-167-73
28	715	43.0	1491	16	US-10-087-167-85
29	681	41.0	2126	14	US-10-295-370-1
30	681	41.0	2126	15	US-10-292-356-1
31	681	41.0	2126	15	US-10-292-324-1
32	660.4	39.7	1934	17	US-10-606-060A-2
33	660.4	39.7	2464	17	US-10-606-060A-3
34	660.4	39.7	2464	17	US-10-606-060A-4
35	652.2	39.2	2711	9	US-09-952-559-2
36	623.4	37.5	1110	9	US-09-965-703-2
37	623.4	37.5	1110	17	US-10-239-134-2
38	623.4	37.5	1288	9	US-09-965-703-1
39	623.4	37.5	1288	17	US-10-239-134-1
40	623.4	37.5	1288	17	US-10-468-199-59
41	623.4	37.5	1542	9	US-09-965-703-58
42	623.4	37.5	1542	17	US-10-239-134-49
43	623.2	37.5	948	17	US-10-606-060A-6
44	617	37.1	1054	9	US-09-965-703-3
45	617	37.1	1054	17	US-10-239-134-3

ALIGNMENTS

RESULT 1
US-10-087-167-104
Sequence 104, Application US/10087167
Publication No. US20030154509A1
GENERAL INFORMATION:
APPLICANT: Pascal, Erica
APPLICANT: Valentine, Scott
APPLICANT: Brown, Jeffrey
APPLICANT: Cockrell, Adam
APPLICANT: Johnson, Brian
TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
FILE REFERENCE: 50018A
CURRENT APPLICATION NUMBER: US/10/087,167
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/242,969
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PatentIn version 3.1
SEQ ID NO 104
LENGTH: 3972
TYPE: DNA
ORGANISM: synthetic construct
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(3972)
OTHER INFORMATION: GAL4-Manduca ECR-VP16 fragment in pCGS202
NAME/KEY: CDS
LOCATION: (2007)..(3668)
OTHER INFORMATION: GAL4-Manduca ECR-VP16 chimera
US-10-087-167-104
Query Match 100.0%; Score 1662; DB 16; Length 3972;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAAGCTACTGTTCTTCTATCGAACAGCATGCGATATTTTCCGAGCTTAAAAAGCTCAAG	60
Db	2007	ATGAAGCTACTGTTCTTCTATCGAACAGCATGCGATATTTTCCGAGCTTAAAAAGCTCAAG	2066
Qy	61	TGCTCCAAAGAAAAACCGAAGTGGCCCAAGTGTCTGAAGAACAACTCGGGAGTGTCCGTAC	120
Db	2067	TGCTCCAAAGAAAAACCGAAGTGGCCCAAGTGTCTGAAGAACAACTCGGGAGTGTCCGTAC	2126
Qy	121	TCTCCCAAACCAAAGAGTCTCCGCTGACTAGGSCACATCTGACAGAAAGTGGAAATCAAGG	180
Db	2127	TCTCCCAAACCAAAGAGTCTCCGCTGACTAGGSCACATCTGACAGAAAGTGGAAATCAAGG	2186
Qy	181	CTGAAAGACTGGAAACAGCTATTTTCTACTGATTTTTTCTCTCGAAGAACCCTTGACATGATT	240
Db	2187	CTGAAAGACTGGAAACAGCTATTTTCTACTGATTTTTTCTCTCGAAGAACCCTTGACATGATT	2246
Qy	241	TTGAAATATGGATTTCTTACAGGATATAAAAGCATTTGTTAAACAGGATTTATTTGTACAAAGAT	300
Db	2247	TTGAAATATGGATTTCTTACAGGATATAAAAGCATTTGTTAAACAGGATTTATTTGTACAAAGAT	2306
Qy	301	AATGTGAATAAGATGCCGTACACAGATAGATTTGGCTTCAGTGGAGACTGATATGCCCTCTA	360
Db	2307	AATGTGAATAAGATGCCGTACACAGATAGATTTGGCTTCAGTGGAGACTGATATGCCCTCTA	2366
Qy	361	ACATTGAGACAGCTAGAAATAAGTGCACATCATCTCGGAAGAGAGTAGTATACAAAGGT	420
Db	2367	ACATTGAGACAGCTAGAAATAAGTGCACATCATCTCGGAAGAGAGTAGTATACAAAGGT	2426
Qy	421	CAAAAGACAGTTGACTGTATCGACCGCTATGAGGCCCGAGTGCCTCGTCCAGAGTCCACG	480
Db	2427	CAAAAGACAGTTGACTGTATCGACCGCTATGAGGCCCGAGTGCCTCGTCCAGAGTCCACG	2486
Qy	481	TGCAAGAACAAAAGAGAGAAAAGAACACAGAGAGAAAAGACAAACTGCCAGTCAGT	540
Db	2487	TGCAAGAACAAAAGAGAGAAAAGAACACAGAGAGAAAAGACAAACTGCCAGTCAGT	2546
Qy	541	ACGACGACAGTGGACGATCATATGCTTGCCATAATGTCAATGTGACCTTCGCCCCCAGAG	600
Db	2547	ACGACGACAGTGGACGATCATATGCTTGCCATAATGTCAATGTGACCTTCGCCCCCAGAG	2606
Qy	601	CGCGCAGGATTCACGAGTGGTCCCGAGGTTCTTAACGGAGAGAGCTAATGGAGCAGAAC	660
Db	2607	CGCGCAGGATTCACGAGTGGTCCCGAGGTTCTTAACGGAGAGAGCTAATGGAGCAGAAC	2666
Qy	661	AGACTGAAGAAATGTGACCCGCTGTGCGCGAACACAGAAAGTCCCTGATCGCGAGGCTCGTG	720
Db	2667	AGACTGAAGAAATGTGACCCGCTGTGCGCGAACACAGAAAGTCCCTGATCGCGAGGCTCGTG	2726
Qy	721	TGGTACGAGAGGGGTACGACACCGCTCGAGAGAGATCTCAGAGAGTTTACACAGACA	780
Db	2727	TGGTACGAGAGGGGTACGACACCGCTCGAGAGAGATCTCAGAGAGTTTACACAGACA	2786
Qy	781	TGGCAGTTTAGAAGAAGAGAGAGAGGAAACTGCATGCCCCTTTCCGTCAGATCACAGAG	840
Db	2787	TGGCAGTTTAGAAGAAGAGAGAGAGGAAACTGCATGCCCCTTTCCGTCAGATCACAGAG	2846
Qy	841	ATGACGATCTTAAACAGTSCAGCTTTATTTGTAGAAATTCGCAAAAGGACTACCGGGATTTCTCC	900
Db	2847	ATGACGATCTTAAACAGTSCAGCTTTATTTGTAGAAATTCGCAAAAGGACTACCGGGATTTCTCC	2906
Qy	901	AAGATATCTCAGTCCGATCAAAATTACATTTAAGGGCTCATCAAGCGAGTGATCATG	960
Db	2907	AAGATATCTCAGTCCGATCAAAATTACATTTAAGGGCTCATCAAGCGAGTGATCATG	2966
Qy	961	CTGCGAGTGGCGCAGCTGACGACGCGCAGCAGACGCTGCTGTTTCGCGAAACAACCG	1020
Db	2967	CTGCGAGTGGCGCAGCTGACGACGCGCAGCAGACGCTGCTGTTTCGCGAAACAACCG	3026
Qy	1021	GGTTACACGCGCAACACTACCGAAGCGGGCATGTCTTACGTCTATCAGGACCTGCTG	1080
Db	3027	GGTTACACGCGCAACACTACCGAAGCGGGCATGTCTTACGTCTATCAGGACCTGCTG	3086

Qy	1081	CAC	TTCTGT	CGGTGTAT	GTACT	CCATG	AGCAT	GGCA	CAATG	TGCA	CTAC	CGGCT	CTCACC	1144					
Db	3087	CAC	TTCTGT	CGGTGTAT	GTACT	CCATG	AGCAT	GGCA	CAATG	TGCA	CTAC	CGGCT	CTCACC	3146					
Qy	1141	GCC	ATCG	TTATAT	TTCT	CAG	ACGG	CCAGG	CGCT	CGAG	CAAC	CCCTTT	TAGTGG	AGGAATC	1200				
Db	3147	GCC	ATCG	TTATAT	TTCT	CAG	ACGG	CCAGG	CGCT	CGAG	CAAC	CCCTTT	TAGTGG	AGGAATC	3206				
Qy	1201	CAG	AGAT	ACTACT	TTGA	AGAC	CGCT	CGGG	TTTAC	ATTTT	AAAT	CAG	CA	CAGCGG	TCGCCT	1260			
Db	3207	CAG	AGAT	ACTACT	TTGA	AGAC	CGCT	CGGG	TTTAC	ATTTT	AAAT	CAG	CA	CAGCGG	TCGCCT	3266			
Qy	1261	CGT	GCG	CGTGT	TTG	TCG	CA	AGAT	CTCT	CGG	CGT	GCTG	AG	CGA	CTCG	CGC	1320		
Db	3267	CGT	GCG	CGTGT	TTG	TCG	CA	AGAT	CTCT	CGG	CGT	GCTG	AG	CGA	CTCG	CGC	3326		
Qy	1321	ACG	CAG	AACT	CCAC	ATG	TCAT	CTCG	CTCA	AGCT	GAAG	AAAC	AGG	AAACT	TC	CGCC	ATTC	1380	
Db	3327	ACG	CAG	AACT	CCAC	ATG	TCAT	CTCG	CTCA	AGCT	GAAG	AAAC	AGG	AAACT	TC	CGCC	ATTC	3386	
Qy	1381	CTC	GAG	GAGAT	CTGG	ACG	TGG	CGCG	GAAG	TGTC	AC	AGCT	TC	AC	AGCA	AGCT	TG	1440	
Db	3387	CTC	GAG	GAGAT	CTGG	ACG	TGG	CGCG	GAAG	TGTC	AC	AGCT	TC	AC	AGCA	AGCT	TG	3446	
Qy	1441	GT	CAG	CC	TGGG	AG	CA	GCAG	CTC	CA	ATTAG	ACG	CGG	AGG	ACG	TG	CGG	ATC	1500
Db	3447	GT	CAG	CC	TGGG	AG	CA	GCAG	CTC	CA	ATTAG	ACG	CGG	AGG	ACG	TG	CGG	ATC	3506
Qy	1501	GCG	CTA	GAC	CA	CA	TTTC	GAT	CTG	GA	CA	TGTT	CGG	GGG	ACG	GGG	ATTT	1560	
Db	3507	GCG	CTA	GAC	CA	CA	TTTC	GAT	CTG	GA	CA	TGTT	CGG	GGG	ACG	GGG	ATTT	3566	
Qy	1561	AC	CCCC	CA	CA	CA	CT	CCG	CCCC	CT	CG	CG	CT	CT	CG	ATAT	TG	1620	
Db	3567	AC	CCCC	CA	CA	CA	CT	CCG	CCCC	CT	CG	CG	CT	CT	CG	ATAT	TG	3626	
Qy	1621	AT	GTTT	AC	CG	AT	CG	CC	TTT	GG	AA	TTG	AC	AG	AT	AC	GG	1682	
Db	3627	AT	GTTT	AC	CG	AT	CG	CC	TTT	GG	AA	TTG	AC	AG	AT	AC	GG	3688	

RESULT 2

```

US-10-087-167-122
; Sequence 122, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 122
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1767)
; OTHER INFORMATION: Ecdysone receptor chimera G(M) FV
US-10-087-167-122

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Query Match	97.0%;	Score 1612.8;	DB 16;	Length 1767;
Best Local Similarity	98.8%;	Pred. No. 0;		
Matches 1642:	Conservative	0;	Mismatches 2;	Indels 18; Gaps 1;

QY 1 ATGAAGTACTGCTCTTCTATCGAACAAGCATCGGATATTTGCGGACTTTAAAGCTCAAG 60
 DB |||||
 QY 124 ATGAAGTACTGCTCTTCTATCGAACAAGCATCGGATATTTGCGGACTTTAAAGCTCAAG 183
 DB |||||
 QY 61 TGCTCCAAAGAAAAACCGAAGTGCACCAGTGTCTGAAGAACAACTGGGAGTGTGCTTAC 120
 DB |||||
 QY 184 TGCTCCAAAGAAAAACCGAAGTGCACCAGTGTCTGAAGAACAACTGGGAGTGTGCTTAC 243
 DB |||||
 QY 121 TCTCCAAAACCAAAAGGTCTCGCTGACTAGGCGACATCTGACAGAGTGAATCAAGG 180
 DB |||||
 QY 244 TCTCCAAAACCAAAAGGTCTCGCTGACTAGGCGACATCTGACAGAGTGAATCAAGG 303
 DB |||||
 QY 181 CTGAAAGACTGCAACAGCTATTTCTACTGATTTTCTCGAAGAACCTTGCATGATT 240
 DB |||||
 QY 304 CTGAAAGACTGCAACAGCTATTTCTACTGATTTTCTCGAAGAACCTTGCATGATT 363
 DB |||||
 QY 241 TTGAAAATGGAATCTTTTACAGGATATAAAGCAATTTGTTAAAGGATTTTGTACAAGAT 300
 DB |||||
 QY 364 TTGAAAATGGAATCTTTTACAGGATATAAAGCAATTTGTTAAAGGATTTTGTACAAGAT 423
 DB |||||
 QY 301 AATGTGAATAAAGATGCGCTGACAGATAGATTGGCTTCACTGAGAGTACTGCTCTA 360
 DB |||||
 QY 424 AATGTGAATAAAGATGCGCTGACAGATAGATTGGCTTCACTGAGAGTACTGCTCTA 483
 DB |||||
 QY 361 ACATTGAGACAGATAGATAGTGCAGCATCATCATCGAAGAGAGTAGTAACAAAGT 420
 DB |||||
 QY 484 ACATTGAGACAGATAGATAGTGCAGCATCATCATCGAAGAGAGTAGTAACAAAGT 543
 DB |||||
 QY 421 CAAAGACAGTTGACTGTATCGAGCGGTATGAGCGCGAGTGGTCTGCTCCAGAGTCCAG 480
 DB |||||
 QY 544 CAAAGACAGTTGACTGTATCGAGCGGTATGAGCGCGAGTGGTCTGCTCCAGAGTCCAG 603
 DB |||||
 QY 481 TGAAGAACAAAGAAAGAAAGGAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 DB |||||
 QY 604 TGAAGAACAAAGAAAGAAAGGAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 663
 DB |||||
 QY 541 ACAGCAGACAGTGCAGCATCATATGCTGCGCATATGCAATGACCTCGCGCCCGCAGAG 600
 DB |||||
 QY 664 ACAGCAGACAGTGCAGCATCATATGCTGCGCATATGCAATGACCTCGCGCCCGCAGAG 723
 DB |||||
 QY 601 GCGGCAAGGATTCAGAAAGTGGTCCGAGGTTCTTAACGGAGAGAGTAAATGAGAGAGAAC 660
 DB |||||
 QY 724 GCGGCAAGGATTCAGAAAGTGGTCCGAGGTTCTTAACGGAGAGAGTAAATGAGAGAGAAC 783
 DB |||||
 QY 661 AGACTGAAGATGTGAGCGGCTGTGCGGAAACAGAGTCCCTGATCGCGAGGCTCGT 720
 DB |||||
 QY 784 AGACTGAAGATGTGAGCGGCTGTGCGGAAACAGAGTCCCTGATCGCGAGGCTCGT 843
 DB |||||
 QY 721 TGGTACAGAGGGGTACGAGAGCGCTCGAGGAGAGATCTCAAGAGAGTTACACAGACA 780
 DB |||||
 QY 844 TGGTACAGAGGGGTACGAGAGCGCTCGAGGAGAGATCTCAAGAGAGTTACACAGACA 903
 DB |||||
 QY 781 TGGCAGTTAGAAGAAAGAGAGAGGAGAACTGACATGCTCCCTCCGTCAGATCAAGAG 840
 DB |||||
 QY 904 TGGCAGTTAGAAGAAAGAGAGAGGAGAACTGACATGCTCCCTCCGTCAGATCAAGAG 963
 DB |||||
 QY 841 ATGACGATCTTAACAGTGCAGTTATTTGAGAAATTCGCAAGGAGTACCGGATTTCC 900
 DB |||||
 QY 964 ATGACGATCTTAACAGTGCAGTTATTTGAGAAATTCGCAAGGAGTACCGGATTTCC 1023
 DB |||||
 QY 901 AGATATCTCAGTCCGATCAAAATTAATTAAGGCGTATCAAGCGAGTGAATGATG 960
 DB |||||
 QY 1024 AGATATCTCAGTCCGATCAAAATTAATTAAGGCGTATCAAGCGAGTGAATGATG 1083
 DB |||||
 QY 961 CTGCGAGTGGCGGACCGGTACGAGCGCGGCGACGAGCGTGTGTTGCGGAAACCAAG 1020
 DB |||||
 QY 1084 CTGCGAGTGGCGGACCGGTACGAGCGCGGCGACGAGCGTGTGTTGCGGAAACCAAG 1143
 DB |||||
 QY 1021 GCGTACACGCGGACAACTACCGCAAGCGCGGAGTGTCTACGTATCGAGGAGCTGCTG 1080
 DB |||||
 QY 1144 GCGTACACGCGGACAACTACCGCAAGCGCGGAGTGTCTACGTATCGAGGAGCTGCTG 1203
 DB |||||
 QY 1081 CACTTCTGCTGATGTACTCCATGAGCATGAGCAATGACATGCGCTGCTCACC 1140
 DB |||||

DB 1204 CACTTCTGCTGATGTACTCCATGAGCATGACAAATGTGCATACGCGTGTCTACC 1263
 QY |||||
 QY 1141 GCGATCTTATTTCTCAGACCGCGCTCGAGCAACCCCTTTTATGTGGAGGAATC 1200
 DB |||||
 QY 1264 GCGATCTTATTTCTCAGACCGCGCGCTCGAGCAACCCCTTTTATGTGGAGGAATC 1323
 DB |||||
 QY 1201 CAGAGATACTACTTTGAAGACGCTCGGGTTTTACATTTTAAATCAGACAGCGGCTGCGCT 1260
 DB |||||
 QY 1324 CAGAGATACTACTTTGAAGACGCTCGGGTTTTACATTTTAAATCAGACAGCGGCTGCGCT 1383
 DB |||||
 QY 1261 GCGTGGCGGCTGCTGTTGCGCAAGATCTCGCGCTGCTGACGGAACCTGGGACGCTCGG 1320
 DB |||||
 QY 1384 GCGTGGCGGCTGCTGTTGCGCAAGATCTCGCGCTGCTGACGGAACCTGGGACGCTCGG 1443
 DB |||||
 QY 1321 ACGCAGAACTCCAAACATGTGATCTCGTGAAGCTGAAGAAACAGGAAACTTCGCGCATTC 1380
 DB |||||
 QY 1444 ACGCAGAACTCCAAACATGTGATCTCGTGAAGCTGAAGAAACAGGAAACTTCGCGCATTC 1503
 DB |||||
 QY 1381 CTCGAGGAGATCTGGGACGCTGCGCAAGTGTGACGACGAAAGCTTGCCTCCCGACCGAT 1440
 DB |||||
 QY 1504 CTCGAGGAGATCTGGGACGCT-----GAAGCTTGCCTCCCGACCGAT 1545
 DB |||||
 QY 1441 GTCAGCTGGGGACGAGCTCCATTAAGCGCGAGGAGCTGGCGCATGCGCATGCGGAC 1500
 DB |||||
 QY 1546 GTCAGCTGGGGACGAGCTCCATTAAGCGCGAGGAGCTGGCGCATGCGCATGCGGAC 1605
 DB |||||
 QY 1501 GCGCTAGACGATTTGATCTGACATGTTGGGGACGCGGATTTCCCGGCTCCGGATTT 1560
 DB |||||
 QY 1606 GCGCTAGACGATTTGATCTGACATGTTGGGGACGCGGATTTCCCGGCTCCGGATTT 1665
 DB |||||
 QY 1561 ACCCGCCACGACTCCGCGCTTACGCGCTCTGATATGCGGACTTCGAGTTTGAGCAG 1620
 DB |||||
 QY 1666 ACCCGCCACGACTCCGCGCTTACGCGCTCTGATATGCGGACTTCGAGTTTGAGCAG 1725
 DB |||||
 QY 1621 ATGTTTACGATGCTCTTGAATTAACGATGACGATGCGTGGGTAG 1662
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 QY 1726 ATGTTTACGATGCTCTTGAATTAACGATGACGATGCGTGGGTAG 1767
 DB |||||

RESULT 3

US-10-087-167-126
 ; Sequence 126, Application US/10087167
 ; Publication No. US20030154509A1

GENERAL INFORMATION:

; APPLICANT: Pascal, Erica
 ; APPLICANT: Valentine, Scott
 ; APPLICANT: Brown, Jeffrey
 ; APPLICANT: Cockrell, Adam
 ; APPLICANT: Johnson, Brian
 ; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
 ; FILE REFERENCE: 50018A
 ; CURRENT APPLICATION NUMBER: US/10/087,167
 ; CURRENT FILING DATE: 2002-03-01
 ; PRIOR APPLICATION NUMBER: US 60/242,969
 ; PRIOR FILING DATE: 2000-10-24
 ; NUMBER OF SEQ ID NOS: 148
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 126
 ; LENGTH: 1800
 ; TYPE: DNA
 ; ORGANISM: Synthetic Construct
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1800)
 ; OTHER INFORMATION: Ecdysone receptor chimera G(B)MV
 US-10-087-167-126

Query Match 93.4%; Score 1552.2; DB 16; Length 1800;

Best Local Similarity 95.9%; Pred. No. 0;

Matches 1609; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

QY 1 ATGAAGTACTGCTCTTCTATCGAACAAGCATGCGATATTTGCGGAGCTTAAAAAGCTCAAG 60

Db 124 ATGAAGTACTGTCTTCTTATCGAACCAAGCATGCGATATTTGCCGACTTAAAAAGCTCAAG 183
 Qy 61 TGCTCAAGAAAAACCGAAGTGCAGGAGTGTCTGAAGAACAACTGGAGTGTGCTTAC 120
 Db 184 TGCTCAAGAAAAACCGAAGTGCAGGAGTGTCTGAAGAACAACTGGAGTGTGCTTAC 243
 Qy 121 TCTCCCAAAACCAAAAGGTCTCCGCTGACTAGGGCACATCTGACAGAAAGTGGAAATCAAGG 180
 Db 244 TCTCCCAAAACCAAAAGGTCTCCGCTGACTAGGGCACATCTGACAGAAAGTGGAAATCAAGG 303
 Qy 181 CTAGAAAGACTGGAACAGCTATTTCTACTGATTTTCTCTGAGAAAGACTTGACATGATT 240
 Db 304 CTAGAAAGACTGGAACAGCTATTTCTACTGATTTTCTCTGAGAAAGACTTGACATGATT 363
 Qy 241 TTGAAAATGGATCTTTTACAGATATTAAGCAATTTGTTAAACAGGATTTTGTACAAGAT 300
 Db 364 TTGAAAATGGATCTTTTACAGATATTAAGCAATTTGTTAAACAGGATTTTGTACAAGAT 423
 Qy 301 ATGTGTAATGAAGTCCGCTACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTA 360
 Db 424 ATGTGTAATGAAGTCCGCTACAGATAGATTGGCTTCAGTGGAGACTGATATGCTCTA 483
 Qy 361 ACATTGAGACACATAGATAAGTGCACATCATCATCGAAAGAGAGTAGTAACAAGGT 420
 Db 484 ACATTGAGACACATAGATAAGTGCACATCATCATCGAAAGAGAGTAGTAACAAGGT 543
 Qy 421 CAAAGACAGTTGACTGTATGCAAGGTATGAGGCCGAGTGGTGTGCCAGAGTCCAGG 480
 Db 544 CAAAGACAGTTGACTGTATGCAAGGTATGAGGCCGAGTGGTGTGCCAGAGTCCAGG 603
 Qy 481 TCAGAAACAAAG 540
 Db 604 TCAGAAACAAAG 663
 Qy 541 ACAGACAGAGTGGACGATCATATGCTGCCATAATGCAATGTGACCTCCGCCCCAGAG 600
 Db 664 ACAGACAGAGTGGACGATCATATGCTGCCATAATGCAATGTGACCTCCGCCCCAGAG 723
 Qy 601 GCGGCAAGGATTACGAAGTGTGCGAGGTTCTTAACGGAGAGAGTAAATGAGAGAGAGAG 660
 Db 724 GCGGCAAGGATTACGAAGTGTGCGAGGTTCTTAACGGAGAGAGTAAATGAGAGAGAGAG 783
 Qy 661 AGACTGAAGATGTGACGCGCTGTGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 Db 784 AGACTGAAGATGTGACGCGCTGTGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 843
 Qy 721 TGCTACAGAGGGGTACAG 780
 Db 844 TGCTACAGAGGGGTATGACAACTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 903
 Qy 781 TGCGAGTTAG 840
 Db 904 TGCGAGTTCGAG 960
 Qy 841 ATGACAGTCTTACAGTGCAGCTTATGTAGATTTGCAAGAGGAGTACCGGAGTCTCC 900
 Db 961 ATGACAGTCTGACAGTTCAACTCATGTAAGATTCGAAAGGCTTCCAGGCTTCGCC 1020
 Qy 901 AAGATATCTCAGTCCGATCAAAATACATTTAAAGCGCTCATCAAGCGAGTGTGATG 960
 Db 1021 AAGATCTCGAGTCCGATCAAAATACATTTAAAGCGCTTCAAGTGAAGTGTGATG 1080
 Qy 961 CTGCGAGTGGCGGACGGTACGACGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 Db 1081 CTGCGAGTGGCGGCGGTACGACGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
 Qy 1021 GCGTACAGCGGCAACTACCGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 Db 1141 GCGTACTCCGCGCAACTACCGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
 Qy 1081 CACTTCTGTCGGTGTATGTACTCCATGAGATGAGCAATGTGCACTACGCGCTGCTCACC 1140
 Db 1201 CACTTCTGTCGGTGTATGTACTCCATGATGATGATGATGATGATGATGATGATGATGATGATG 1260

Qy 1141 GCCATCGTTATATTTCTCAGACCGGCCAGGCTCGAGCAACCCCTTTTATGTGAGGAAATC 1200
 Db 1261 GCCATGTGATTTTCTCAGACCGGCCCTGGCTCGAGCAACCCCTTTTATGTGAGGAAATC 1320
 Qy 1201 CAGAGATATCTACTTGAAGACGCTCGGGTTTACATTTTAAATCAGCAGCGCGTCCGCT 1260
 Db 1321 CAGCGGTATTAACCTGAAACACGCTCGGGTGTACATCTTTGAACCAAAAAGTGCCTCGCG 1380
 Qy 1261 CGCTGCGCGTGTCTCGGCAAGATCCTCGCGTGTGACGGAACCTCGCACGCTCGGC 1320
 Db 1381 CGCTGCGCGTGTCTCGGCAAGATCCTCGGATATTTGACGAGCTCGGACCTCGGC 1440
 Qy 1321 ACGAGAACTCCAACATGTGATCTGCTGAAGTGAAGAACAGGAAATCTTCGCGCATTC 1380
 Db 1441 ATGAGAACTCCAACATGTGATCTGCTGAAGTGAAGAACAGGAAATCTTCGCGCATTC 1500
 Qy 1381 CTCGAGAGATCTCGGAGCTGCCGAGTGTGACGAGCAAGAGCTTGCCTCCCGACCGAT 1440
 Db 1501 CTCGAGAGATCTCGGAGCTGCCGAGTGTGACGAGCAAGAGCTTGCCTCCCGACCGAT 1554
 Qy 1441 GTCAGCTTGGGGAGAGCTCCACTTAGACGCGAGAGAGCTGGCGATGCGCATGCGCGAC 1500
 Db 1555 GTCAGCTTGGGGAGAGCTCCACTTAGACGCGAGAGAGCTGGCGATGCGCGATGCGCGAC 1614
 Qy 1501 GCGCTAGACGATTTTCGATCTGACATGTTGGGGGAGCGGGATTTCCCGGATTTT 1560
 Db 1615 GCGCTAGACGATTTTCGATCTGACATGTTGGGGGAGCGGGATTTCCCGGATTTT 1674
 Qy 1561 ACCCCCCAGACTCCGCCCCCTACCGGCTCTGGATATGCGCGACTTCGAGTTTGAGCAG 1620
 Db 1675 ACCCCCCAGACTCCGCCCCCTACCGGCTCTGGATATGCGCGACTTCGAGTTTGAGCAG 1734
 Qy 1621 ATGTTTACGATGCTTGGATTTGACGAGTACGTTGGGTAG 1662
 Db 1735 ATGTTTACGATGCTTGGATTTGACGAGTACGTTGGGTAG 1776

RESULT 5

US-10-087-167-136
 ; Sequence 136, Application US/10087167
 ; Publication No. US20030154509A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pascal, Erica
 ; APPLICANT: Valentine, Scott
 ; APPLICANT: Brown, Jeffrey
 ; APPLICANT: Cockrell, Brian
 ; APPLICANT: Johnson, Brian
 ; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
 ; FILE REFERENCE: 50018A
 ; CURRENT APPLICATION NUMBER: US/10/087,167
 ; CURRENT FILING DATE: 2002-03-01
 ; PRIOR APPLICATION NUMBER: US 60/242,969
 ; PRIOR FILING DATE: 2000-10-24
 ; NUMBER OF SEQ ID NOS: 148
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 136
 ; LENGTH: 1863
 ; TYPE: DNA
 ; ORGANISM: Synthetic Construct
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1863)
 ; OTHER INFORMATION: Ecdysone receptor chimera G(M)MD
 US-10-087-167-136

Query Match 86.1%; Score 1431.8; DB 16; Length 1863;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 1439; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 Qy 1 ATGAAGTACTGTCTTCTTATCGAAACAGCATGCGATATTTGCCGACTTAAAAAGCTCAAG 60
 Db 124 ATGAAGTACTGTCTTCTTATCGAAACAGCATGCGATATTTGCCGACTTAAAAAGCTCAAG 183


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QY 241 TTGAAATGGATTCTTTACAGATATAAAAGCATTGTTAAACAGGATTTATTGTACAAGAT 300
DB 242 |||||
DB 364 TTGAAATGGATTCTTTACAGATATAAAAGCATTGTTAAACAGGATTTATTGTACAAGAT 423
QY 301 AATGTGAATAAAGATGCGCGTCAAGATAGATTGGCTTCAGTGGAGCTGATATGCTCTTA 360
DB 424 AATGTGAATAAAGATGCGCGTCAAGATAGATTGGCTTCAGTGGAGCTGATATGCTCTTA 483
QY 361 ACATTGAGACAGCATAGATAAAGTTCGACATCATCTCGGAAGAGAGTAGTAACAAAGGT 420
DB 484 ACATTGAGACAGCATAGATAAAGTTCGACATCATCTCGGAAGAGAGTAGTAACAAAGGT 543
QY 421 CAAAGACAGTTGACTGTATCGACGCGTATGAGCGCCGAGTGGCTCGTCCCGAGAGTCCACG 480
DB 544 CAAAGACAGTTGACTGTATCGACGCGTATGAGCGCCGAGTGGCTCGTCCCGAGAGTCCACG 603
QY 481 TGCAGAAACAAAGAGAGAAAGGAAGCAGACAGAGAGAAAGACAAACACTGCGAGTCAGT 540
DB 604 TGCAGAAACAAAGAGAGAAAGGAAGCAGACAGAGAGAAAGACAAACACTGCGAGTCAGT 663
QY 541 ACGACAGATGGAGCATCATATGCTGCCATAATGCAATGTGACCCCTCCGCCCCCAGAG 600
DB 664 ACGACAGATGGAGCATCATATGCTGCCATAATGCAATGTGACCCCTCCGCCCCCAGAG 723
QY 601 GCGCAAGGATTCAGAAAGTGTCCGAGGTTCTTAACGGAAGTAAATGAGCAGAGAAC 660
DB 724 GCGCAAGGATTCAGAAAGTGTCCGAGGTTCTTAACGGAAGTAAATGAGCAGAGAAC 783
QY 661 AGACTGAAGAAATGTACGCGCGTGTGCGGCAACACAGAGTCCCTGATCGCAGGTCGTG 720
DB 784 AGACTGAAGAAATGTACGCGCGTGTGCGGCAACACAGAGTCCCTGATCGCAGGTCGTG 843
QY 721 TGGTACCAGAGGGGTACAGACAGCGCTCGGAGGAAAGATCTCAAGAGAGTTACACAGACA 780
DB 844 TGGTACCAGAGGGGTACAGACAGCGCTCGGAGGAAAGATCTCAAGAGAGTTACACAGACA 903
QY 781 TGGCAGTTAGAGAGAGAGAGAGAGAGAACTGACATGCCCTTCGTCAGATACAGAG 840
DB 904 TGGCAGTTAGAGAGAGAGAGAGAGAGAACTGACATGCCCTTCGTCAGATACAGAG 963
QY 841 ATGACGATCTTAACAGTCAGCTTATTGTAGAAATTCGCAAGGGAGTACCGGATTTCTCC 900
DB 964 ATGACGATCTTAACAGTCAGCTTATTGTAGAAATTCGCAAGGGAGTACCGGATTTCTCC 1023
QY 901 AAGATATCTCAGTCCGATCAAAATTACATTTAAAGCGCTCATCAAGCGAAGTGATG 960
DB 1024 AAGATATCTCAGTCCGATCAAAATTACATTTAAAGCGCTCATCAAGCGAAGTGATG 1083
QY 961 CTGCGAGTCGCGGAGGTACGACGCGGACGAGCAGCGTGTGTTCCGGAACACACAG 1020
DB 1084 CTGCGAGTCGCGGAGGTACGACGCGGACGAGCAGCGTGTGTTCCGGAACACACAG 1143
QY 1021 GCGTACACGCGGACAACTACCGCAAGGGGGCATGTCTTACGTCACTCGAGGACCTGCTG 1080
DB 1144 GCGTACACGCGGACAACTACCGCAAGGGGGCATGTCTTACGTCACTCGAGGACCTGCTG 1203
QY 1081 CACTTCTGTCGGTGTATGATCTCCATGAGCATGGAACAATGTGCACTACGCGTGTCTCACC 1140
DB 1204 CACTTCTGTCGGTGTATGATCTCCATGAGCATGGAACAATGTGCACTACGCGTGTCTCACC 1263
QY 1141 GCCATGTTATATCTCAGACCGGCGAGCGCTCGAGCAACCCCTTTTGTGGAGGAATC 1200
DB 1264 GCCATGTTATATCTCAGACCGGCGAGCGCTCGAGCAACCCCTTTTGTGGAGGAATC 1323
QY 1201 CAGAGATACCTACTTGAAGAGCTGCGGGTTTACATTTTAAATCAGACACGCGTGCCT 1260
DB 1324 CAGAGATACCTACTTGAAGAGCTGCGGGTTTACATTTTAAATCAGACACGCGTGCCT 1383
QY 1261 CGCTGCGCGCTGTGTTGCGCAAGATCTCGCGGTGTGTCGGAACCTGCGCACGCTCGGC 1320
DB 1384 CGCTGCGCGCTGTGTTGCGCAAGATCTCGCGGTGTGTCGGAACCTGCGCACGCTCGGC 1443
QY 1321 ACCGAGNACTCCAACATGTGCTCTCGTGAAGCTGAGAGACAGGAACCTTCCGCCATTC 1380
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RESULT 7

US-10-087-167-128

; Sequence 128, Application US/10087167

; Publication No. US20030154509A1

; GENERAL INFORMATION:

; APPLICANT: Pascal, Erica

; APPLICANT: Valentine, Scott

; APPLICANT: Brown, Jeffrey

; APPLICANT: Cockrell, Adam

; APPLICANT: Johnson, Brian

; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS

; FILE REFERENCE: 50018A

; CURRENT APPLICATION NUMBER: US/10/087,167

; CURRENT FILING DATE: 2002-03-01

; PRIOR APPLICATION NUMBER: US 60/242,969

; PRIOR FILING DATE: 2000-10-24

; NUMBER OF SEQ ID NOS: 148

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 128

; LENGTH: 1428

; TYPE: DNA

; ORGANISM: Synthetic Construct

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1428)

; OTHER INFORMATION: G(M)M (GAL4 DNA Binding Domain fused to the Manduca BcR Hinge an

; OTHER INFORMATION: Ligand Binding Domain)

US-10-087-167-128

Query Match 85.7%; Score 1425; DB 16; Length 1428;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGAAGCTACTGCTCTTCTATCGAAACAAGCATCGATATTTGCCGACTTAAAGCTCAAG 60
DB 1 ATGAAGCTACTGCTCTTCTATCGAAACAAGCATCGATATTTGCCGACTTAAAGCTCAAG 60
QY 61 TGCTCCAAAGAAAAACCGAAGTGCAGCAAGTGTCTGGAAGAACACTGGGAGTGTCCCTAC 120
DB 61 TGCTCCAAAGAAAAACCGAAGTGCAGCAAGTGTCTGGAAGAACACTGGGAGTGTCCCTAC 120
QY 121 TCTCCCAAAACCAAAGGTCTCGCTGACTAGGGCACATCTGACAGAAGTGAATCAAGG 180
DB 121 TCTCCCAAAACCAAAGGTCTCGCTGACTAGGGCACATCTGACAGAAGTGAATCAAGG 180
QY 181 CTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTTTCTCGAAGAACCTTGCATGATT 240
DB 181 CTAGAAAGACTGGAAACAGCTATTTCTACTGATTTTTTCTCGAAGAACCTTGCATGATT 240
QY 241 TTGAAATCGATTCTTTACAGGATATAAAGCAATTGTTAAACAGGATTTTGTACAAGAT 300
DB 241 TTGAAATCGATTCTTTACAGGATATAAAGCAATTGTTAAACAGGATTTTGTACAAGAT 300
QY 301 AATGTGAATAAAGATGCCCTCAAGATAGATTGGCTTTCAGTGGAGACTGATATGCTCTTA 360
DB 301 AATGTGAATAAAGATGCCCTCAAGATAGATTGGCTTTCAGTGGAGACTGATATGCTCTTA 360
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QY 361 ACATTGAGACAGCATAGTAATAGTGGACATCATCTCGAAGAGAGTAGTAACAAAGGT 420
Db |||||||
QY 361 ACATTGAGACAGCATAGTAATAGTGGACATCATCTCGAAGAGAGTAGTAACAAAGGT 420
Db |||||||
QY 421 CAAGACAGTTGACTGTATCGACGGTATAGGCCGAGTCCGTGCTCCAGAGTCCACG 480
Db |||||||
QY 421 CAAGACAGTTGACTGTATCGACGGTATAGGCCGAGTCCGTGCTCCAGAGTCCACG 480
Db |||||||
QY 481 TCGAAGAAACAAAGAGAAAGAGAACGACAGAGAGAGAGAAACAACTGCCAGTCAGT 540
Db |||||||
QY 481 TCGAAGAAACAAAGAGAAAGAGAACGACAGAGAGAGAGAAACAACTGCCAGTCAGT 540
Db |||||||
QY 541 ACGACGACAGTGGACGATCATATGCTCCGCAATATGCAATGATGACCCCTCCGCCCCACAG 600
Db |||||||
QY 541 ACGACGACAGTGGACGATCATATGCTCCGCAATATGCAATGATGACCCCTCCGCCCCACAG 600
Db |||||||
QY 601 CGCGCAAGGATTACGAAAGTGTCCCGAGGTTCTTAACGAGAGAACTAATGGAGCAGAAC 660
Db |||||||
QY 601 CGCGCAAGGATTACGAAAGTGTCCCGAGGTTCTTAACGAGAGAACTAATGGAGCAGAAC 660
Db |||||||
QY 661 AGACTGAAGATGTGACGCGCTGTCGGCGAACGAGAGTCCCTGATCGCGAGGCTCGTG 720
Db |||||||
QY 661 AGACTGAAGATGTGACGCGCTGTCGGCGAACGAGAGTCCCTGATCGCGAGGCTCGTG 720
Db |||||||
QY 721 TGGTACCAAGGGGTACGAGCGCTGTCGGAGGAGATCTCAAGAGAGTTTACACAGACA 780
Db |||||||
QY 721 TGGTACCAAGGGGTACGAGCGCTGTCGGAGGAGATCTCAAGAGAGTTTACACAGACA 780
Db |||||||
QY 781 TGGCAGTTAGAGAGAGAGAGAGGAGAACTGACATGCCCTTCCGTCAGATCACAGAG 840
Db |||||||
QY 781 TGGCAGTTAGAGAGAGAGAGAGGAGAACTGACATGCCCTTCCGTCAGATCACAGAG 840
Db |||||||
QY 841 ATGACGATCTTAAAGTGCAGCTTATGTAGAAATTCGCAAGGAGTACCCGGATTCTCC 900
Db |||||||
QY 841 ATGACGATCTTAAAGTGCAGCTTATGTAGAAATTCGCAAGGAGTACCCGGATTCTCC 900
Db |||||||
QY 901 AGATATCTCAGTCCGATCAATTAATTTAAAGGGGTATCAAGGAAAGTATGATG 960
Db |||||||
QY 901 AGATATCTCAGTCCGATCAATTAATTTAAAGGGGTATCAAGGAAAGTATGATG 960
Db |||||||
QY 961 CTGCGAGTGGCGCAGCTGACGACGCGCGACGAGCGGTGCTTTTCGCGAAACAAACG 1020
Db |||||||
QY 961 CTGCGAGTGGCGCAGCTGACGACGCGCGACGAGCGGTGCTTTTCGCGAAACAAACG 1020
Db |||||||
QY 1021 GCGTACACGCGCAAACTACCGCAAGGGCGCATGCTCAGTCATCGAGGACCTGCTG 1080
Db |||||||
QY 1021 GCGTACACGCGCAAACTACCGCAAGGGCGCATGCTCAGTCATCGAGGACCTGCTG 1080
Db |||||||
QY 1081 CACTTCTGTCGGTGTATGTACTCCATGAGCATGGACAATGTGCACTACGCGCTGCTCACC 1140
Db |||||||
QY 1081 CACTTCTGTCGGTGTATGTACTCCATGAGCATGGACAATGTGCACTACGCGCTGCTCACC 1140
Db |||||||
QY 1141 GCCATCGTTTATTTCTCAGACCGGCGCAGGCTCGAGCAACCCCTTTTATGTGAGGAAATC 1200
Db |||||||
QY 1141 GCCATCGTTTATTTCTCAGACCGGCGCAGGCTCGAGCAACCCCTTTTATGTGAGGAAATC 1200
Db |||||||
QY 1201 CAGAGATCTACTGAGACGCTGCGGGTTTACATTTTAAATCAGCAGCGCGTCGCT 1260
Db |||||||
QY 1201 CAGAGATCTACTGAGACGCTGCGGGTTTACATTTTAAATCAGCAGCGCGTCGCT 1260
Db |||||||
QY 1261 CGCTGCGCGCTGCTGTTGCGCAAGATCTCTCGCGTGTGCTGACGGAACTCGCAACGCTCGGC 1320
Db |||||||
QY 1261 CGCTGCGCGCTGCTGTTGCGCAAGATCTCTCGCGTGTGCTGACGGAACTCGCAACGCTCGGC 1320
Db |||||||
QY 1321 ACGCAGAACTCCAAATGTGCAATCTGCTGAAGCTGAGAGACAGGAACTTCGCGCATTC 1380
Db |||||||
QY 1321 ACGCAGAACTCCAAATGTGCAATCTGCTGAAGCTGAGAGACAGGAACTTCGCGCATTC 1380
Db |||||||
QY 1381 CTCGAGGAGATCTGGGAGCGTGGCCGAAAGTGTGACGACGAAAGCTT 1425
Db |||||||
QY 1381 CTCGAGGAGATCTGGGAGCGTGGCCGAAAGTGTGACGACGAAAGCTT 1425
Db |||||||
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RESULT 8
US-10-087-167-120
; Sequence 120, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1767)
; OTHER INFORMATION: Ecdysone receptor chimera G (M) EV
US-10-087-167-120
```

```
Query Match      85.7%; Score 1424; DB 16; Length 1767;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1524; Conservative 0; Mismatches 120; Indels 18; Gaps 1;

QY 1 ATGAAGCTACTGCTCTTCTATCGAACCAAGCATGCGATATTTGCCGACTTAAAAAGCTCAAG 60
Db |||||||
QY 124 ATGAAGCTACTGCTCTTCTATCGAACCAAGCATGCGATATTTGCCGACTTAAAAAGCTCAAG 183
Db |||||||
QY 61 TGCCTCAAAGAAAAACCGAAGTGCGCCAGTGTCTGAAGAAACAACTGGGAGTGTGCGTAC 120
Db |||||||
QY 184 TGCCTCAAAGAAAAACCGAAGTGCGCCAGTGTCTGAAGAAACAACTGGGAGTGTGCGTAC 243
Db |||||||
QY 121 TCTCCCAAAACCAAAAGGTCTCGCTGACTAGGGCACTCTGACAGAAAGTGGAAATCAAG 180
Db |||||||
QY 244 TCTCCCAAAACCAAAAGGTCTCGCTGACTAGGGCACTCTGACAGAAAGTGGAAATCAAG 303
Db |||||||
QY 181 CTAGAAAGACTGGAAACAGCTTATTTCTACTGATTTTCTCTCGAGAAGACCTTGACATGATT 240
Db |||||||
QY 304 CTAGAAAGACTGGAAACAGCTTATTTCTACTGATTTTCTCTCGAGAAGACCTTGACATGATT 363
Db |||||||
QY 241 TTGAAAATGGATTTCTTTACAGGATATAAAAGCATTTGTTAAACAGGATTTATTTGTACAAGAT 300
Db |||||||
QY 364 TTGAAAATGGATTTCTTTACAGGATATAAAAGCATTTGTTAAACAGGATTTATTTGTACAAGAT 423
Db |||||||
QY 301 AATGTGAATAAAGATCCGTCACAGATAGATTGGCTTTCAGTGGAGACTGATATGCCTCTA 360
Db |||||||
QY 424 AATGTGAATAAAGATCCGTCACAGATAGATTGGCTTTCAGTGGAGACTGATATGCCTCTA 483
Db |||||||
QY 361 ACATTGACAGCAGCATAGAATAAGTGCACATCATCATCGGAAGAGAGTAGTAACAAAGGT 420
Db |||||||
QY 484 ACATTGACAGCAGCATAGAATAAGTGCACATCATCATCGGAAGAGAGTAGTAACAAAGGT 543
Db |||||||
QY 421 CAAAGACAGTTGACTGTATCGACCGTATGAGGCCGAGTGCCTGCCAGAGTCCACG 480
Db |||||||
QY 544 CAAAGACAGTTGACTGTATCGACCGTATGAGGCCGAGTGCCTGCCAGAGTCCACG 603
Db |||||||
QY 481 TCGAAGAAACAAAGAGAGAAAGAGAACGACAGAGAGAGAGAAACAACTGCCAGTCAGT 540
Db |||||||
QY 604 TCGAAGAAACAAAGAGAGAGAGAGAACGACAGAGAGAGAGAAACAACTGCCAGTCAGT 663
Db |||||||
QY 541 ACGACGACAGTGGACGATCATATGCTGCCAATAATGCAATGTGTGACCCCTCGCCCCCAGAG 600
Db |||||||
QY 664 ACGACGACAGTGGACGATCATATGCTGCCAATAATGCAATGTGTGACCCCTCGCCCCCAGAG 723
Db |||||||
QY 601 CGCGCAAGGATTACGAAAGTGTGCTCCCGAGGTTCTTAACGAGAGAGAGTAAATGGAGCAGAAC 660
Db |||||||
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Db 724 GCGGCAAGGATTCACGAAGTGTGCGAGTTCTTAACGGGAAGCTAATGAGCAGAAC 783
QY 661 AGACTGAAGAAATGTGACGCGCTGTGCGGAAACCAAGAGTCCCTGATCGGAGGCTCGTG 720
Db 784 AGACTGAAGAAATGTGACGCGCTGTGCGGAAACCAAGAGTCCCTGATCGGAGGCTCGTG 843
QY 721 TGGTACCAAGGGGTACGAGCAGCGCTCGGAGGAAGATCTCAAGAGAGTTACACAGACA 780
Db 844 TGGTACCAAGGGGTACGAGCAGCGCTCGGAGGAAGATCTCAAGAGAGTTACACAGACT 903
QY 781 TGGCAGTTAGAAAGAAAGAGAGGAGGAAATGACATGCCCTTCGTCAGATCAAGAG 840
Db 904 TGGCAATCAGCAGATGAAGAACGAGAACTCAGACATGCCATTCGCGCAGATCAAGAA 963
QY 841 ATGACGATCTTAACAGTCAGCTTATTGTAGAAATTCGCAAGGGAGTACCGGATTCCTCC 900
Db 964 ATGACCATCTCACAGTACAGCTAATAGTCGAGTTTGGCAAGGGCTACCTGGTTCATCA 1023
QY 901 AAGATATCTCAGTCCGATCAAAATTAATTAAGGGCGTCAATCAAGCGAAGTATGATG 960
Db 1024 AAGATCTCAACCTGACAGATCAATTAATTAAGGGCGATGCTCAAGCGAAGTATGATG 1083
QY 961 CTGCGAGTGGCGGACGATACGACGCGGCGAGCAGCGTGTCTGTCGCAACCAACAG 1020
Db 1084 CTGCGAGTGGCGGACGATACGACGCGGCGTGTCTGTCGCAACCAACAG 1143
QY 1021 GCGTACACGCGGACAACTACGCAAGGCGGATGTCTGTCGTCATCAAGAGACCTGCTG 1080
Db 1144 GCGTACACTCGGACAACTACGCAAGGCGGATGTCTGTCGCAACCAACAG 1203
QY 1081 CACTTCTGCGGTGTATGTACTCCATGACGATGCAATGTGCATCAAGCGTGTCTCACC 1140
Db 1204 CACTTCTGCGGTGTATGTACTCCATGACGATGCAATGTGCATCAAGCGTGTCTCACC 1263
QY 1141 GCATCGTTATATCTCAGACGCGGCGGCGCTCGAGCAACCCCTTTTGTGGAGGAAATC 1200
Db 1264 GCATCGTTATATCTCAGACGCGGCGGCGCTAGAGCAGCCACAGCTAGTGAAGAGATC 1323
QY 1201 CAGAGATCTACTTGAAGACGCTGCGGGTTTACATTTTAAATCAGACAGCGGCTGCTC 1260
Db 1324 CAGCGGTATTACCTGAACACGCTGCGGGTGTACATCATGAACCAAGCAGCGGCTGCGCG 1383
QY 1261 CGTGGCGGCTGTGTTGCGCAAGATCTCGGCGTGTCTGCGGAACTGCGCAGCTCGCG 1320
Db 1384 CGTGGCGGCTGTATCTACGCAAGATCTCTGCGGTGTCTTACCGAGTTGCGGACGCTGGGC 1443
QY 1321 ACGCAGAACTCCAAACATGTGATCTCGCTGAAGCTGAAGAACAGGAACTTCGCGCATTC 1380
Db 1444 ATGCAAAATTCGAACATGTGATCTCGCTGAAGCTCAAGAACAGGAGCTGCGCGCTTC 1503
QY 1381 CTGAGGAGATCTGGGACGCTGGCGAAGTGTGACAGCAGAAAGCTTCCCGCCCGCAGCCGAT 1440
Db 1504 CTGAGGAGATCTGGGACGCT-----GAAGCTTCCCGCCCGCAGCCGAT 1545
QY 1441 GTAGCCTGGGAGACGAGCTCCTACTTAGACGCGGAGACGCTGCGATGGCGATCGCGAC 1500
Db 1546 GTAGCCTGGGAGACGAGCTCCTACTTAGACGCGGAGACGCTGCGATGGCGATCGCGAC 1605
QY 1501 GCGCTAGACCATTTGATCTGGACATGTTGGGGGACGGGGATTCGCGGGTTCGGGATTT 1560
Db 1606 GCGCTAGACCATTTGATCTGGACATGTTGGGGGACGGGGATTCGCGGGTTCGGGATTT 1665
QY 1561 ACCCCCCAGACTCCGCGCTCTAGGATATGCGGCTCTGATATGCGGCTTTCGAGTTTGAAGCAG 1620
Db 1666 ACCCCCCAGACTCCGCGCTCTAGGATATGCGGCTCTGATATGCGGCTTTCGAGTTTGAAGCAG 1725
QY 1621 ATGTTTACGATGCGCTTGAATTTGACGATACGTTGGGTAG 1662
Db 1726 ATGTTTACGATGCGCTTGAATTTGACGATACGTTGGGTAG 1767

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US-10-087-167-142
; Sequence 142, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 1809
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1809)
; OTHER INFORMATION: Bcdysone receptor chimera VG(M)M
US-10-087-167-142

Query Match      85.6%; Score 1422; DB 16; Length 1809;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AAGTACTGTCTTCTATCGAACAGCATGCGATTTTCGCGACTTAAAGAGCTCAAGTGC 63
Db 385 AAGTACTGTCTTCTATCGAACAGCATGCGATTTTCGCGACTTAAAGAGCTCAAGTGC 444
QY 64 TCCAAAGAAAAACCGAAGTGGCCAAAGTGTCTGTAAGAAACAACCTGGAGTGTGCTACTCT 123
Db 445 TCCAAAGAAAAACCGAAGTGGCCAAAGTGTCTGTAAGAAACAACCTGGAGTGTGCTACTCT 504
QY 124 CCCAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAGAGTGGAAATCAAGGCTA 183
Db 505 CCCAAACCAAAAGGTCTCCGCTGACTAGGCGACATCTGACAGAGAGTGGAAATCAAGGCTA 564
QY 184 GAAAGACTGGAAACAGCTATTTCTACTGATTTTTCCTCGAGAGAGCTTGACATGATTTTG 243
Db 565 GAAAGACTGGAAACAGCTATTTCTACTGATTTTTCCTCGAGAGAGCTTGACATGATTTTG 624
QY 244 AAAATGGATTCTTTTACAGGATATAAAAGCATTTGTTAAACAGGATTTTGTACAGATAAT 303
Db 625 AAAATGGATTCTTTTACAGGATATAAAAGCATTTGTTAAACAGGATTTTGTACAGATAAT 684
QY 304 GTGAATAAAGATGCCGTACAGATAGATTTGGTTCAGTGGAGCTGATATGCTCTTAACA 363
Db 685 GTGAATAAAGATGCCGTACAGATAGATTTGGTTCAGTGGAGCTGATATGCTCTTAACA 744
QY 364 TTGACAGACATAGAAATAGTCCGACATCATCATCGAAGAGAGTAGTAAACAAAGCTCAA 423
Db 745 TTGACAGACATAGAAATAGTCCGACATCATCATCGAAGAGAGTAGTAAACAAAGCTCAA 804
QY 424 AGACAGTTGACTGTATCGACGCTATGAGGCCGAGTGTGCTCCAGAGTCCAGCTGC 483
Db 805 AGACAGTTGACTGTATCGACGCTATGAGGCCGAGTGTGCTCCAGAGTCCAGCTGC 864
QY 484 AAGAACAAAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
Db 865 AAGAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 924
QY 544 ACGCAGTGGAGCATCATATGCTGCCATTAATGCAATGTGACCTCCGCGCCCGCAGAGGCG 603
Db 925 ACGCAGTGGAGCATCATATGCTGCCATTAATGCAATGTGACCTCCGCGCCCGCAGAGGCG 984
QY 604 GCAAGGATTACGAAAGTGTGCTCCGAGGTTCTTAACGAGAGAGCTAATGAGAGAGAGAG 663

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Db 985 GCAAGGATTCACGAAGTGGTCCCGAGGTTCTTAACGGAGAAGCTAAATGGAGCAGACAGA 1044
Qy 664 CTGAAGATGTGACGCCGCTGTCCGGCAACAGAAAGTCCCTGATCGGAGGCTCGTGG 723
Db 1045 CTGAAGATGTGACGCCGCTGTCCGGCAACAGAAAGTCCCTGATCGGAGGCTCGTGG 1104
Qy 724 TACCAGGAGGGTACGAGCAGCGCTCGGAGGAAGATCTCAAGAGAGTTTACACAGACATGG 783
Db 1105 TACCAGGAGGGTACGAGCAGCGCTCGGAGGAAGATCTCAAGAGAGTTTACACAGACATGG 1164
Qy 784 CAGTTAGAGAGAGAGAGAGAGAACTGACATGCCCCCTTCCTGATCGATCAGAGATG 843
Db 1165 CAGTTAGAGAGAGAGAGAGAGAACTGACATGCCCCCTTCCTGATCGATCAGAGATG 1224
Qy 844 ACGATCTTAAAGTGCAGCTTATTGTAGAAATTCGAAGGAGACTACCGGATTCCTCAAG 903
Db 1225 ACGATCTTAAAGTGCAGCTTATTGTAGAAATTCGAAGGAGACTACCGGATTCCTCAAG 1284
Qy 904 ATATCTCAGTCCGATCAAAATTACATTTAATAAGGCGTCAATCAAGCGAAGTGATGCTG 963
Db 1285 ATATCTCAGTCCGATCAAAATTACATTTAATAAGGCGTCAATCAAGCGAAGTGATGCTG 1344
Qy 964 CAGTGGCGGACGGTACGACGCGCGGACGAGCAGCGTGTCTTTCGCGAACAACACAGCG 1023
Db 1345 CAGTGGCGGACGGTACGACGCGCGGACGAGCAGCGTGTCTTTCGCGAACAACACAGCG 1404
Qy 1024 TACACGCGGACAACTACCGAAGCGGCGCATGCTACGTCATCGAGGACCTGCTGCAC 1083
Db 1405 TACACGCGGACAACTACCGAAGCGGCGCATGCTACGTCATCGAGGACCTGCTGCAC 1464
Qy 1084 TTCTGTCGGTGTATGCTACTCCATGAGCATGGAACAATGTGCACTACGCGCTGCTCACGCG 1143
Db 1465 TTCTGTCGGTGTATGCTACTCCATGAGCATGGAACAATGTGCACTACGCGCTGCTCACGCG 1524
Qy 1144 ATCGTTATTTCTAGACGCGCGGCGCTCGAGCAACCCCTTTTAGTGGAGGAATCCAG 1203
Db 1525 ATCGTTATTTCTAGACGCGCGGCGCTCGAGCAACCCCTTTTAGTGGAGGAATCCAG 1584
Qy 1204 AGATACTACTTGAAGACGCTGGGGTTTACATTTTAAATCAGCAGCGCGTGGCTCGC 1263
Db 1585 AGATACTACTTGAAGACGCTGGGGTTTACATTTTAAATCAGCAGCGCGTGGCTCGC 1644
Qy 1264 TCGCGCGTGTCTTCGGAAGATCTCGCGGTGCTGACGGAACCTGCGCACGCTCGGACG 1323
Db 1645 TCGCGCGTGTCTTCGGAAGATCTCGCGGTGCTGACGGAACCTGCGCACGCTCGGACG 1704
Qy 1324 CAGAACTCCAACTGTCATCTCGCTGAAGCTGGAAGACAGGAACTTCGCGCATTCCTC 1383
Db 1705 CAGAACTCCAACTGTCATCTCGCTGAAGCTGGAAGACAGGAACTTCGCGCATTCCTC 1764
Qy 1384 GAGGAGATCTGGAGCTGGCGCAAGTGTGACGACGAAAGCTT 1425
Db 1765 GAGGAGATCTGGAGCTGGCGCAAGTGTGACGACGAAAGCTT 1806
```

RESULT 10

US-10-087-167-124

; Sequence 124, Application US/10087167

; Publication No. US20030154509A1

; GENERAL INFORMATION:

; APPLICANT: Pascal, Erica

; APPLICANT: Valentine, Scott

; APPLICANT: Brown, Jeffrey

; APPLICANT: Cockrell, Adam

; APPLICANT: Johnson, Brian

; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS

; FILE REFERENCE: 50018A

; CURRENT APPLICATION NUMBER: US/10/087,167

; CURRENT FILING DATE: 2002-03-01

; PRIOR APPLICATION NUMBER: US 60/242,969

; PRIOR FILING DATE: 2000-10-24

; NUMBER OF SEQ ID NOS: 148

; SOFTWARE: PatentIn version 3.1

```
; SEQ ID NO 124
; LENGTH: 1782
; TYPE: DNA
; ORGANISM: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1782)
; OTHER INFORMATION: Ecdysone receptor chimera G(B) EV
US-10-087-167-124
```

Query Match 79.1%; Score 1314.2; DB 16; Length 1782;

Best Local Similarity 87.7%; Pred. No. 0;

Matches 1471; Conservative 0; Mismatches 173; Indels 33; Gaps 2;

Qy 1 ATGAAGTACTGTCTTCTATCGAACCAAGCATGCGATATTTCGCGACTTAAAAAGCTCAAG 60

Db 124 ATGAAGTACTGTCTTCTATCGAACCAAGCATGCGATATTTCGCGACTTAAAAAGCTCAAG 183

Qy 61 TGTCTCAAGAAAAAACCGAAGTGGCGGAGTCTGGAAGAACTGGGAGTGTGCTAC 120

Db 184 TGTCTCAAGAAAAAACCGAAGTGGCGGAGTCTGGAAGAACTGGGAGTGTGCTAC 243

Qy 121 TCTCCCAAAACCAAAAGTCTCCGCTGACTAGGCGCACATCTGACAGAGTGGAAATCAAG 180

Db 244 TCTCCCAAAACCAAAAGTCTCCGCTGACTAGGCGCACATCTGACAGAGTGGAAATCAAG 303

Qy 181 CTAGAAGAGCTGGAAACAGCTATTCTACTGATTTTCTCAGAGAAGACCTTGACATGATT 240

Db 304 CTAGAAGAGCTGGAAACAGCTATTCTACTGATTTTCTCAGAGAAGACCTTGACATGATT 363

Qy 241 TTGAAATGATGTTTACAGGATATAAAGCAATGTTTAACAGGATTTTGTACAGAT 300

Db 364 TTGAAATGATGTTTACAGGATATAAAGCAATGTTTAACAGGATTTTGTACAGAT 423

Qy 301 AATGTGAATAAAGATCGCTCAGATAGATTGGCTTCAGTGAGACTGATATGCCTCTA 360

Db 424 AATGTGAATAAAGATCGCTCAGATAGATTGGCTTCAGTGAGACTGATATGCCTCTA 483

Qy 361 ACATTGAGACAGCATAGAATAAGTGGCAATCATATCGGAAGAGAGTAGTAACAAAGGT 420

Db 484 ACATTGAGACAGCATAGAATAAGTGGCAATCATATCGGAAGAGAGTAGTAACAAAGGT 543

Qy 421 CAAAGACAGTTGACTGTATCGACGCGTATGAGCGCGGAGTGGTCCGAGAGTCCACG 480

Db 544 CAAAGACAGTTGACTGTATCGACGCGTATGAGCGCGGAGTGGTCCGAGAGTCCACG 603

Qy 481 TGCAAGAAACAAAGAGAGAAAGGACACAGAGAGAAAAAGACAAACTGCCAGTCAGT 540

Db 604 TGTGCGCAAAAAGAGAGAGAGAGAGACACAGAGAGAAAAAGACAAACTGCCAGTCAGT 663

Qy 541 ACAGACAGTGGACGATCATATGCTTGCCTGCTCAATTAATGCAATGTGACCCCTCGCCCCCAGAG 600

Db 664 ACAACGACGTAGACGATCATATGCCCCCAATATGTCAGTGTGATCCACACCCCGGAG 723

Qy 601 CGGCAAGGATT-----CACGAAATGTCCTCCGAGGTTCTTAACGAGAGAG 645

Db 724 GCAGCGAGGATTCGGAATGTTTGCAGCATGAAGTGTCCCGGTTCTCTCGAGAGAG 783

Qy 646 CTAAATGAGCAGAACACAGACTGAAGAAATGACGCGCTGTGCGGCAACCCAGAGTCCCTG 705

Db 784 CTGATGAGAGCAATCGCTGAGAGACATACCCCCCTCACCGCAACCCAGCAGTCTCTG 843

Qy 706 ATCGGAGGCTGCTGTTACAGAGGGGTACAGAGCGGCTCGGAGGAAGATCTCAAG 765

Db 844 ATCGGAGGCTGCTGTTACAGAGGGGTACAGAGCGGCTCGGAGGAAGATCTCAAG 903

Qy 766 AGAGTTACAGACATCGCAGTTAGAGAAAGAGAGAGGAGAACTGACATGCCCTTC 825

Db 904 AGGTTGACGAGACTTGGCAATCAGCAGATGGAAGACGAGACTCAGACATGCCATTC 963

Qy 826 CGTCAGATCAGAGAGATGACGATCTTAACAGTGCAGCTTTATTGTAGAAATTCGCAAGGGA 885

Db 964 CGCCAGATCAGAGAAATGACCATCTCTCACAGTACAGCTAATAGTCGAGTTTGTCCAAAGGC 1023

QY	886	CTACCGGATTTCTCAAGATATCTCAGTCCGATCAATTAATTAAGCGGTCATCA	945
DB	1024	CTACCTGGTTTTTCAAGATCTCAACACCTGACCAAGATCAATTAATTAAGCGGTCATCA	1083
QY	946	AGCGAAGTGTATGCTCGAGTGGCGGACGCTACGACGGGGGACGACGAGCGTGTG	1005
DB	1084	AGCGAAGTGTATGCTCGAGTGGCGGACGCTACGACGGGGGACGACGAGCGTGTG	1143
QY	1006	TTTCGGAACAACAGCGGTACACGGCGCAAACTACCGAAGCGGGGATGTCCTACGTC	1065
DB	1144	TTTCGGAACAACAGCGGTACACTCGCAAACTACCGAAGCGGGGATGTCCTACGTC	1203
QY	1066	ATCGAGGACCTGCTGCACTTCTGTCGGTGTATGTAATCATGAGCATGCAATATGTCAC	1125
DB	1204	ATCGAAGACCTGCTGCACTTCTGTCGGTGTATGTAATCATGAGCATGCAATATGTCAC	1263
QY	1126	TACGCGTCTCACCGCATCTGTAATATCTCAGACCGGCCAGGCTCGAGCAACCCCTT	1185
DB	1264	TACGCGTCTCACCTGTCATCTGTAATATCTCAGACCGGCCAGGCTCGAGCAACCCCTT	1323
QY	1186	TTAGTGGAGAAATCCAGAGATACCTTTGAAGACGCTGCGGGTTTACATTTAAATCAG	1245
DB	1324	CTAGTAGAAGATCCAGCGGTATTACCTGAACACGCTGCGGGTGTACATCATGAACAG	1383
QY	1246	CACAGCGCTGCTGCTGCTGCGCGCTGCTGTTGCGCAAGATCCTCGCGTGTGACGNA	1305
DB	1384	CACAGCGCTGCTGCTGCTGCGCGCTGCTGTTGCGCAAGATCCTCGCGTGTGACGNA	1443
QY	1306	CTGCGACGCTGCGGACGAGAACTCCAAACATGTGATCTCGCTGAAGCTGAAGAACAGG	1365
DB	1444	TTGCGGACCTGCGGACGAGAACTCCAAACATGTGATCTCGCTGAAGCTGAAGAACAGG	1503
QY	1366	AAACTTCCGCCATTCCTCGAGGAGATCTGGGACGCTGGCCGAAGTGTGACGACGAAGTT	1425
DB	1504	AGCTGCCGCGCTTCTCGAGGAGATCTGGGACGCTGGCCGAAGTGTGACGACGAAGTT	1545
QY	1426	GGCCCCCGACGATGTGCTGAGCTGGGGACGAGCTCCACTTAGACGGCGAGGACGTCGCG	1485
DB	1546	GGCCCCCGACGATGTGCTGAGCTGGGGACGAGCTCCACTTAGACGGCGAGGACGTCGCG	1605
QY	1486	ATGGGCGATGCGGACGCTAGACGATTTGATCTGCAATGTTGGGGACGCGGATTC	1545
DB	1606	ATGGGCGATGCGGACGCTAGACGATTTGATCTGCAATGTTGGGGACGCGGATTC	1665
QY	1546	CCGGTCCGGGATTTACCCCCCAGACTCCGCCCCCTACGGCGCTCTGGATATGGCCGAC	1605
DB	1666	CCGGTCCGGGATTTACCCCCCAGACTCCGCCCCCTACGGCGCTCTGGATATGGCCGAC	1725
QY	1606	TTGAGTTTGGAGAGATGTTTACCGATGCTTGGAAATGACGAGTACGGTGGGTAG	1662
DB	1726	TTGAGTTTGGAGAGATGTTTACCGATGCTTGGAAATGACGAGTACGGTGGGTAG	1782

RESULT 11

US-10-087-167-93
; Sequence 93, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 93

;	LENGTH: 1518	
;	TYPE: DNA	
;	ORGANISM: Synthetic construct	
;	FEATURE:	
;	NAME/KEY: CDS	
;	LOCATION: (1)..(1518)	
;	OTHER INFORMATION: Ecdysone Receptor chimera MMV	
;	US-10-087-167-93	
Query Match	73.2%; Score 1216.6; DB 16; Length 1518;	
Best Local Similarity	99.7%; Pred. No. 0;	
Matches 1219; Conservative	0; Mismatches 4; Indels 0; Gaps 0;	
QY	440	CGACGCGTATGAGGCCCGAGTCCGTCTCCAGAGTCCAGTGCAGAAACAAAAGAGAG 499
DB	296	CGTGGGATGAGGCCCGAGTCCGTCTCCAGAGTCCAGTGCAGAAACAAAAGAGAG 355
QY	500	AAAAGAAAGCAAGAGAGAAAAGCAAACTGCCAGTCACTACGACGACAGTGGACGATC 559
DB	356	AAAAGAAAGCAAGAGAGAAAAGCAAACTGCCAGTCACTACGACGACAGTGGACGATC 415
QY	560	ATATGCCCTGCCATATGCAATGTGACCTCCGCCCCAGAGCGGCAAGGATTCACGAAG 619
DB	416	ATATGCCCTGCCATATGCAATGTGACCTCCGCCCCAGAGCGGCAAGGATTCACGAAG 475
QY	620	TGGTCCCGAGGTTCTTAACGGAGAAAGCTAATGGAGCAGAACAGACTGAAGAAATGTGACGC 679
DB	476	TGGTCCCGAGGTTCTTAACGGAGAAAGCTAATGGAGCAGAACAGACTGAAGAAATGTGACGC 535
QY	680	CGCTGTCGGCGAAACAGAAAGTCCCTGATGCGAGGCTGCTGTGGTACAGGAGGGGTAGC 739
DB	536	CGCTGTCGGCGAAACAGAAAGTCCCTGATGCGAGGCTGCTGTGGTACAGGAGGGGTAGC 595
QY	740	AGCAGCGCTCGGAGGAAAGTCTCAAGAGATTTACAGACATGGCAGTTAGAAAGAAAG 799
DB	596	AGCAGCGCTCGGAGGAAAGTCTCAAGAGATTTACAGACATGGCAGTTAGAAAGAAAG 655
QY	800	AAGAGGAGAAACTGACATGCTCCGTCCGTCCGTCCGTCCGTCCGTCCGTCCGTCCGTCCGT 859
DB	656	AAGAGGAGAAACTGACATGCTCCGTCCGTCCGTCCGTCCGTCCGTCCGTCCGTCCGTCCGT 715
QY	860	AGCTTATGTAGAAATTCGCAAAAGGAGCTACCGGGATTTCCAGAGATATCTCAGTCCGATC 919
DB	716	AGCTTATGTAGAAATTCGCAAAAGGAGCTACCGGGATTTCCAGAGATATCTCAGTCCGATC 775
QY	920	AAATACATATTAAGGCGTCAATCAAGCGAAGTGAATGATGCTCCAGTGGCGGACGCT 979
DB	776	AAATACATATTAAGGCGTCAATCAAGCGAAGTGAATGATGCTCCAGTGGCGGACGCT 835
QY	980	ACGACGCGGACGAGACGCTGCTGTTCCGAAACCAACAGGCGTACACGCGGCAAACT 1039
DB	836	ACGACGCGGACGAGACGCTGCTGTTCCGAAACCAACAGGCGTACACGCGGCAAACT 895
QY	1040	ACCGAAGCGGCGATGCTCCTACGTCATCGAGACCTGCTGCACTTCTGCTGGGTATGT 1099
DB	896	ACCGAAGCGGCGATGCTCCTACGTCATCGAGACCTGCTGCACTTCTGCTGGGTATGT 955
QY	1100	ACTCCATGAGCATGGAATGTCATGCTACGCTGCTCAGCGCTGCTCAGCGCATCTTATCTCAG 1159
DB	956	ACTCCATGAGCATGGAATGTCATGCTACGCTGCTCAGCGCTGCTCAGCGCATCTTATCTCAG 1015
QY	1160	ACCGGCGAGGCTCGAGCAACCCCTTTTATGAGGAAATCCAGAGATACTTCTGAAGA 1219
DB	1016	ACCGGCGAGGCTCGAGCAACCCCTTTTATGAGGAAATCCAGAGATACTTCTGAAGA 1075
QY	1220	CGCTGCGGGTTACATTTTAAATCAGACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1279
DB	1076	CGCTGCGGGTTACATTTTAAATCAGACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1135
QY	1280	GCAAGATCTCGGCGTGTGACGGAATCGGACGCTCGGACGAGAACTCCAAACATGT 1339
DB	1136	GCAAGATCTCGGCGTGTGACGGAATCGGACGCTCGGACGAGAACTCCAAACATGT 1195

QY 1340 GCATCTCGTCAAGCTGAGAACAGGAACTTCCGCGCATTCCTCGAGAGATCTGGGACG 1399
 DB 1196 GCATCTCGTCAAGCTGAGAACAGGAACTTCCGCGCATTCCTCGAGAGATCTGGGACG 1255
 QY 1400 TGGCCGAAGTGTGACACGACGAAGCTTGGCCCGGACCGATGTCAGCGCTGGGGACGAGC 1459
 DB 1256 TGGCCGAAGTGTGACACGACGAAGCTTGGCCCGGACCGATGTCAGCGCTGGGGACGAGC 1315
 QY 1460 TCCACTTAGACGGGACGAGACGTGGCGATGGCGCATCGGACGCGCTAGACGATTCGATC 1519
 DB 1316 TCCACTTAGACGGGACGAGACGTGGCGATGGCGCATCGGACGCGCTAGACGATTCGATC 1375
 QY 1520 TGGACATGTTGGGGACGGGATTCGCCGGTTCGGGATTTACCCCGACGACTCCGCCC 1579
 DB 1376 TGGACATGTTGGGGACGGGATTCGCCGGTTCGGGATTTACCCCGACGACTCCGCCC 1435
 QY 1580 CCTACGGCGCTCTGGATATGGCCGACTTCGAGTTTGGACGAGATGTTTACCGATGCCCTTG 1639
 DB 1436 CCTACGGCGCTCTGGATATGGCCGACTTCGAGTTTGGACGAGATGTTTACCGATGCCCTTG 1495
 QY 1640 GAATTGACGAGTACGGTGGGTAG 1662
 DB 1496 GAATTGACGAGTACGGTGGGTAG 1518

RESULT 12

US-10-087-167-69
 ; Sequence 69, Application US/10087167
 ; Publication No. US20030154509A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pascal, Erica
 ; APPLICANT: Valentine, Scott
 ; APPLICANT: Brown, Jeffrey
 ; APPLICANT: Cockrell, Adam
 ; APPLICANT: Johnson, Brian
 ; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
 ; FILE REFERENCE: 50018A
 ; CURRENT APPLICATION NUMBER: US/10/087,167
 ; CURRENT FILING DATE: 2002-03-01
 ; PRIOR APPLICATION NUMBER: US 60/242,969
 ; PRIOR FILING DATE: 2000-10-24
 ; NUMBER OF SEQ ID NOS: 148
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 69
 ; LENGTH: 1500
 ; TYPE: DNA
 ; ORGANISM: Synthetic construct
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1500)
 ; OTHER INFORMATION: Ecdysone Receptor chimera MFV
 US-10-087-167-69
 Query Match 70.2%; Score 1167.4; DB 16; Length 1500;
 Best Local Similarity 98.0%; Pred. No. 0;
 Matches 1199; Conservative 0; Mismatches 6; Indels 18; Gaps 1;
 QY 440 CGACGGTATGAGCCGCGAGTCCGTCCTCCAGAGTCCACGTGCAAGAACAAAGAGAG 499
 DB 296 CGGTGGGATGAGCCGCGAGTCCGTCCTCCAGAGTCCACGTGCAAGAACAAAGAGAG 355
 QY 500 AAAAGGACACAGAGAGAAAGCAAACTGCCAGTCACTACGACGACGAGTGGACGATC 559
 DB 356 AAAAGGACACAGAGAGAAAGCAAACTGCCAGTCACTACGACGACGAGTGGACGATC 415
 QY 560 ATATGCTCCCAATATGCAATGTGACCTTCGCCCGGAGCGGCGGAGGATTCAGAG 619
 DB 416 ATATGCTCCCAATATGCAATGTGACCTTCGCCCGGAGCGGCGGAGGATTCAGAG 475
 QY 620 TGGTCCCGAGGTTCTTAACGGAGAGCTAATGGACGAGAACTGGAAGATGTGACGC 679
 DB 476 TGGTCCCGAGGTTCTTAACGGAGAGCTAATGGACGAGAACTGGAAGATGTGACGC 535

RESULT 13

US-10-087-167-147
 ; Sequence 147, Application US/10087167
 ; Publication No. US20030154509A1

QY 680 CGCTGTCCGCGAACCAAGTCCCTGATCGCGAGGTCGTGTGGTACCAAGAGGGGTACG 739
 DB 536 CGCTGTCCGCGAACCAAGTCCCTGATCGCGAGGTCGTGTGGTACCAAGAGGGGTACG 595
 QY 740 AGCAGCCGTCCGAGGAGATCTCAAGAGTTCACAGACATCGCAGTTAGAGAGAGAG 799
 DB 596 AGCAGCCGTCCGAGGAGATCTCAAGAGTTCACAGACATCGCAGTTAGAGAGAGAG 655
 QY 800 AACAGAGGAACTGACATGCGCTTCCTCGTCAAGATACAGAGATGAGATCTTAAACAGTGC 859
 DB 656 AACAGAGGAACTGACATGCGCTTCCTCGTCAAGATACAGAGATGAGATCTTAAACAGTGC 715
 QY 860 AGCTTATTTAGAAATTCGAAAGGACTACCGGATTCCTCAAGATATCTCAGTCCGATC 919
 DB 716 AGCTTATTTAGAAATTCGAAAGGACTACCGGATTCCTCAAGATATCTCAGTCCGATC 775
 QY 920 AAATTACATTTAAAGGCGTCATCAAGCGAAGTGTGCTGCGAGTGGCGGCGCGGT 979
 DB 776 AAATTACATTTAAAGGCGTCATCAAGCGAAGTGTGCTGCGAGTGGCGGCGCGGT 835
 QY 980 ACCGCGCGGACGCGACGCGTCTGTTCCGCAACCAAGGCGTACACGCGGACAACT 1039
 DB 836 ACCGCGCGGACGCGACGCGTCTGTTCCGCAACCAAGGCGTACACGCGGACAACT 895
 QY 1040 ACCGCAAGCGGCGATGTCCTCATCATGAGACCTGCTGCACTTCTGTCGGTGTATGT 1099
 DB 896 ACCGCAAGCGGCGATGTCCTCATCATGAGGACCTGCTGCACTTCTGTCGGTGTATGT 955
 QY 1100 ACTCCATGACATGGACATGTGCATCTACGCGTGTCCGCGCATCTGTTATATTCAG 1159
 DB 956 ACTCCATGACATGGACATGTGCATCTACGCGTGTCCGCGCATCTGTTATATTCAG 1015
 QY 1160 ACCGCGCGGCGCTCGAGCAACCCCTTTAGTGGAGGAAATCCAGAGATCTACTTTGAAGA 1219
 DB 1016 ACCGCGCGGCGCTCGAGCAACCCCTTTAGTGGAGGAAATCCAGAGATCTACTTTGAAGA 1075
 QY 1220 CGTTCGGGTTTAAATTTAAATCAGACAGCGGTCGCTCGTTCGCGCGTGTGTTCG 1279
 DB 1076 CGTTCGGGTTTAAATTTAAATCAGACAGCGGTCGCTCGTTCGCGCGTGTGTTCG 1135
 QY 1280 GCAAGATCTCGGCGTCTGACGAACTGCGCGCTCGGCGCAGCAACTCCCAACATGT 1339
 DB 1136 GCAAGATCTCGGCGTCTGACGAACTGCGCGCTCGGCGCAGCAACTCCCAACATGT 1195
 QY 1340 GCATCTCGTCAAGCTGAAGAACAGGAACTTCGCGCATCTCTCGAGAGATCTGGGACG 1399
 DB 1196 GCATCTCGTCAAGCTGAAGAACAGGAACTTCGCGCATCTCTCGAGAGATCTGGGACG 1255
 QY 1400 TGGCCGAAGTGTGACACGACGAAGCTTGGCCCGGACCGATGTCAGCGCTGGGGACGAGC 1459
 DB 1256 T-----GAAAGCTTGGCCCGGACCGATGTCAGCGTGGGGACGAGC 1297
 QY 1460 TCCACTTAGACGGGACGAGTGGCGATGGCGATGGCGATGGCGATGGCGATGGCGATGGCGATC 1519
 DB 1298 TCCACTTAGACGGGACGAGTGGCGATGGCGATGGCGATGGCGATGGCGATGGCGATGGCGATC 1357
 QY 1520 TGGACATGTTGGGGGACGGGATTCGCCGGGTCCGGGATTTACCCCGACGACTCCGCGCC 1579
 DB 1358 TGGACATGTTGGGGGACGGGATTCGCCGGGTCCGGGATTTACCCCGACGACTCCGCGCC 1417
 QY 1580 CCTACGGCGCTCTGGATATGGCGACTTCGAGTTTGGACGAGATGTTTACCGATGCCCTTG 1639
 DB 1418 CCTACGGCGCTCTGGATATGGCGACTTCGAGTTTGGACGAGATGTTTACCGATGCCCTTG 1477
 QY 1640 GAATTGACGAGTACGGTGGGTAG 1662
 DB 1478 GAATTGACGAGTACGGTGGGTAG 1500

GENERAL INFORMATION:
 APPLICANT: Pascal, Erica
 APPLICANT: Valentine, Scott
 APPLICANT: Brown, Jeffrey
 APPLICANT: Cockrell, Adam
 APPLICANT: Johnson, Brian
 TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
 FILE REFERENCE: 50018A
 CURRENT APPLICATION NUMBER: US/10/087,167
 CURRENT FILING DATE: 2002-03-01
 PRIOR APPLICATION NUMBER: US 60/242,969
 PRIOR FILING DATE: 2000-10-24
 NUMBER OF SEQ ID NOS: 148
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 147
 LENGTH: 1800
 TYPE: DNA
 ORGANISM: Synthetic Construct
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1800)
 OTHER INFORMATION: Ecdysone receptor chimera GV(M)M
 US-10-087-167-147

Query Match 70.2%; Score 1166; DB 16; Length 1800;
 Best Local Similarity 85.1%; Pred. No. 0;
 Matches 1425; Conservative 0; Mismatches 0; Indels 249; Gaps 1;

QY	1	ATGAAGCTACTGTTCTTATCGAACAAGCATGCGATATTGCGGACTTAAAAAGCTCAAG	60
DB	124	ATGAAGCTACTGTTCTTATCGAACAAGCATGCGATATTGCGGACTTAAAAAGCTCAAG	183
QY	61	TGCTCCAAAGAAACCGGAGTGGCCAAAGTGTCTGAAGAAACAACTGGGAGTGTGCTTAC	120
DB	184	TGCTCCAAAGAAACCGGAGTGGCCAAAGTGTCTGAAGAAACAACTGGGAGTGTGCTTAC	243
QY	121	TCCTCCAAACCAAGAGTCTCCGCTGACTAGGGACATCTGACAGAGTGAATCAAGG	180
DB	244	TCCTCCAAACCAAGAGTCTCCGCTGACTAGGGACATCTGACAGAGTGAATCAAGG	303
QY	181	CTAGAAAGACTGGAAACAGCTATTCTTACTGATTTTCTCGAAGACCTTGACATGATT	240
DB	304	CTAGAAAGACTGGAAACAGCTATTCTTACTGATTTTCTCGAAGACCTTGACATGATT	363
QY	241	TTGAAATGGATTCTTTACGGATATAAAGCATTTGTTAACAGGATATTGTACAGAT	300
DB	364	TTGAAATGGATTCTTTACGGATATAAAGCATTTGTTAACAGGATATTGTACAGAT	423
QY	301	AATGTGAATAAGATGCCGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCCCTTA	360
DB	424	AATGTGAATAAGATGCCGTACAGATAGATTGGCTTCAGTGGAGACTGATATGCCCTTA	483
QY	361	ACATTGAGACAGCATAGATAAGTGGACATCATCTCGAAGAGAGTAGTAACAAAGGT	420
DB	484	ACATTGAGACAGCATAGATAAGTGGACATCATCTCGAAGAGAGTAGTAACAAAGGT	543
QY	421	CAAAGACAGTTGATGTATCGACGGGTATAGAGCCCGAGTGGCTGCTCCAGAGTC----	476
DB	544	CAAAGACAGTTGATGTATCGACGGGTATAGAGCCCGAGTGGCTGCTCCAGAGTCACG	603
QY	477	-----	476
DB	604	TGCAAGCTTCCCGCCCGACCGATGTGACGCTGGGGGACGAGCTCCACTTAGACGGGAG	663
QY	477	-----	476
DB	664	GACGTGGGATGGGCATGCCGCGCTAGACGATTTTCGATCTGGACATGTTGGGGGAC	723
QY	477	-----	476
DB	724	GGGGATTCGGGTCGGGATTTACCCCGCCAGACTCCCGCCCGCTACGGCGCTCTGGAT	783
QY	477	-----	476

Db	784	ATGCCGACTTCCGAGTTTGAGCAGATGTTTACCGATGCCCTTGGAATTGACGAGTACGGT	843
QY	477	-----CAGCTGCAAGACAAAGAAAGAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	531
Db	844	GGGAACACAGTGCAGAAACAAAGAAAGAAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	903
QY	532	CCAGTCAGTCAGCAGCAGTGCAGATCATATGCTGCCATAATGCAATGAGACCTCCG	591
Db	904	CCAGTCAGTCAGCAGCAGTGCAGATCATATGCTGCCATAATGCAATGAGACCTCCG	963
QY	592	CCCCAGAGCGGCAAGGATTCAGAAAGTGTCCGAGGTTCCCTAACCGAGAGAGTAAATG	651
Db	964	CCCCAGAGCGGCAAGGATTCAGAAAGTGTCCGAGGTTCCCTAACCGAGAGAGTAAATG	1023
QY	652	GAGCAGACAGACTGAGAAATGTACGCGCTGTCCGCGAACCAGAACTCCCTGATCCG	711
Db	1024	GAGCAGACAGACTGAGAAATGTACGCGCTGTCCGCGAACCAGAACTCCCTGATCCG	1083
QY	712	AGGCTCGTGTGTACCCAGAGGGGTACGAGCAGCGCTCGGAGGAGATCTCAAGAGATT	771
Db	1084	AGGCTCGTGTGTACCCAGAGGGGTACGAGCAGCGCTCGGAGGAGATCTCAAGAGATT	1143
QY	772	ACACAGACATGCGCAGTTAGAAAGAAAGAGAGAGAACTGCATGCCCTTCCGTCAG	831
Db	1144	ACACAGACATGCGCAGTTAGAAAGAAAGAGAGAGAACTGCATGCCCTTCCGTCAG	1203
QY	832	ATCAGAGATGACGATCTTAACAGTGCAGCTTATTGTAGAAATTCGCAAGAGGACTACCG	891
Db	1204	ATCAGAGATGACGATCTTAACAGTGCAGCTTATTGTAGAAATTCGCAAGAGGACTACCG	1263
QY	892	GGATTCTCCAGATATCTCAGTCCGATCAAAATTAATTTAAAGCGCTCATCAAGCGAA	951
Db	1264	GGATTCTCCAGATATCTCAGTCCGATCAAAATTAATTTAAAGCGCTCATCAAGCGAA	1323
QY	952	GTGATGATGCTGCGAGTGGCGGCGGTAACGAGCGGCGAGCAGCGTGTGTTCGG	1011
Db	1324	GTGATGATGCTGCGAGTGGCGGCGGTAACGAGCGGCGAGCAGCGTGTGTTCGG	1383
QY	1012	AACAACAGGCGGTACACGGCGGACAACTACCGAGAGGGCGGCTCTCTAGTCATCCAG	1071
Db	1384	AACAACAGGCGGTACACGGCGGACAACTACCGAGAGGGCGGCTCTCTAGTCATCCAG	1443
QY	1072	GACCTGCTGCACTTCTGTCGGTGTATGTAATCTCCATGAGCATGGACAAATGTGCACTACGG	1131
Db	1444	GACCTGCTGCACTTCTGTCGGTGTATGTAATCTCCATGAGCATGGACAAATGTGCACTACGG	1503
QY	1132	CTGCTCACCGCCATCGTTATATTTTCAGACCGGCGGCGCTCGAGCAACCCCTTTTAGTG	1191
Db	1504	CTGCTCACCGCCATCGTTATATTTTCAGACCGGCGGCGCTCGAGCAACCCCTTTTAGTG	1563
QY	1192	GAGGAATTCAGAGATACCTTTGAAGAGCGTCCGGGTTTACATTTTAATCAGCACAGC	1251
Db	1564	GAGGAATTCAGAGATACCTTTGAAGAGCGTCCGGGTTTACATTTTAATCAGCACAGC	1623
QY	1252	GGGTGCGCTCGTCCGCGGCTGCTGTTTCGCAAGATCTCCGGGCTGTGACGAACTGCGC	1311
Db	1624	GGGTGCGCTCGTCCGCGGCTGCTGTTTCGCAAGATCTCCGGGCTGTGACGAACTGCGC	1683
QY	1312	ACGCTCGGCACGAGAACTCCAAATGTGCAATCTCGCTGAAGCTGAAAGAACAGGAACTTT	1371
Db	1684	ACGCTCGGCACGAGAACTCCAAATGTGCAATCTCGCTGAAGCTGAAAGAACAGGAACTTT	1743
QY	1372	CGGCATTTCTCGAGAGATCTGGAGCGTGGCGGAGTGTCCACGACGAGCTT	1425
Db	1744	CGGCATTTCTCGAGAGATCTGGAGCGTGGCGGAGTGTCCACGACGAGCTT	1797

RESULT 14
 US-10-087-167-79
 ; Sequence 79, Application US/10087167
 ; Publication No. US20030154509A1
 ; GENERAL INFORMATION:

```

; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Synthetic construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
; OTHER INFORMATION: Ecdysone Receptor chimera EMV
US-10-087-167-79

Query Match      66.8%; Score 1109.8; DB 16; Length 1533;
Best Local Similarity 92.8%; Pred. No. 1.2e-313; Indels 15; Gaps 1;
Matches 1181; Conservative 0; Mismatches 77;

QY 405 GAGTAGTAACAAAGGTCAAAGACAGTGTGACTGTATCGACGCGTATGAGGCCGCGAGTGGT 464
DB 261 GAAATGTCAAGATGCGCGTTGMAAGAGTGTAGCGGTGGCATGAGGCCGCGAGTGGT 320
QY 465 CGTCCAGAGTCCAGTCAAGAACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 524
DB 321 GGTGTCAGAAAGCGAGTGTGCGCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 380
QY 525 CAAATCTGCAGTCAAGTACGACAGTGCAGATCATATGCTGCGCAATATGCAATGTGA 584
DB 381 CAAATACAGTACGACAAAGACAGTACGATCATATGCTGCGCAATATGCAATGTGA 440
QY 585 CCCTCCGCCGCCAGAGCGCGCAAGGATT-----CACGAAGTGGTCCCGAG 629
DB 441 TCCACACCCCGGAGGAGCGAGGATTCTGGAATGTTTGACGATGAAGTGGTCCCGCG 500
QY 630 GTTCTTAACGGAGAGCTAATGGACAGAAAGAGATGTGACGCGCGTGTGGC 689
DB 501 GTTCTCTCGGAGAGAGCTGATGGAGCAAGATCGGCTGAAGAAACATACCCCGCTCACCGC 560
QY 690 GAACAGAGAGTCCCTGATCGGAGGCTGCTGTGTGTACAGAGGCGGTACGAGCAGCGGTC 749
DB 561 CAACAGAGAGTCCCTGATCGGAGGCTGCTGTGTGTACAGAGGCGGTACGAGCAGCGGTC 620
QY 750 GGAGGAAGATCTCAAGAGAGGTTTACACAGATGCGAGTTAGAGAAAGAAAGAGAGGAGGA 809
DB 621 GGAGGAAGATCTCAAGAGAGGTTTACACAGATGCGAGTTAGAGAAAGAAAGAGAGGAGGA 680
QY 810 AACTACATGCGCTTCGCTCAGATCACAGATGACGATCTTACAGTGCAGCTTATGT 869
DB 681 AACTGACATGCGCTTCGCTCAGATCACAGATGACGATCTTACAGTGCAGCTTATGT 740
QY 870 AGAATTCGAAAGGAGTACCGGGATCTTCCAAAGATATCTCAGTCCGATCAAAATTACATT 929
DB 741 AGAATTCGAAAGGAGTACCGGGATCTTCCAAAGATATCTCAGTCCGATCAAAATTACATT 800
QY 930 ATTAAGGCGTCAATCAAGGAAGTATGATGTGCGAGTGGCGGACGGTACGAGCGGCG 989
DB 801 ATTAAGGCGTCAATCAAGGAAGTATGATGTGCGAGTGGCGGACGGTACGAGCGGCG 860
QY 990 GACGACAGCGTGTGCTGCGCAACACACAGGCGTACAGCGCGCAACTACCGCAAGGC 1049
DB 861 GACGACAGCGTGTGCTGCGCAACACACAGGCGTACAGCGCGCAACTACCGCAAGGC 920
QY 1050 GGGCATGTCTACGTCAATCGAGGACCTGCTGCACTTCTGTGGTGTATGTACTCCATGAG 1109

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DB 921 GGGCATGTCTACGTCAATCGAGGACCTGCTGCACATTTCTGTGGTGTATGTACTCCATGAG 980
QY 1110 CATGGACAATGTGCACTACGCGTCTCACCSCCATCGTTATATTCTCAGACCGGCGAGG 1169
DB 981 CATGGACAATGTGCACTACGCGTCTCACCSCCATCGTTATATTCTCAGACCGGCGAGG 1040
QY 1170 CCTCGAGCAACCCCTTTTGTAGTGGAGAAATCCAGAGATACTACTTGAAGACGCTGCGGGT 1229
DB 1041 CTTGAGCAACCCCTTTTGTAGTGGAGAAATCCAGAGATACTACTTGAAGACGCTGCGGGT 1100
QY 1230 TTACATTTTAAATCAGACAGCGCTGCGCTCGCTCGCGCGTCTGTTGGGCAAGATCCT 1289
DB 1101 TTACATTTTAAATCAGACAGCGCTGCGCTCGCTCGCGCGTCTGTTGGGCAAGATCCT 1160
QY 1290 CGGCGTGTGACGGAACTCGGCACGCTCGGCACGAGAACTCCCAACATGTGCATCTCGCT 1349
DB 1161 CGGCGTGTGACGGAACTCGGCACGCTCGGCACGAGAACTCCCAACATGTGCATCTCGCT 1220
QY 1350 GAAGCTGAAGAACAGGAACTTCCGCGCATTTCTCGAGGAGATCTGGGACGTGGCCGAAGT 1409
DB 1221 GAAGCTGAAGAACAGGAACTTCCGCGCATTTCTCGAGGAGATCTGGGACGTGGCCGAAGT 1280
QY 1410 GTCGACGACGAAGCTTTCGCCCGCCGACCGATGTCAGCTTGGGGGACGAGCTCCACTTAGA 1469
DB 1281 GTCGACGACGAAGCTTTCGCCCGCCGACCGATGTCAGCTTGGGGGACGAGCTCCACTTAGA 1340
QY 1470 CGGCGAGGACGTGGCGATGCGCATGCCGACGCGTAGACGATTTTCGATCTGGACATGTT 1529
DB 1341 CGGCGAGGACGTGGCGATGCGCATGCCGACGCGTAGACGATTTTCGATCTGGACATGTT 1400
QY 1530 GGGGACGCGGGAATTCGCCCGGTCGGGATTTTACCCCCCAGACTCCGCCCGCTTACGCGC 1589
DB 1401 GGGGACGCGGGAATTCGCCCGGTCGGGATTTTACCCCCCAGACTCCGCCCGCTTACGCGC 1460
QY 1590 TCTGGATATGCGCGACTTTCGAGTTTTCGAGCAGATGTTTACCGATGCGCTTGGAAATGACGA 1649
DB 1461 TCTGGATATGCGCGACTTTCGAGTTTTCGAGCAGATGTTTACCGATGCGCTTGGAAATGACGA 1520
QY 1650 GTACGGTGGGTAG 1662
DB 1521 GTACGGTGGGTAG 1533

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RESULT 15
US-10-087-167-65
; Sequence 65, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Synthetic construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1509)
; OTHER INFORMATION: Ecdysone Receptor chimera MBV
US-10-087-167-65

```

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Query Match      59.9%; Score 996.2; DB 16; Length 1509;
Best Local Similarity 89.6%; Pred. No. 2.3e-280;

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Matches 1096; Conservative 0; Mismatches 118; Indels 9; Gaps 2;	
Qy	440 CGACCGGTATGAGGCCCGAGTGCCTGTCCTCCAGAGTCCACGTGTCAGAACAAAGAGAG 499
Db	1367 TGGACATGTTGGGGGACGGGGATTCCCGGGTCCGGGATTTTACCCCCACGACTCCGCCC 1426
Qy	296 CGGTGGCATGAGGCCCGAGTGCCTGTCCTCCAGAGTCCACGTGTCAGAACAAAGAGAG 355
Qy	500 AAAAGGAGCAGAGAGAAAAGAACAACTGCCAGTCAAGTACGACGACGACGAGTGGACGATC 559
Db	1427 CCTACGGCGCTCTCGATATGGCCGACTTCGAGTTTGAGCAGATGTTTACCGATGCCCTTG 1486
Qy	356 AAAAGGAGCAGAGAGAAAAGAACAACTGCCAGTCAAGTACGACGACGACGAGTGGACGATC 415
Qy	560 ATATCCCTGCCATATGCAATGTGACCTCCGCCCCCAGAGCGCAAGGATTTACGAAG 619
Db	1487 GAATTGACGAGTACGGTGGGTAG 1509
Qy	416 ATATCCCTGCCATATGCAATGTGACCTCCGCCCCCAGAGCGCGCAAGGATTTACGAAG 475
Qy	620 TGGTCCCGAGGTTCTTAACGAGAGAGCTTAATGGACAGAACAGACTGAAGATGTGACGC 679
Db	1520 TGGACATGTTGGGGGACGGGGATTCCCGGGTCCGGGATTTTACCCCCACGACTCCGCCC 1579
Qy	476 TGGTCCCGAGGTTCTTAACGAGAGAGCTTAATGGAGCAGAACAGACTGAAGATGTGACGC 535
Qy	680 CGCTGTCGGCGAACAGAGAGTCCCTGATCGCGAGGCTCGTGTGTACAGGAGGGGTACG 739
Db	1367 TGGACATGTTGGGGGACGGGGATTCCCGGGTCCGGGATTTTACCCCCACGACTCCGCCC 1426
Qy	536 CGCTGTCGGCGAACAGAGAGTCCCTGATCGCGAGGCTCGTGTGTACAGGAGGCTATG 595
Qy	740 AGCAGCCGTCGGAGGAGATCTCAAGAGAGTTACACAGATGGCAGTTAGAAGAAG 799
Db	1580 CCTACGGCGCTCTCGATATGGCCGACTTCGAGTTTGAGCAGATGTTTACCGATGCCCTTG 1639
Qy	596 AACAACTTCAGAGGAGACCTCAAGAGGTCAGCGACCTGGCAGTCGGACGAGGATG 655
Qy	800 AAGAGGAGGAACTGACATGCCCTTCCGTCAGATCACAGAGATGACGATCTTAACAGTGC 859
Db	1427 CCTACGGCGCTCTCGATATGGCCGACTTCGAGTTTGAGCAGATGTTTACCGATGCCCTTG 1486
Qy	656 AAGAGGAGTCA--GATATGCCGTTCCGCGCAGATCACCGAGATGACGATCCTGACAGTTC 712
Qy	860 AGCTTATGTAGAAATCGCAAGGAGTACCGGGATTCCTCAAGATATCTCAGTCCGATC 919
Db	1520 TGGACATGTTGGGGGACGGGGATTCCCGGGTCCGGGATTTTACCCCCACGACTCCGCCC 1579
Qy	713 AAATCATGTAGAAATCGCAAGGAGTTCGCGAGGCTTCGCGAGGATCTCGCAGTCCGATC 772
Qy	920 AAATACATTTATAAGGCGTCAATCAAGCGAAGTGATGATGTCGCGAGTGGCGCGACGCT 979
Db	1487 GAATTGACGAGTACGGTGGGTAG 1509
Qy	773 AAATCAGTTACTAAGGCGTGTCAAGTGAGTGATGATGCTCCGAGTGGCCGCGCGT 832
Qy	980 ACAGCGCGCGACGAGACGCTGCTTCCGAAACAAACAGGCGTACAGCGCGCAACT 1039
Db	1580 CCTACGGCGCTCTCGATATGGCCGACTTCGAGTTTGAGCAGATGTTTACCGATGCCCTTG 1639
Qy	833 ACAGCGCGCGACGAGACGCTGCTTCCGAAACAAACAGGCGTACTCCCGCGCAACT 892
Qy	1040 ACCGCAAGCGGCGATGCTCTAGCTCATCGAGACCTGCGACATCTCTGTCGGTGTATGT 1099
Db	1367 TGGACATGTTGGGGGACGGGGATTCCCGGGTCCGGGATTTTACCCCCACGACTCCGCCC 1426
Qy	893 ACCGCAAGCGGCGATGCTCTAGCTCATCGAGATCTCTTGACATCTCTGTCGGTGTATGT 952
Qy	1100 ACTCCATGAGTGGACAATGTGCACTACGCGTCTCACCGCCATCGTTATATCTCAG 1159
Db	1427 CCTACGGCGCTCTCGATATGGCCGACTTCGAGTTTGAGCAGATGTTTACCGATGCCCTTG 1486
Qy	953 ACTCCATGATGATGGATACGTGCACTACGCGTGTCTACGGCCATGTTCATTTCTCAG 1012
Qy	1160 ACCGGCCAGGCGCTCGAGCAACCCCTTTAGTGGAGGAATCCAGAGATACTACTTGAAGA 1219
Db	1520 TGGACATGTTGGGGGACGGGGATTCCCGGGTCCGGGATTTTACCCCCACGACTCCGCCC 1579
Qy	1013 ACCGGCTCGGCTCGAGCAACCCCTTTAGTGGAGGAATCCAGCGGTATTACCTGAACA 1072
Qy	1220 CGCTGCGGGTTTACATTTTAAATCAGCAGACGCGTCCGCTCGCTCGCGCGCTGCTGTTCCG 1279
Db	1427 CCTACGGCGCTCTCGATATGGCCGACTTCGAGTTTGAGCAGATGTTTACCGATGCCCTTG 1486
Qy	1073 CGCTGCGGGTTTACATTTTAAATCAGCAGACGCGTCCGCTCGCTCGCGCGCTGCTGTTCCG 1132
Qy	1280 GCAAGATCTCTCGCGTGTGACGGAACCTGCGCACGCTCGGCACGACAGAACTCCAAATGT 1339
Db	1367 TGGACATGTTGGGGGACGGGGATTCCCGGGTCCGGGATTTTACCCCCACGACTCCGCCC 1426
Qy	1133 CCAAGATCTCGGGGATTTGACCGGAGCTGGGACCTTCGGCATGCGAGACTCCAAATGT 1192
Qy	1340 GCATCTCGTGAAGCTGAAGAACAGGAACTTCGCGCATTCCTCGAGGAGATCTGGGACG 1399
Db	1580 CCTACGGCGCTCTCGATATGGCCGACTTCGAGTTTGAGCAGATGTTTACCGATGCCCTTG 1639
Qy	1193 GCATCTCGTGAAGCTGAAGAACAGGAACTTCGCGCATTCCTCGAGGAGATCTGGGACG 1252
Qy	1400 TGGCGGAGTGTGACGACGAGCTTGCCTCCCGCCGACCGATGTGACGCTGGGGAGCGGC 1459
Db	1427 CCTACGGCGCTCTCGATATGGCCGACTTCGAGTTTGAGCAGATGTTTACCGATGCCCTTG 1486
Qy	1253 TG-----GAATCCCGGGAGGCTTGCCTCCCGCCGACCGATGTGACGCTGGGGAGCGGC 1306
Qy	1460 TCCACTTAGACGGCGAGGCTGCGGATGCGGATGCGGATGCGGCTAGACGATTTGATC 1519
Db	1367 TGGACATGTTGGGGGACGGGGATTCCCGGGTCCGGGATTTTACCCCCACGACTCCGCCC 1426
Qy	1307 TCCACTTAGACGGCGAGGCTGCGGATGCGGATGCGGATGCGGCTAGACGATTTGATC 1366

Search completed: April 14, 2005, 19:22:25
Job time : 1007.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 14, 2005, 12:19:35 ; Search time 173 Seconds
(without alignments)
1236.292 Million cell updates/sec

Title: US-10-087-167-105

Perfect score: 2856

Sequence: 1 MKLLSSIEQACIDICRLKLLK.....ADFFEFQMFDALGIDEYGG 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2856	100.0	553	5	ABJ05371 Ecdysone
2	2856	100.0	553	7	ADP49177
3	2803	98.1	588	5	ABJ05374 Chimeric
4	2803	98.1	588	7	ADP49195
5	2786.5	97.6	599	5	ABJ05376 Chimeric
6	2786.5	97.6	599	7	ADP49199
7	2738.5	95.9	591	5	ABJ05372 Chimeric
8	2738.5	95.9	591	7	ADP49191
9	2731	95.6	588	5	ABJ05373 Chimeric
10	2731	95.6	588	7	ADP49193
11	2661.5	93.2	593	5	ABJ05375 Chimeric
12	2661.5	93.2	593	7	ADP49197
13	2442.5	85.5	615	5	ABJ05378 Chimeric
14	2442.5	85.5	615	7	ADP49207
15	2440	85.4	620	5	ABJ05379 Chimeric
16	2440	85.4	620	7	ADP49209
17	2433	85.2	475	5	ABJ05377 Chimeric
18	2433	85.2	475	7	ADP49201
19	2428	85.0	602	5	ABJ05380 Chimeric
20	2428	85.0	602	7	ADP49215
21	2381.5	83.4	599	5	ABJ05381 Chimeric
22	2381.5	83.4	599	7	ADP49220
23	2100	73.5	505	5	ABJ05369 Chimeric
24	2100	73.5	505	7	ADP49166
25	2047	71.7	499	5	ABJ05357 Chimeric

26	2047	71.7	499	7	ADP49142	Adf49142 Ecdysone
27	2030.5	71.1	510	5	ABJ05362	Abj05362 Chimeric
28	2030.5	71.1	510	7	ADP49152	Adf49152 Ecdysone
29	1982.5	69.4	502	5	ABJ05355	Abj05355 Chimeric
30	1982.5	69.4	502	7	ADP49138	Adf49138 Ecdysone
31	1975	69.2	499	5	ABJ05356	Abj05356 Chimeric
32	1975	69.2	499	7	ADP49140	Adf49140 Ecdysone
33	1913	67.0	507	5	ABJ05361	Abj05361 Chimeric
34	1913	67.0	507	7	ADP49150	Adf49150 Ecdysone
35	1905.5	66.7	504	5	ABJ05360	Abj05360 Chimeric
36	1905.5	66.7	504	7	ADP49148	Adf49148 Ecdysone
37	1816	63.6	521	5	ABJ05367	Abj05367 Chimeric
38	1816	63.6	521	7	ADP49162	Adf49162 Ecdysone
39	1791.5	62.7	516	5	ABJ05358	Abj05358 Chimeric
40	1791.5	62.7	516	7	ADP49144	Adf49144 Ecdysone
41	1763	61.7	487	5	ABJ05364	Abj05364 Chimeric
42	1763	61.7	487	7	ADP49156	Adf49156 Ecdysone
43	1725.5	60.4	500	5	ABJ05368	Abj05368 Chimeric
44	1725.5	60.4	500	7	ADP49164	Adf49164 Ecdysone
45	1712	59.9	501	5	ABJ05354	Abj05354 Chimeric

ALIGNMENTS

RESULT 1

ABJ05371
ID ABJ05371 standard; protein; 553 AA.

AC ABJ05371;

DT 07-NOV-2002 (first entry)

DE Ecdysone receptor encoded by vector pCGS202 SEQ ID NO: 105.

XX Plant; gene expression control; insect; hormone receptor; fertility;
KW ecdysone receptor.

OS Synthetic.

XX WO200261102-A2.

XX 08-AUG-2002.

XX 24-OCT-2001; 2001WO-US051417.

XX 24-OCT-2000; 2000US-0242969P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

XX WPI; 2002-619259/66.

XX N-ESDB; ABT07353.

XX New receptor cassette encoding a chimeric receptor polypeptide, useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility.

XX Claim 27; Page 258-261; 319pp; English.

XX The present invention relates to a receptor cassette encoding a chimeric receptor polypeptide comprising at least one DNA binding domain, a hinge domain of an ecdysone receptor (Ecr) of an insect, a ligand binding domain of an insect Ecr, where the ligand binding domain is heterologous with respect to the hinge domain and an activation domain. The chimeric insect hormone receptors and receptor cassettes are useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility. The method is useful for decreasing or increasing plant gene expression. The present sequence is a protein described in the exemplification of the invention

QY	541	MFTDALGIDEYGG 553	
DB	541	MFTDALGIDEYGG 553	
RESULT 3			
ABJ05374			
ID	ABJ05374	standard; protein; 588 AA.	
XX	ABJ05374;		
XX	AC		
XX	29-AUG-2003	(revised)	
DT	07-NOV-2002	(first entry)	
XX	Chimeric ecdysone receptor SEQ ID NO: 123.		
XX	Plant; gene expression control; insect; hormone receptor; fertility;		
KW	ecdysone receptor.		
XX	Manduca sexta.		
OS	Spodoptera frugiperda.		
OS	Chimeric.		
XX	WO200261102-A2.		
XX	08-AUG-2002.		
PD	24-OCT-2001;	2001WO-US051417.	
XX	24-OCT-2000;	2000US-0242969P.	
XX	(SYGN) SYNGENTA PARTICIPATIONS AG.		
PA	Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;		
PI	WPI; 2002-619259/66.		
XX	N-PSDB; ABT07368.		
DR			
XX			
PT	New receptor cassette encoding a chimeric receptor polypeptide, useful in		
PT	regulating expression of target polypeptides in plants in the presence of		
XX	appropriate ligands that may be used in controlling plant fertility.		
XX	Example 23; Page 278-280; 319pp; English.		
XX	The present invention relates to a receptor cassette encoding a chimeric		
CC	receptor polypeptide comprising at least one DNA binding domain, a hinge		
CC	domain of an ecdysone receptor (ECR) of an insect, a ligand binding		
CC	domain of an insect ECR, where the ligand binding domain is heterologous		
CC	with respect to the hinge domain and an activation domain. The chimeric		
CC	insect hormone receptors and receptor cassettes are useful in regulating		
CC	expression of target polypeptides in plants in the presence of		
CC	appropriate ligands that may be used in controlling plant fertility. The		
CC	method is useful for decreasing or increasing plant gene expression. The		
CC	present sequence is a protein described in the exemplification of the		
CC	invention. (Updated on 29-AUG-2003 to standardise OS field)		
XX	Sequence 588 AA;		
SQ			
Query Match			
Best Local Similarity 98.1%; Score 2803; DB 5; Length 588;			
Matches 545; Conservative 1; Mismatches 1; Indels 6; Gaps 1;			
QY	1	MKLLSSISOACDICRLKKLCKSEKPKCAKCKKNNWECRYSPKTRSPKTRAHLTEVESR 60	
DB	42	MKLLSSISOACDICRLKKLCKSEKPKCAKCKKNNWECRYSPKTRSPKTRAHLTEVESR 101	
QY	61	LERLEQLFLLIFPREDLMDKMSLDQIKALLTGLFVQDNVNNKDAVTDRLASVETDML 120	
DB	102	LERLEQLFLLIFPREDLMDKMSLDQIKALLTGLFVQDNVNNKDAVTDRLASVETDML 161	
QY	121	TLRQHRISATSSSESSNKGORQLTVSTRMPECVVPSTCKNKRREKEAOREKDKLPVS 180	
DB	162	TLRQHRISATSSSESSNKGORQLTVSTRMPECVVPSTCKNKRREKEAOREKDKLPVS 221	
us-10-087-167-105.rag			
QY	181	TTTVDDHMPAIMQCDDPPPPPEAARIHEVVPRFLTEKLMQNLKNVTPLSANQKSLIARLV 240	
DB	222	TTTVDDHMPAIMQCDDPPPPPEAARIHEVVPRFLTEKLMQNLKNVTPLSANQKSLIARLV 281	
QY	241	WYQEGYEQPSEEDLKRVTTQWOLEEEEEEDTDFRQITENTILTQVLIIVEFAKGLPGFS 300	
DB	282	WYQEGYEQPSEEDLKRVTTQWOLEEEEEEDTDFRQITENTILTQVLIIVEFAKGLPGFS 341	
QY	301	KISQSDQITLLKASSSEVMMLRVARRDYDAATDSVLFANNOAYTRDNYRKAGMSYVIEDLL 360	
DB	342	KISQSDQITLLKASSSEVMMLRVARRDYDAATDSVLFANNOAYTRDNYRKAGMSYVIEDLL 401	
QY	361	HFRCMYSMSMDNVHYALLTAIVIFSDRPGLEQLLVVEEIQRYYLKTURVYILNQHSASP 420	
DB	402	HFRCMYSMSMDNVHYALLTAIVIFSDRPGLEQLLVVEEIQRYYLKTURVYILNQHSASP 461	
QY	421	RCAVLFGKILGVLTELRTLTGTONSNMCISLKNRKLPPFLEEIWDVAEVTSTKLAPTD 480	
DB	462	RCAVLFGKILGVLTELRTLTGTONSNMCISLKNRKLPPFLEEIWDV-----KLAPTD 515	
QY	481	VSLGDELHLDGEDVMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDMADFEFEQ 540	
DB	516	VSLGDELHLDGEDVMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDMADFEFEQ 575	
QY	541	MFTDALGIDEYGG 553	
DB	576	MFTDALGIDEYGG 588	
RESULT 4			
ID	ADF49195	standard; protein; 588 AA.	
XX	ADF49195;		
DT	12-FEB-2004	(first entry)	
XX	Ecdysone receptor/VP16 transactivation domain seq id 123.		
DE	receptor cassette; chimeric receptor polypeptide; DNA binding domain;		
KW	hinge domain; ecdysone receptor; ECR; ligand binding domain;		
KW	activation domain; transgenic seed; transgenic plant; plant line;		
KW	herbicide; pesticide; chimeric ecdysone receptor; ECR;		
XX	yeast GAL4 DNA binding domain; VP16 transactivation domain.		
OS	Synthetic.		
OS	Manduca sexta.		
OS	Ascomycota.		
OS	Spodoptera frugiperda.		
XX	Herpes simplex virus unknown type.		
FN	US2003154509-A1.		
XX	14-AUG-2003.		
XX	24-OCT-2001;	2001US-00087167.	
XX	24-OCT-2001;	2001US-00087167.	
PA	(PASC/) PASCAL E J.		
PA	(VALE/) VALENTINE S A.		
PA	(BROW/) BROWN J A.		
PA	(COCK/) COCKRELL A S.		
PA	(JOHN/) JOHNSON B D.		
XX	Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;		
PI	WPI; 2003-897756/82.		
XX	N-PSDB; ADF49194.		
DR			
XX	New receptor cassette encoding a chimeric receptor polypeptide, useful		
PT	for regulating the expression of target polypeptides in plants in the		

Db 402 IEDLLHFCRCMYSMNDNVHALLTAIVIFSDRPGLEQPLLVVEIQRYYLKLRLVYILNQ 461

Qy 416 HSASPRCAVLFGKILGVLTELRTLTQNSNMCISLKNRKLPPPLEBIWDVAEVSSTKL 475

Db 462 HSASPRCAVLFGKILGVLTELRTLTQNSNMCISLKNRKLPPPLEBIWDVAEVSSTKL 521

Qy 476 APPTDVSIGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGTTPHDSAPYGALDNAD 535

Db 522 APPTDVSIGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGTTPHDSAPYGALDNAD 581

Qy 536 FEFEQMFDTALGIDEYGG 553

Db 582 FEFEQMFDTALGIDEYGG 599

RESULT 6

ADF49199

ID ADF49199 standard; protein; 599 AA.

XX

AC ADF49199;

XX

DT 12-FEB-2004 (first entry)

XX

DE Ecdysone receptor/VP16 transactivation domain seq id 127.

XX

Kw receptor cassette; chimeric receptor polypeptide; DNA binding domain; hinge domain; ecdysone receptor; EcR; ligand binding domain; activation domain; transgenic seed; transgenic plant; plant line; herbicide; pesticide; chimeric ecdysone receptor; EcR; yeast GAL4 DNA binding domain; VP16 transactivation domain.

XX

OS Synthetic.

OS Ostrinia nubilalis.

OS Ascomycota.

OS Manduca sexta.

OS Herpes simplex virus unknown type.

XX

XX US2003154509-A1.

XX

XX 14-AUG-2003.

XX

XX 24-OCT-2001; 2001US-00087167.

XX

XX 24-OCT-2001; 2001US-00087167.

XX

XX (PASC/) PASCAL E J.

XX (VALE/) VALENTINE S A.

XX (BROW/) BROWN J A.

XX (COCK/) COCKRELL A S.

XX (JOHN/) JOHNSON B D.

XX

PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

XX

DR WPI; 2003-897756/82.

DR N-PSDB; ADF49198.

XX

XX New receptor cassette encoding a chimeric receptor polypeptide, useful for regulating the expression of target polypeptides in plants in the presence of appropriate chemical ligands.

PT

PT Example 23; SEQ ID NO 127; 186pp; English.

PS

XX The invention describes a receptor cassette encoding a chimeric receptor polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge (D) domain of an ecdysone receptor (EcR) of an insect, a ligand binding (B) domain that is heterologous with respect to the D domain, and an activation domain. The receptor cassette and method are useful in regulating the expression of target polypeptides in plants in the presence of appropriate chemical ligands. The transgenic seeds and plants can be used for the breeding of improved plant lines that, for e.g., increase the effectiveness of conventional methods such as herbicide or pesticide treatment. This is the amino acid sequence of an ecdysone receptor-VP16 transactivation domain fusion protein.

XX SQ Sequence 599 AA;

Query Match

Best Local Similarity 97.6%; Score 2786.5; DB 7; Length 599;

Matches 540; Conservative 7; Mismatches 23; Indels 5; Gaps 1;

Qy 1 MKLSSIEQAQCDICRLKKLKCSEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60

Db 42 MKLSSIEQAQCDICRLKKLKCSEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 101

Qy 61 LERLEQLFLIFPREDLDMLKMSLDQIKALLTGLFVQDNVNVKDAVTRDLASVETDML 120

Db 102 LERLEQLFLIFPREDLDMLKMSLDQIKALLTGLFVQDNVNVKDAVTRDLASVETDML 161

Qy 121 TLQHRISATSSSESSNKGQRLTVSTRMPECVVPESTCKNRREKAEQKDKLPVS 180

Db 162 TLQHRISATSSSESSNKGQRLTVSTRMPECVVPESTCKNRREKAEQKDKLPVS 221

Qy 181 TTTVDHMPAIMQCDDPPPPPEAARI-----HEVVPRFLTEKLMQNRKLNVTPLSANQKSL 235

Db 222 TTTVDHMPAIMQCDDPPPPPEAARI-----HEVVPRFLTEKLMQNRKLNVTPLSANQKSL 281

Qy 236 IARLVWYQEGYEQSEEDLKRVTQTWOLEEEEEETDMPFRQITEMTILTVQLIVEFAG 295

Db 282 IARLVWYQEGYEQSEEDLKRVTQTWOLEEEEEETDMPFRQITEMTILTVQLIVEFAG 341

Qy 296 LPGFSKISQSDQITLLKASSSEVMMLRVARYDAATSVLFANNOAYTRDNVYKAGMSYV 355

Db 342 LPGFSKISQSDQITLLKASSSEVMMLRVARYDAATSVLFANNOAYTRDNVYKAGMSYV 401

Qy 356 IEDLLHFCRCMYSMNDNVHALLTAIVIFSDRPGLEQPLLVVEIQRYYLKLRLVYILNQ 415

Db 402 IEDLLHFCRCMYSMNDNVHALLTAIVIFSDRPGLEQPLLVVEIQRYYLKLRLVYILNQ 461

Qy 416 HSASPRCAVLFGKILGVLTELRTLTQNSNMCISLKNRKLPPPLEBIWDVAEVSSTKL 475

Db 462 HSASPRCAVLFGKILGVLTELRTLTQNSNMCISLKNRKLPPPLEBIWDVAEVSSTKL 521

Qy 476 APPTDVSIGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGTTPHDSAPYGALDNAD 535

Db 522 APPTDVSIGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGTTPHDSAPYGALDNAD 581

Qy 536 FEFEQMFDTALGIDEYGG 553

Db 582 FEFEQMFDTALGIDEYGG 599

RESULT 7

ABJ05372

ID ABJ05372 standard; protein; 591 AA.

AC ABJ05372;

XX

DT 29-AUG-2003 (revised)

DT 07-NOV-2002 (first entry)

XX

DE Chimeric ecdysone receptor SEQ ID NO: 119.

XX

KW Plant; gene expression control; insect; hormone receptor; fertility; ecdysone receptor.

XX

OS Manduca sexta.

OS Agrotis ipsilon.

OS Chimeric.

XX

PN WO200261102-A2.

XX

PD 08-AUG-2002.

XX

XX 24-OCT-2001; 2001WO-US051417.

PF

PR 24-OCT-2000; 2000US-0242969P.

XX

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XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
XX WPI; 2002-619259/66.
XX N-PSDB; ABT07366.
XX
XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
XX regulating expression of target polypeptides in plants in the presence of
XX appropriate ligands that may be used in controlling plant fertility.
XX
XX Example 23; Page 268-270; 319pp; English.
XX
XX The present invention relates to a receptor cassette encoding a chimeric
XX receptor polypeptide comprising at least one DNA binding domain, a hinge
XX domain of an ecdysone receptor (EcR) of an insect, a ligand binding
XX domain of an insect EcR, where the ligand binding domain is heterologous
XX with respect to the hinge domain and an activation domain. The chimeric
XX insect hormone receptors and receptor cassettes are useful in regulating
XX expression of target polypeptides in plants in the presence of
XX appropriate ligands that may be used in controlling plant fertility. The
XX method is useful for decreasing or increasing plant gene expression. The
XX present sequence is a protein described in the exemplification of the
XX invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 591 AA;
XX
XX Query Match 95.9%; Score 2738.5; DB 5; Length 591;
XX Best Local Similarity 96.2%; Pred. No. 5.7e-219;
XX Matches 532; Conservative 8; Mismatches 10; Indels 3; Gaps 2;
XX
XX 1 MKLLSSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
XX Db
XX 42 MKLLSSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 101
XX
XX 61 LERLEQLFLLIFFPREDLDMILKMSLQDIKALLTGLFVQDNVNKDVAVTDRLASVETDML 120
XX Db
XX 102 LERLEQLFLLIFFPREDLDMILKMSLQDIKALLTGLFVQDNVNKDVAVTDRLASVETDML 161
XX
XX 121 TLQRHRISATSSSESSNKGQRQITVSTRMPECVPESTCKNKRREKAEQKDLPLVS 180
XX Db
XX 162 TLQRHRISATSSSESSNKGQRQITVSTRMPECVPESTCKNKRREKAEQKDLPLVS 221
XX
XX 181 TTTVDHHPATMQCDPPPEAARHEVVPRLTEKLEQNRLKNVTPLSANQKSLIARLV 240
XX Db
XX 222 TTTVDHHPATMQCDPPPEAARHEVVPRLTEKLEQNRLKNVTPLSANQKSLIARLV 281
XX
XX 241 WYQGEYQPSSEDLKRVTTQWLBESEETDMPFROITMTILTVOIVEFAKGLPGFS 300
XX Db
XX 282 WYQGEYQPSSEDLKRVTTQW-SDEDEESDMPFROITMTILTVOIVEFAKGLPGFA 340
XX
XX 301 KISQSDQITLLKASSEVMMLRVARRYDAATDSVLFANNQAYTRDNYRKAGMSYVIEDLL 360
XX Db
XX 341 KISQSDQITLLKASSEVMMLRVARRYDAATDSVLFANNQAYSRDNYRKAGMSYVIEDLL 400
XX
XX 361 HFRCMYSMDNHYHALLTAIVFSDRPGLEQLLVEEIQRYVLTIRVILNQHSAP 420
XX Db
XX 401 HFRCMYSMDNHYHALLTAIVFSDRPGLEQLLVEEIQRYVLTIRVILNQHSAP 460
XX
XX 421 RCVLFGLIGLVTGLRTGLTQNSNMICSLKLNKRLPPFLFEEIWDVAEVSSTTKLAPTD 480
XX Db
XX 461 RCPVVFAGILIGLITGLRTGLTQNSNMICSLKLNKRLPPFLFEEIWDVVE--SRGKLAPTD 518
XX
XX 481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYGLADMADFFFEQ 540
XX Db
XX 519 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYGLADMADFFFEQ 578
XX
XX 541 MFTDALGIDEYGG 553
XX Db
XX 579 MFTDALGIDEYGG 591
XX
XX RESULT 8
XX ADF49191
XX ID ADF49191 standard; protein; 591 AA.
XX
XX AC ADF49191;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX DE Ecdysone receptor/VP16 transactivation domain seq id 119.
XX
XX KW receptor cassette; chimeric receptor polypeptide; DNA binding domain;
XX hinge domain; ecdysone receptor; EcR; ligand binding domain;
XX KW activation domain; transgenic seed; transgenic plant; plant line;
XX herbicide; pesticide; chimeric ecdysone receptor; EcR;
XX KW yeast GAL4 DNA binding domain; VP16 transactivation domain.
XX
XX OS Synthetic.
XX OS Manduca sexta.
XX OS Ascomycota.
XX OS Agrotis ipsilon.
XX OS Herpes simplex virus unknown type.
XX
XX PN US2003154509-A1.
XX
XX PD 14-AUG-2003.
XX
XX PF 24-OCT-2001; 2001US-00087167.
XX
XX PR 24-OCT-2001; 2001US-00087167.
XX
XX PA (PASC/) PASCAL E J.
XX PA (VALE/) VALENTINE S A.
XX PA (BROW/) BROWN J A.
XX PA (COCK/) COCKRELL A S.
XX PA (JOHN/) JOHNSON B D.
XX
XX PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
XX WPI; 2003-897756/82.
XX N-PSDB; ADF49190.
XX
XX New receptor cassette encoding a chimeric receptor polypeptide, useful
XX for regulating the expression of target polypeptides in plants in the
XX presence of appropriate chemical ligands.
XX
XX Example 23; SEQ ID NO 119; 186pp; English.
XX
XX The invention describes a receptor cassette encoding a chimeric receptor
XX polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
XX (D) domain of an ecdysone receptor (EcR) of an insect, a ligand binding
XX (E) domain that is heterologous with respect to the D domain, and an
XX activation domain. The receptor cassette and method are useful in
XX regulating the expression of target polypeptides in plants in the
XX presence of appropriate chemical ligands. The transgenic seeds and plants
XX can be used for the breeding of improved plant lines that, for e.g.
XX increase the effectiveness of conventional methods such as herbicide or
XX pesticide treatment. This is the amino acid sequence of an ecdysone
XX receptor-VP16 transactivation domain fusion protein.
XX
XX Sequence 591 AA;
XX
XX Query Match 95.9%; Score 2738.5; DB 7; Length 591;
XX Best Local Similarity 96.2%; Pred. No. 5.7e-219;
XX Matches 532; Conservative 8; Mismatches 10; Indels 3; Gaps 2;
XX
XX 1 MKLLSSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
XX Db
XX 42 MKLLSSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 101
XX
XX 61 LERLEQLFLLIFFPREDLDMILKMSLQDIKALLTGLFVQDNVNKDVAVTDRLASVETDML 120
XX Db
XX 102 LERLEQLFLLIFFPREDLDMILKMSLQDIKALLTGLFVQDNVNKDVAVTDRLASVETDML 161
XX
```

QY 121 TLQHRISATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRREKEAQRKDKLPVS 180
DB 162 TLQHRISATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRREKEAQRKDKLPVS 221
QY 181 TTTVDHMPAQMCDPPPEAARIEHVVPFLTEKLMQNRLKNVTPLSANQKSLIARLV 240
DB 222 TTTVDHMPAQMCDPPPEAARIEHVVPFLTEKLMQNRLKNVTPLSANQKSLIARLV 281
QY 241 WYQGYEQPSBEDLKRVTQTWQLEBEEEDMDPRQITMTILTVQLIVFAKGLPGFS 300
DB 282 WYQGYEQPSBEDLKRVTQTWQ-SPEDEESDMPRQITMTILTVQLIVFAKGLPGFA 340
QY 301 KISQSDQITLLKASSEVMMLRVARRYDAATDSVLFANNQAYTRDNRKAGMSYVIEDLL 360
DB 341 KISQSDQITLLKACSEVMMLRVARRYDAATDSVLFANNQAYSRDNRKAGMSYVIEDLL 400
QY 361 HFCRCMYSMDNVHYALLTAIVFSDRPGLEQPLVVEIORYYLKTIRVYLNOHSASP 420
DB 401 HFCRCMYSMDNVHYALLTAIVFSDRPGLEQPLVVEIORYYLKTIRVYLNOHSASP 460
QY 421 RCVLFGKILGVLTELRTLTGQNSNMCI SLKLNKRLPPFLEEIWDVAEVS TTKLAPPTD 480
DB 461 RCPVVFALIGLTELRTLTGQNSNMCI SLKLNKRLPPFLEEIWDVE--SRGKLAPPTD 518
QY 481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYCALDMADFEFEQ 540
DB 519 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYCALDMADFEFEQ 578
QY 541 MFTDALGIDEYGG 553
DB 579 MFTDALGIDEYGG 591

RESULT 9
ABJ05373
ID ABJ05373 standard; protein; 588 AA.

XX ABJ05373;
AC 29-AUG-2003 (revised)
DT 07-NOV-2002 (first entry)
XX Chimeric ecdysone receptor SEQ ID NO: 121.
DE Plant; gene expression control; insect; hormone receptor; fertility;
KW ecdysone receptor.
XX Manduca sexta.
OS Ostrinia nubilalis.
OS Chimeric.
XX WO200261102-A2.
PN 08-AUG-2002.
PD 24-OCT-2001; 2001WO-US051417.
PF 24-OCT-2000; 2000US-0242969P.
PR (SYGN) SYNGENTA PARTICIPATIONS AG.
PA Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
PI WPI: 2002-619259/66.
DR N-PSDB; ABT07367.
XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
PT regulating expression of target polypeptides in plants in the presence of
PT appropriate ligands that may be used in controlling plant fertility.
XX Claim 6; Page 273-275; 319pp; English.
XX The present invention relates to a receptor cassette encoding a chimeric

CC receptor polypeptide comprising at least one DNA binding domain, a hinge
CC domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
CC domain of an insect Ecr, where the ligand binding domain is heterologous
CC with respect to the hinge domain and an activation domain. The chimeric
CC insect hormone receptors and receptor cassettes are useful in regulating
CC expression of target polypeptides in plants in the presence of
CC appropriate ligands that may be used in controlling plant fertility. The
CC method is useful for decreasing or increasing plant gene expression. The
CC present sequence is a protein described in the exemplification of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX Sequence 588 AA;
SQ

Query Match 95.6%; Score 2731; DB 5; Length 588;
Best Local Similarity 95.3%; Pred. No. 2.4e-218;
Matches 527; Conservative 10; Mismatches 10; Indels 6; Gaps 1;
QY 1 MKLLSSIEQACDLCRLKLLKCKSEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
DB 42 MKLLSSIEQACDLCRLKLLKCKSEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 101
QY 61 LERLEQLFLIFPREDLMDILKMSLODIKALLTGLFVQDNVNVKDAVTDRLASVETDMLP 120
DB 102 LERLEQLFLIFPREDLMDILKMSLODIKALLTGLFVQDNVNVKDAVTDRLASVETDMLP 161
QY 121 TLQHRISATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRREKEAQRKDKLPVS 180
DB 162 TLQHRISATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRREKEAQRKDKLPVS 221
QY 181 TTTVDHMPAQMCDPPPEAARIEHVVPFLTEKLMQNRLKNVTPLSANQKSLIARLV 240
DB 222 TTTVDHMPAQMCDPPPEAARIEHVVPFLTEKLMQNRLKNVTPLSANQKSLIARLV 281
QY 241 WYQGYEQPSBEDLKRVTQTWQLEBEEEDMDPRQITMTILTVQLIVFAKGLPGFS 300
DB 282 WYQGYEQPSBEDLKRVTQTWQSADEEDSDMPRQITMTILTVQLIVFAKGLPGFS 341
QY 301 KISQSDQITLLKASSEVMMLRVARRYDAATDSVLFANNQAYTRDNRKAGMSYVIEDLL 360
DB 342 KISQSDQITLLKACSEVMMLRVARRYDAVSDSVLFANNQAYTRDNRKAGWAYVIEDLL 401
QY 361 HFCRCMYSMDNVHYALLTAIVFSDRPGLEQPLVVEIORYYLKTIRVYLNOHSASP 420
DB 402 HFCRCMYSMDNVHYALLTAIVFSDRPGLEQPLVVEIORYYLKTIRVYLNOHSASP 461
QY 421 RCVLFGKILGVLTELRTLTGQNSNMCI SLKLNKRLPPFLEEIWDVAEVS TTKLAPPTD 480
DB 462 RCVIYAKILSVLTELRTLTGQNSNMCI SLKLNKRLPPFLEEIWDV-----KLAPPTD 515
QY 481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYCALDMADFEFEQ 540
DB 516 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYCALDMADFEFEQ 575
QY 541 MFTDALGIDEYGG 553
DB 576 MFTDALGIDEYGG 588

RESULT 10
ADF49193
ID ADF49193 standard; protein; 588 AA.

XX ADF49193;
AC ADF49193;
XX 12-FEB-2004 (first entry)
DT Ecdysone receptor/VP16 transactivation domain seq id 121.
DE receptor cassette; chimeric receptor polypeptide; DNA binding domain;
KW hinge domain; ecdysone receptor; Ecr; ligand binding domain;
KW activation domain; transgenic seed; transgenic plant; plant line;
KW herbicide; pesticide; chimeric ecdysone receptor; Ecr;
KW yeast GAL4 DNA binding domain; VP16 transactivation domain.

XX OS Synthetic.
OS OS Manduca sexta.
OS OS Ascomycota.
OS OS Ostrinia nubilalis.
OS OS Herpes simplex virus unknown type.
XX XX US2003154509-A1.
XX XX 14-AUG-2003.
XX XX 24-OCT-2001; 2001US-00087167.
XX XX 24-OCT-2001; 2001US-00087167.
XX XX (PASC/) PASCAL E J.
XX XX (VALE/) VALENTINE S A.
XX XX (BROW/) BROWN J A.
XX XX (COCK/) COCKRELL A S.
XX XX (JOHN/) JOHNSON B D.
XX XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX XX WPI; 2003-897756/82.
XX XX N-PSDB; ADF49192.
XX XX New receptor cassette encoding a chimeric receptor polypeptide, useful
XX XX for regulating the expression of target polypeptides in plants in the
XX XX presence of appropriate chemical ligands.
XX XX Example 23; SEQ ID NO 121; 186pp; English.
XX XX The invention describes a receptor cassette encoding a chimeric receptor
XX XX polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
XX XX (D) domain of an ecdysone receptor (EcR) of an insect, a ligand binding
XX XX (E) domain that is heterologous with respect to the D domain, and an
XX XX activation domain. The receptor cassette and method are useful in
XX XX regulating the expression of target polypeptides in plants in the
XX XX presence of appropriate chemical ligands. The transgenic seeds and plants
XX XX can be used for the breeding of improved plant lines that, for e.g.,
XX XX increase the effectiveness of conventional methods such as herbicide or
XX XX pesticide treatment. This is the amino acid sequence of an ecdysone
XX XX receptor-VP16 transactivation domain fusion protein.
XX XX Sequence 588 AA;
XX XX
XX XX Query Match 95.6%; Score 2731; DB 7; Length 588;
XX XX Best Local Similarity 95.3%; Pred. No. 2.4e-218;
XX XX Matches 527; Conservative 10; Mismatches 10; Indels 6; Gaps 1;
QY 1 MKLLSSISQACDICELKXKCKSEKPKCAKCKNNWECRYSPKTRSPPLTRAHLTEVESR 60
DB 42 MKLLSSISQACDICELKXKCKSEKPKCAKCKNNWECRYSPKTRSPPLTRAHLTEVESR 101
QY 61 LERLEQLFLLIPPRDLMLKMDLSLQIKALLTGLFQVDNVNKAQVTDRLASVETDML 120
DB 102 LERLEQLFLLIPPRDLMLKMDLSLQIKALLTGLFQVDNVNKAQVTDRLASVETDML 161
QY 121 TLQRHRIATSSSESSNGRQLTVSTRMPECVPESTCKNKRREKAEQKDLPLVS 180
DB 162 TLQRHRIATSSSESSNGRQLTVSTRMPECVPESTCKNKRREKAEQKDLPLVS 221
QY 181 TTTVDHHPAQMCDPPPEAARIEHVVPFRFTEKLMQNRKKNVTPLSANQKSLIARLV 240
DB 222 TTTVDHHPAQMCDPPPEAARIEHVVPFRFTEKLMQNRKKNVTPLSANQKSLIARLV 281
QY 241 WYQEGVEQPSDDLKRVVTQTWQLEBEEBETDMPFRQITEMTLTVQLVIVFAKGLPGFS 300
DB 282 WYQEGVEQPSDDLKRVVTQTWQLEBEEBETDMPFRQITEMTLTVQLVIVFAKGLPGFS 341
QY 301 KISQSDQITLLKASSEVMMLVARRYDAATDVLVFNQATRDYRNYRKAGMSVYIEDLL 360
DB 342 KISQSDQITLLKASSEVMMLVARRYDAATDVLVFNQATRDYRNYRKAGMSVYIEDLL 401

QY 361 HFCRCMYSMDNVHYALLTAIVIFSDRPGLEQPLVVEIQRYLKTLLRVILNOHSASP 420
DB 402 HFCRCMYSMDNVHYALLTAIVIFSDRPGLEQPLVVEIQRYLKTLLRVILNOHSASP 461
QY 421 RCAVLFGKILGVLTELRTLTQNSMNCISILKKNRKLPPFLEEIWDVAEVSSTTKLAPPTD 480
DB 462 RCAVIYAKILSVLTELRTLTGMQNSMNCISILKKNRKLPPFLEEIWDV-----KLAPPTD 515
QY 481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSGPGFTPHDSAPYGALDMADFEFEQ 540
DB 516 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSGPGFTPHDSAPYGALDMADFEFEQ 575
QY 541 MFTDALGIDEYGG 553
DB 576 MFTDALGIDEYGG 588

RESULT 11
ABJ05375
ID ABJ05375 standard; protein; 593 AA.
XX AC ABJ05375;
XX XX 29-AUG-2003 (revised)
XX XX 07-NOV-2002 (first entry)
XX XX Chimeric ecdysone receptor SEQ ID NO: 125.
XX XX Plant; gene expression control; insect; hormone receptor; fertility;
XX XX ecdysone receptor.
XX XX Ostrinia nubilalis.
XX XX Ostrinia nubilalis.
XX XX Chimeric.
XX XX WO200261102-A2.
XX XX 08-AUG-2002.
XX XX 24-OCT-2001; 2001WO-US051417.
XX XX 24-OCT-2000; 2000US-0242969P.
XX XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX XX WPI; 2002-619259/66.
XX XX N-PSDB; ABT07369.
XX XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
XX XX regulating expression of target polypeptides in plants in the presence of
XX XX appropriate ligands that may be used in controlling plant fertility.
XX XX Example 23; Page 283-285; 319pp; English.
XX XX The present invention relates to a receptor cassette encoding a chimeric
XX XX receptor polypeptide comprising at least one DNA binding domain, a hinge
XX XX domain of an ecdysone receptor (EcR) of an insect, a ligand binding
XX XX domain of an insect EcR, where the ligand binding domain is heterologous
XX XX with respect to the hinge domain and an activation domain. The chimeric
XX XX insect hormone receptors and receptor cassettes are useful in regulating
XX XX expression of target polypeptides in plants in the presence of
XX XX appropriate ligands that may be used in controlling plant fertility. The
XX XX method is useful for decreasing or increasing plant gene expression. The
XX XX present sequence is a protein described in the exemplification of the
XX XX invention. (Updated on 29-AUG-2003 to standardise OS field)
XX XX Sequence 593 AA;
XX XX
XX XX Query Match 93.2%; Score 2661.5; DB 5; Length 593;
XX XX Best Local Similarity 92.1%; Pred. No. 1.9e-212;

Query Match	93.2%	Score 2661.5;	DB 7;	Length 593;
Best Local Similarity	92.1%	Pred. No. 1.5e-212;		
Matches 514;	Conservative 17;	Mismatches 16;	Indels 11;	Gaps 2

Qy	1	MKLLSSIEQACDI	CRLLKKL	KCKSKPKCAK	CLKNWECRYSP	TKTSPL	TRAHL	TEVSR	60
Db	42	MKLLSSIEQACDI	ICRLKKL	KCKSKPKCAK	CLKNWECRYSP	TKTSPL	TRAHL	TEVSR	101
Qy	61	LERLSQLFLI	FPRED	LDMLIK	MSLODI	KALLTGL	FVQNV	NKDAV	120
Db	102	LERLSQLFLI	FPRED	LDMLIK	MSLODI	KALLTGL	FVQNV	NKDAV	161

Query Match	93.2%	Score	2661.5	DB	7	Length	593
Best Local Similarity	92.1%	Pred. No.	1.5e-212				
Matches	514	Conservative	17	Mismatches	16	Indels	11
Gaps							
QY	1	MKLLSSISQACDI	CRLLKXKSKKPKCAKCLKNWECRYSPKTKSP	LAHLTEVESR	60		
DB	42	MKLLSSISQACDI	CRLLKXKSKKPKCAKCLKNWECRYSPKTKSP	LAHLTEVESR	101		
QY	61	LERLEQLFLLIP	REDLDMILKMDSLQDIKALLTGLFVQDNVNKDAVTD	RLASVETDMLP	120		
DB	102	LERLEQLFLLIP	REDLDMILKMDSLQDIKALLTGLFVQDNVNKDAVTD	RLASVETDMLP	161		
QY	121	TLRQHRISATSS	BESSNKGORQLTVSTRMPCEVCVPPESTCKNKR	EKAQREKDKLPVS	180		
DB	162	TLRQHRISATSS	BESSNKGORQLTVSTRMPCEVCVPPESTCKNKR	EKAQREKDKLPVS	221		
QY	181	TTTTVDHHPA	IMQCDPPPPPEAARI-----HEVPRFLTEKLMQNRLKNV	TPLSANQKSL	235		
DB	222	TTTTVDHHPA	IMQCDPPPPPEAARILECLOHEVVPFLSEKLMQNRLKN	PPLTANQOFL	281		
QY	236	IARLVVYQEGVE	QSEEDLKRVTOTWOLEEBEETDMPFRQITEMTILTVQ	LIVFPAKG	295		
DB	282	IARLVVYQEGVE	QSEEDLKRVTOTWQSADEEDSDMPFRQITEMTILTVQ	LIVFPAKG	341		
QY	296	LPGFSKI	SQSQDITLLKASSSEVMMLRVARRYDAATDSVLFANNOA	YTRONRYKAGMSYV	355		
DB	342	LPGFSKI	SQSQDITLLKACSSSEVMMLRVARRYDAVSVLFANNOA	YTRONRYKAGMAYV	401		
QY	356	IEDLLHFRCR	CMYSMSMDNVHYALLTAIVIFSDRPGLEQPLLVEEIQ	RYILKTLRVYILNQ	415		
DB	402	IEDLLHFRCR	CMYSMSMDNVHYALLTAIVIFSDRPGLEQPLLVEEIQ	RYILKTLRVYIMNQ	461		
QY	416	HSASPRCAVL	FGKILGVLTTELRTIGTONSNWCISLKNKRLPPFL	EEIWDVAEVSTTKL	475		
DB	462	HSASPRCAVI	YAKILSVLTTELRTIGMQNSNCCISLKNKRLPPFL	EEIWDV-----KL	515		
QY	476	APPTDVSIG	DELHLDGEDVANAHADALDDFDLMDGDS	PGPGFPHDSAPYCALDMAD	535		
DB	516	APPTDVSIG	DELHLDGEDVANAHADALDDFDLMDGDS	PGPGFPHDSAPYCALDMAD	575		
QY	536	FEFEQMF	TDALGIDBYGG	553			
DB	576	FEFEQMF	TDALGIDBYGG	593			

```

RESULT 13
ABJ05378
ID ABJ05378 standard; protein; 615 AA.
XX
AC ABJ05378;
XX
XX
DT 29-AUG-2003 (revised)
DT 07-NOV-2002 (first entry)
XX
XX Chimeric ecdysone receptor SEQ ID NO: 135.
XX
XX Plant; gene expression control; insect; hormone receptor; fertility;
XX ecdysone receptor.
XX
XX Manduca sexta.
XX OS Manduca sexta.
XX OS Chimeric.
XX
XX WO200261102-A2.
XX
XX 08-AUG-2002.
XX
XX 24-OCT-2001; 2001WO-US051417.
XX
XX 24-OCT-2000; 2000US-0242969P.
XX
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
XX WPI; 2002-619259/66.
XX
XX N-PSDB; ABT07376.
XX
XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
XX regulating expression of target polypeptides in plants in the presence of
XX appropriate ligands that may be used in controlling plant fertility.
XX
XX Example 25; Page 299-301; 319pp; English.
XX
XX The present invention relates to a receptor cassette encoding a chimeric
XX receptor polypeptide comprising at least one DNA binding domain, a hinge
XX domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
XX domain of an insect Ecr, where the ligand binding domain is heterologous
XX with respect to the hinge domain and an activation domain. The chimeric
XX insect hormone receptors and receptor cassettes are useful in regulating
XX expression of target polypeptides in plants in the presence of
XX appropriate ligands that may be used in controlling plant fertility. The
XX method is useful for decreasing or increasing plant gene expression. The
XX present sequence is a protein described in the exemplification of the
XX invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 615 AA;
XX
Query Match 85.5%; Score 2442.5; DB 5; Length 615;
Best Local Similarity 94.0%; Pred. No. 2.7e-194;
Matches 486; Conservative 1; Mismatches 25; Indels 5; Gaps 2;
XX
QY 1 MKLLSSIEQACDICRLKKLCKSEKPKCAKCLKNNWECRYSPKTKRSPPLTRAHLTEVESR 60
DB 42 MKLLSSIEQACDICRLKKLCKSEKPKCAKCLKNNWECRYSPKTKRSPPLTRAHLTEVESR 101
XX
QY 61 LERLEQLPLLPREDLDMILKMSLDQIKALLTGLFVQDNVNNKDAVTDRLASVETDMLP 120
DB 102 LERLEQLPLLPREDLDMILKMSLDQIKALLTGLFVQDNVNNKDAVTDRLASVETDMLP 161
XX
QY 121 TLQHRISATSSBESSNKGORQLTVSTRMPECVPESTCKNKRKEAOREKDKLPVS 180
DB 162 TLQHRISATSSBESSNKGORQLTVSTRMPECVPESTCKNKRKEAOREKDKLPVS 221
XX
QY 181 TTTVDHMPAIMQCDPPPEAARIEHVVPRLTEKLMEQNRLKNVTPLSANQKSLIARLV 240
XX

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DB 222 TTTVDHMPAIMQCDPPPEAARIEHVVPRLTEKLMEQNRLKNVTPLSANQKSLIARLV 281
QY 241 WYQEGYBOPSEEDLKRVTQTWOLEEEEEETDMPFROIETMTILTVOIIVEFAKGLPGFS 300
DB 282 WYQEGYBOPSEEDLKRVTQTWOLEEEEEETDMPFROIETMTILTVOIIVEFAKGLPGFS 341
QY 301 KISQSDQITLLKASSSEVMMLRVARRYDAATDSVLFANNQAYTRDNYRKAGMSYVIEDLL 360
DB 342 KISQSDQITLLKASSSEVMMLRVARRYDAATDSVLFANNQAYTRDNYRKAGMSYVIEDLL 401
QY 361 HFRCMYSMSMDNVHYALLTAIVIFSDRPGLEQPLVVEEIQRYVYLKTLRVYILNQHSASP 420
DB 402 HFRCMYSMSMDNVHYALLTAIVIFSDRPGLEQPLVVEEIQRYVYLKTLRVYILNQHSASP 461
QY 421 RCAVLFGKILGVLTGLTGTQNSNMCISLKNRKLPPFLEEIWDVAEVTTKLAPPTD 480
DB 462 RCAVLFGKILGVLTGLTGTQNSNMCISLKNRKLPPFLEEIWDVAEVTTKLAPPTD 519
QY 481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGDSPG 517
DB 520 VRCTGGLFFPHRDTTPAHA---GETATPMAGGGGGGG 553

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RESULT 14

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ADF49207
ID ADF49207 standard; protein; 615 AA.
XX
AC ADF49207;
XX
XX 12-FEB-2004 (first entry)
XX
XX Ecdysone receptor/CI transactivation domain seq id 135.
XX
XX receptor cassette; chimeric receptor polypeptide; DNA binding domain;
XX hinge domain; ecdysone receptor; Ecr; ligand binding domain;
XX activation domain; transgenic seed; transgenic plant; plant line;
XX herbicide; pesticide; chimeric ecdysone receptor; ECR;
XX yeast GAL4 DNA binding domain; CI transactivation domain.
XX
XX Synthetic.
XX OS Manduca sexta.
XX OS Ascomycota.
XX OS Zea mays.
XX
XX US2003154509-A1.
XX
XX 14-AUG-2003.
XX
XX 24-OCT-2001; 2001US-00087167.
XX
XX 24-OCT-2001; 2001US-00087167.
XX
XX (PASC/) PASCAL E J.
XX (VALE/) VALENTINE S A.
XX (BROW/) BROWN J A.
XX (COCK/) COCKRELL A S.
XX (JOHN/) JOHNSON B D.
XX
XX Pascal EU, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
XX WPI; 2003-897756/82.
XX
XX New receptor cassette encoding a chimeric receptor polypeptide, useful
XX for regulating the expression of target polypeptides in plants in the
XX presence of appropriate chemical ligands.
XX
XX Example 25; SEQ ID NO 135; 186pp; English.
XX
XX The invention describes a receptor cassette encoding a chimeric receptor
XX polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
XX (D) domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
XX (E) domain that is heterologous with respect to the D domain, and an
XX activation domain. The receptor cassette and method are useful in

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CC regulating the expression of target polypeptides in plants in the
 CC presence of appropriate chemical ligands. The transgenic seeds and plants
 CC can be used for the breeding of improved plant lines that, for e.g.
 CC increase the effectiveness of conventional methods such as herbicide or
 CC pesticide treatment. This is the amino acid sequence of an ecdysone
 CC receptor-C1 transactivation domain fusion protein.
 XX
 SQ Sequence 615 AA;

Query Match 85.5%; Score 2442.5; DB 7; Length 615;
 Best Local Similarity 94.0%; Pred. No. 2.7e-194;
 Matches 486; Conservative 1; Mismatches 25; Indels 5; Gaps 2;
 QY 1 MKLLSSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPKTRSPPLTRAHLTEVERSR 60
 DB 42 MKLLSSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPKTRSPPLTRAHLTEVERSR 101
 QY 61 LERLQFLFLIPREDLMILKMSLODIKALLTGLFVQDNVNDKAVTDRLASVETDML 120
 DB 102 LERLQFLFLIPREDLMILKMSLODIKALLTGLFVQDNVNDKAVTDRLASVETDML 161
 QY 121 TLQHRISATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRKEAQRKDKLPVS 180
 DB 162 TLQHRISATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRKEAQRKDKLPVS 221
 QY 181 TTTVDDHMPALMQCDPPPPPEAARIHEVVPRLTEKLMQNRLKNVTPLSANQKSLIARLV 240
 DB 222 TTTVDDHMPALMQCDPPPPPEAARIHEVVPRLTEKLMQNRLKNVTPLSANQKSLIARLV 281
 QY 241 WYQEGYEQPSEEDLKRVTTQWLEEEEEETDMPFROITMTILTQVLIQVFAKGLPGFS 300
 DB 282 WYQEGYEQPSEEDLKRVTTQWLEEEEEETDMPFROITMTILTQVLIQVFAKGLPGFS 341
 QY 301 KISQSDQITLLKASSSEVMMLRVARYDAATDSVLFANNQAYTRDNRKAGMSYVIEDLL 360
 DB 342 KISQSDQITLLKASSSEVMMLRVARYDAATDSVLFANNQAYTRDNRKAGMSYVIEDLL 401
 QY 361 HFRCWYMSMDNVHYALLTAIVIFSDRPGLEQPLLVVEEIQRYLLKTLRVYLNQHSASP 420
 DB 402 HFRCWYMSMDNVHYALLTAIVIFSDRPGLEQPLLVVEEIQRYLLKTLRVYLNQHSASP 461
 QY 421 RCVLFGKILGVLTELTGTQNSNMCISLKLKNRKLPPFLEEWDVAEVSSTKLAPPTD 480
 DB 462 RCVLFGKILGVLTELTGTQNSNMCISLKLKNRKLPPFLEEWDVAEVSSTKLAPPTD 519
 QY 481 VSLGDELHLDGSDVAMAHADALDDPFLDMLGDGSPG 517
 DB 520 VRCGTGLFFHRTDTPAHA---GETATPMAGGGGGG 553

RESULT 15
 ABJ05379
 ID ABJ05379 standard; protein; 620 AA.
 XX
 AC ABJ05379;
 XX
 DT 29-AUG-2003 (revised)
 DT 07-NOV-2002 (first entry)
 XX
 XX Chimeric ecdysone receptor SEQ ID NO: 137.
 DE Plant; gene expression control; insect; hormone receptor; fertility;
 KW ecdysone receptor.
 XX
 OS Manduca sexta.
 OS Manduca sexta.
 OS Chimeric.
 XX
 PN WO200261102-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 24-OCT-2001; 2001WO-US051417.

XX 24-OCT-2000; 2000US-0242969P.
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 PI WPI; 2002-619259/66.
 XX N-PSDB; ABT07377.
 DR New receptor cassette encoding a chimeric receptor polypeptide, useful in
 DR regulating expression of target polypeptides in plants in the presence of
 PT appropriate ligands that may be used in controlling plant fertility.
 PT Example 25; Page 304-306; 319pp; English.
 PS The present invention relates to a receptor cassette encoding a chimeric
 XX receptor polypeptide comprising at least one DNA binding domain, a hinge
 CC domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
 CC domain of an insect Ecr, where the ligand binding domain is heterologous
 CC with respect to the hinge domain and an activation domain. The chimeric
 CC insect hormone receptors and receptor cassettes are useful in regulating
 CC expression of target polypeptides in plants in the presence of
 CC appropriate ligands that may be used in controlling plant fertility. The
 CC method is useful for decreasing or increasing plant gene expression. The
 CC present sequence is a protein described in the exemplification of the
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 620 AA;

Query Match 85.4%; Score 2440; DB 5; Length 620;
 Best Local Similarity 88.3%; Pred. No. 4.4e-194;
 Matches 492; Conservative 7; Mismatches 34; Indels 24; Gaps 4;
 QY 1 MKLLSSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPKTRSPPLTRAHLTEVERSR 60
 DB 42 MKLLSSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPKTRSPPLTRAHLTEVERSR 101
 QY 61 LERLQFLFLIPREDLMILKMSLODIKALLTGLFVQDNVNDKAVTDRLASVETDML 120
 DB 102 LERLQFLFLIPREDLMILKMSLODIKALLTGLFVQDNVNDKAVTDRLASVETDML 161
 QY 121 TLQHRISATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRKEAQRKDKLPVS 180
 DB 162 TLQHRISATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRKEAQRKDKLPVS 221
 QY 181 TTTVDDHMPALMQCDPPPPPEAARIHEVVPRLTEKLMQNRLKNVTPLSANQKSLIARLV 240
 DB 222 TTTVDDHMPALMQCDPPPPPEAARIHEVVPRLTEKLMQNRLKNVTPLSANQKSLIARLV 281
 QY 241 WYQEGYEQPSEEDLKRVTTQWLEEEEEETDMPFROITMTILTQVLIQVFAKGLPGFS 300
 DB 282 WYQEGYEQPSEEDLKRVTTQWLEEEEEETDMPFROITMTILTQVLIQVFAKGLPGFS 341
 QY 301 KISQSDQITLLKASSSEVMMLRVARYDAATDSVLFANNQAYTRDNRKAGMSYVIEDLL 360
 DB 342 KISQSDQITLLKASSSEVMMLRVARYDAATDSVLFANNQAYTRDNRKAGMSYVIEDLL 401
 QY 361 HFRCWYMSMDNVHYALLTAIVIFSDRPGLEQPLLVVEEIQRYLLKTLRVYLNQHSASP 420
 DB 402 HFRCWYMSMDNVHYALLTAIVIFSDRPGLEQPLLVVEEIQRYLLKTLRVYLNQHSASP 461
 QY 421 RCVLFGKILGVLTELTGTQNSNMCISLKLKNRKLPPFLEEWDVAEVSSTKLAPPTD 480
 DB 462 RCVLFGKILGVLTELTGTQNSNMCISLKLKNRKLPPFLEEWDVAEVSSTKLAPPTD 521
 QY 481 VSLGDELHLDGSDVAMAHADALDDPFLDMLGDG---DPSGPGFT 521
 DB 522 ADPGKATATTTTSTSEITTTGALSDSLAHLLOQGTEDAEAVLGLSLDPSGAKA 581
 QY 522 PHDSA-----PYGALDM 533
 DB 582 VLDDSDSFVWPAASFD 598

Search completed: April 14, 2005, 12:23:32
Job time : 175 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 14, 2005, 12:19:35 ; Search time 48 Seconds
(without alignments)
1108.497 Million cell updates/sec

Title: US-10-087-167-105
Perfect score: 2856
Sequence: 1 MKLLSIEQACDICKLKKL.....ADFFEQMTDALGIDEYGG 553

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: Piri: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1029	36.0	536	2 A56590	ecdysteroid recept
2	986.5	34.5	878	2 A41055	ecdysone receptor
3	764.5	26.8	881	1 RGEYGA	regulatory protein
4	452.5	15.8	447	2 I38975	nuclear orphan rec
5	451.5	15.8	445	2 A56043	steroid hormone re
6	438	15.3	446	2 I59354	retinoid X recepto
7	436	15.3	446	2 I49021	orphan nuclear rec
8	423	14.8	479	1 IXBELF	alpha trans-induci
9	423	14.8	490	1 IYBEL7	alpha trans-induci
10	419	14.7	461	2 J40114	steroid hormone-nu
11	320.5	11.2	484	2 I49018	retinoid X recepto
12	312	10.9	469	2 A56918	farnesoid x-activa
13	302.5	10.6	490	1 IYBE33	alpha trans-induci
14	302.5	10.6	490	2 J50689	virion protein 16
15	290	10.2	448	2 A43786	retinoic acid rece
16	287.5	10.1	452	2 S78481	retinoic acid rece
17	287.5	10.1	458	2 S06123	retinoic acid rece
18	287	10.0	448	2 B56558	retinoic acid rece
19	287	10.0	455	2 S13512	retinoic acid rece
20	286.5	10.0	459	2 A19777	retinoic acid rece
21	286.5	10.0	464	2 A56558	retinoic acid rece
22	285.5	10.0	448	2 S02827	retinoic acid rece
23	285	10.0	448	2 S05051	retinoic acid rece
24	284	9.9	462	1 A29491	retinoic acid rece
25	284	9.9	955	4 C40045	probable transcrip
26	283	9.9	453	2 I50674	retinoic acid rece
27	282	9.9	462	2 S05050	retinoic acid nucl
28	279.5	9.8	454	2 S06124	retinoic acid rece
29	276	9.7	447	2 B34714	retinoic acid rece

ALIGNMENTS

RESULT 1

A56590 ecdysteroid receptor homolog cEcRH - midge (Chironomus tentans)
C:Species: Chironomus tentans

C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004

A:Accession: A56590

R:Imhof, M.O.; Rusconi, S.; Lezzi, M.

Insect Biochem. Mol. Biol. 23, 115-124, 1993

A:Title: Cloning of a Chironomus tentans cDNA encoding a protein (cEcRH) homologous to

A:Reference number: A56590; MUID:93250857; PMID:8485513

A:Accession: A56590

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-536 <IMH>

A:Cross-references: UNIPROT:P49882; GB:S60739; NID:g385893; PIDN:AAC0500.1; PID:g385894

A>Note: sequence extracted from NCBI backbone (NCBIN:132124, NCBI:P132127)

C:Superfamily: unassigned erba-related proteins; erba transforming protein homology

C:Keywords: DNA binding; steroid hormone receptor; zinc finger

F:113-432/Domain: erba transforming protein homology <ERBA>

Query Match 36.0%; Score 1029; DB 2; Length 536;

Best Local Similarity 52.0%; Pred. No. 2.5e-61;

Matches 210; Conservative 67; Mismatches 83; Indels 44; Gaps 5;

Qy	97	FVQDNVKNDAVTDRLASVETDMLTLRQHRISATSSSESSNKQORQLTVSRMRPECVV	156
Db	138	FRRSVTKNAVYCKFGHECDMTMRR-----KQCEKRLKCLAVGMRPECVV	186
Qy	157	PESTCKNKRREKAQREKDLF-----VSTTVT-----DDHMPAIM	192
Db	187	PENQCAIKRKEKKAQKEDKYPGIVGSNTSSSLLNQSLNGLKNLEISYREELLEQLM	246
Qy	193	QCDPPPEAARIHEVVPFRFLTEKLEQNRKNVTPLSANQKSLIARLVWYEGYQPSSE	252
Db	247	KCDPPP-----HPMQQLPEKLMENRAGTGPOLTANQAVIYKLIWYQDGYQPSSE	299
Qy	253	DLKEVTQTWLEEESEBETDMPFQITMTILTQVLIVEFAKGLPGESKISOSDQITLLK	312
Db	300	DLKRIT--ELEEEDEHEANFRYTEVITLTQVLIVEFAKGLPAFTIKIPEODQITLLK	357
Qy	313	ASSEVVMMLRVARYDAATSVLPANNOAYTRDNYRKAGMSYVIEDLHFCRCMYSMSMD	372
Db	358	ACSEVVMMLRVARYDHDSDSILFANNYATKYQYQLAGMBETIDDLHFCRCMYALSID	417
Qy	373	NVHALLTAIVIPSDRPGLEQPLVBEIQRYLLKTLRVYILNQHSAPRCVAFKILGV	432
Db	418	NVEYALLTAIVIPSDRPGLEKAEWVDIIQSYTETLKYIVNRRHGESRCSVQPAKLGI	477
Qy	433	LTELRTGTQNSNMCISILKLNKRLPFLBEIWDVAEVSITKLA	476
Db	478	LTELRTGKNKNSECMFCFLKLNKRLPFLBEVWDVGVNQTQA	521

nuclear orphan receptor LXR-alpha - human

C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 16-Aug-2004
C:Accession: I38975
R:Willy, P.J.; Umesono, K.; Ong, E.S.; Evans, R.M.; Heyman, R.A.; Mangelsdorf, D.J.
Genes Dev. 9, 1033-1045, 1995
A:Title: LXR, a nuclear receptor that defines a distinct retinoid response pathway.
A:Reference number: I38975; MUID:95262897; PMID:7744246
A:Accession: I38975
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-447 <RES>
A:CROSS-references: UNIPROT:Q13133; EMBL:U22662; NID:g726512; PIDN:AAA8586.1; PID:g7265
C:Superfamily: erba transforming protein homology
C:Keywords: zinc finger
F:96-367/Domain: erba transforming protein homology <ERBA>

Query Match 15.8%; Score 452.5; DB 2; Length 447;
Best Local Similarity 34.0%; Pred. No. 8e-23;
Matches 111; Conservative 60; Mismatches 108; Indels 47; Gaps 9;

QY 150 MRPECVPESTCKNK--RREKAQREKDKLPVSTTTVDHMPAINQCDDPPPEAARIHEV 207
DB 163 MREECVLSSEQIRLKKLRQEEQAHATSLPPRRSS-----PP-----QI 202
QY 208 VPRFTEKLMQNRLKNVTPLSANQKSLIARLVYQEGYQEPSEEDLKRVTQTWQL--EE 265
DB 203 LPQ-----LSPEQLGMIEKLVAAQOCNRRSFSDDLRLVT-PWPMADP 244
QY 266 EBEETDMPFRQITMTILTQVILVEFAKGLPGFSKISQSDQITLLKASSEVMMLRVAR 325
DB 245 HSREARQORFAHFTLAIYSQVIEVDFAKQLPGFLQSLREDQIALKTSIEVMLLETSR 304
QY 326 RYDAATDVLFANNOAYTRDNYRKAGMSY-VIEDLLHFRCRCMYSMDNVHYALLTAIV 384
DB 305 RYNGPESITFLKDFSYNRDFAKGLQVEFINPIFEFSRANMLQLNDAEFALLIAIS 364
QY 385 FS-DRPGLQEPQLVVEIQRYLTKLRVILNQHSSAPRCVAVLFGKILGLVLTSLRTLGTON 443
DB 365 FSADRPNVQDQLQVERLQHTYVEALHAYVSIH---PHDRLMFPRLMKLVSLRTLSVH 421
QY 444 SNMCISLKLKNRKLPPFLEEIWDVAE 469
DB 422 SEQVFAIRLQDKKLPPLLSIWDVHE 447

RESULT 5
A56043
steroid hormone receptor-like protein R1D-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C:Accession: A56043
R:Apfel, R.; Benbrook, D.; Lernhardt, B.; Ortiz, M.A.; Salbert, G.; Pfahl, M.
Mol. Cell. Biol. 14, 7025-7035, 1994
A:Title: A novel orphan receptor specific for a subset of thyroid hormone-responsive ele
A:Reference number: A56043; MUID:95021230; PMID:7935418
A:Accession: A56043
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-445 <APP>
A:CROSS-references: UNIPROT:Q62685; GB:U11685; NID:g555751; PIDN:AAA53633.1; PID:g555752
A:Note: authors translated the codon GAG for residue 73 as Ser
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: steroid hormone receptor; zinc finger
F:94-365/Domain: erba transforming protein homology <ERBA>

Query Match 15.8%; Score 451.5; DB 2; Length 445;
Best Local Similarity 33.3%; Pred. No. 9.3e-23;
Matches 108; Conservative 62; Mismatches 111; Indels 43; Gaps 7;

QY 150 MRPECVPESTCKNKREKAQREKDKLPVSTTTVDHMPAINQCDDPPPEAARIHEV 209
DB 161 MREECVLSSEQIRLKKLRQEEQAHATSLPPRRSS-----PPVSSPPQVLP 202

QY 210 RFLTEKLMQNRLKNVTPLSANQKSLIARLVYQEGYQEPSEEDLKRVTQTWQL--EBEE 267
DB 203 Q-----LSPEQLGMIEKLVAAQOCNRRSFSDDLRLVT-PWPIADPQS 244
QY 268 EBEETDMPFRQITMTILTQVILVEFAKGLPGFSKISQSDQITLLKASSEVMMLRVARY 327
DB 245 REARQORFAHFTLAIYSQVIEVDFAKQLPGFLQSLREDQIALKTSIAEVMMLLETSSRY 304
QY 328 DAATDVLFANNOAYTRDNYRKAGMSY-VIEDLLHFRCRCMYSMDNVHYALLTAIVIFS 386
DB 305 NPGSESITFLKDFSYNRDFAKGLQVEFINPIFEFSRANMLQLNDAEFALLIAISIFS 364
QY 387 -DRPGLQEPQLVVEIQRYLTKLRVILNQHSSAPRCVAVLFGKILGLVLTSLRTLGTONS 445
DB 365 ADRPNVQDQLQVERLQHTYVEALHAYVSIH---PHDRLMFPRLMKLVSLRTLSVHSE 421
QY 446 MCISLKLKNRKLPPFLEEIWDVAE 469
DB 422 QVFAIRLQDKKLPPLLSIWDVHE 445

RESULT 6
I49021
retinoid X receptor interacting protein No.15 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
C:Accession: I49021
R:Seol, W.; Choi, H.S.; Moore, D.D.
Mol. Endocrinol. 9, 72-85, 1995
A:Title: Isolation of proteins that interact specifically with the retinoid X receptor:
A:Reference number: A57664; MUID:95280959; PMID:7760852
A:Accession: I49021
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-446 <RES>
A:CROSS-references: UNIPROT:Q60644; EMBL:U09419; NID:g691713; PIDN:AAC52164.1; PID:g6917
C:Genetics: RIP15
C:Superfamily: erba transforming protein homology
C:Keywords: zinc finger
F:76-366/Domain: erba transforming protein homology <ERBA>

Query Match 15.3%; Score 438; DB 2; Length 446;
Best Local Similarity 33.6%; Pred. No. 7.5e-22;
Matches 110; Conservative 62; Mismatches 123; Indels 32; Gaps 7;

QY 150 MRPECVPESTCKNKREKAQREKDKLPVSTTTVDHMPAINQCDDPPPEAARIHEV 209
DB 145 MRECVLSSEQIRKKRIKQKQKQ-----PPPSBPAASSSGRP 183
QY 210 RF---LTEKLMQNRLKNVTPLSANQKSLIARLVYQEGYQEPSEEDLKRVTQTWQL--E 264
DB 184 AASPTSEASSQSGEGEGEIGLTAAQELMIQOLVAAQOCNKRFSFDQPKVT-PWPLGAD 242
QY 265 EBEETDMPFRQITMTILTQVILVEFAKGLPGFSKISQSDQITLLKASSEVMMLRVA 324
DB 243 PQSDARQORFAHFTLAIYSQVIEVDFAKQLPGFLQSLREDQIALKTSIEIMLLTA 302
QY 325 RRYDAATDVLFANNOAYTRDNYRKAGMSY-VIEDLLHFRCRCMYSMDNVHYALLTAIV 383
DB 303 RRYNHETECITFLKDFSYNRDFAKGLQVEFINPIFEFSRANMLRLGLDDAEYALLIAIN 362
QY 384 IFS-DRPGLQEPQLVVEIQRYLTKLRVILNQHSSAPRCVAVLFGKILGLVLTSLRTLTGTQ 442
DB 363 IFSADRPNVQEPSRVEALQQPYVEALLSY---TRIKRPDQQLRFPRLMKLVSLRTLSV 419
QY 443 NSNWCISLKLKNRKLPPFLEEIWDVAE 469
DB 420 HSEQVFAIRLQDKKLPPLLSIWDVHE 446

RESULT 7

A:Molecule type: mRNA
A:Residues: 1-461 <SHI>
A:Cross-references: UNIPROT:P55055; GB:U07132; NID:G641961; PIDN:AAA61783.1; PID:G641962
A:Experimental source: osteosarcoma cells SAOS-2/B10
C:Genetics:
A:Gene: GDB:UNR

A:Cross-references: GDB:389570; OMIM:600380

A:Map position: 19q13.3-19q13.3

C:Superfamily: erba transforming protein homology

C:Keywords: steroid hormone receptor

F:85-381/Domain: erba transforming protein homology <ERBA>

F:87-154/Domain: DNA binding #status predicted <BIN>

Query Match 14.7%; Score 419; DB 2; Length 461;

Best Local Similarity 33.0%; Pred. No. 1.5e-20;

Matches 108; Conservative 63; Mismatches 130; Indels 26; Gaps 7;

QY 150 MRPECVPESTCKNKRKEAQRKDLPVSTTTVDHMPALMQCDPPPPPEAARHIEVVP 209

DB 154 MREQCVLSEQIRKKIRKQQQESQSQSQ-----PVGPGQSSSSASGP 198

QY 210 RFL---TEKLMQNRLKNVTPLSANQSLIARLVWYQEGYQPSBEDLKRVTQTWQL--E 264

DB 199 GASPGEAGSGSGEGEVQTAQELMIQQLVAQAQCNKRFSFQPKVT-PWPLGAD 257

QY 265 EEEBETDMPFRQITTEMTILTVQIVFAKGLPGFSKISQSDQITLLKASSSEVMMLRVA 324

DB 258 PQSDARQORFAHFTFLAIIISVQEIYVDFAKVPGFQLGREGDQIALAKASTIEIMLETA 317

QY 325 RYDAATOSVLFANNOAYTRDNYRKAGMSY-VIEDLLHFCRCMYSMDNVHYALLTAIV 383

DB 318 RRYNHETECITLKDFTYSKDDFHRAGLQVEFINPIFEFSRAMRLGLDDAAYALLIIN 377

QY 384 IFS-DRPGLQPLVEEIQRYVLTLYVILNQHSASPRCAVLFGKILGLVLTGLTQ 442

DB 378 IFSADRPNVQEPGRVEALQOPVEALLSY---TRIKRPDQQLRFPRLMKLVSLRTLSSV 434

QY 443 NSNMICISLKLKNRKLPPPLEEIDVDAE 469

DB 435 HSEQVFAQLQDKLPPPLSEIWDVHE 461

RESULT 11

I49018

retinoid X receptor interacting protein No.6 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004

C:Accession: I49018

R:Seol, W.; Choi, H.S.; Moore, D.D.

Mol. Endocrinol. 9, 72-85, 1995

A:Title: Isolation of proteins that interact specifically with the retinoid X receptor:

A:Reference number: A57664; MUID:95280959; PMID:7760852

A:Accession: I49018

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-484 <RES>

A:Cross-references: UNIPROT:Q60641; EMBL:U09416; NID:G691707; PIDN:AAC53066.1; PID:G69171

C:Genetics:

A:Gene: RPI4-1(6)

C:Superfamily: erba transforming protein homology

C:Keywords: zinc finger

F:136-405/Domain: erba transforming protein homology <ERBA>

Query Match 11.2%; Score 320.5; DB 2; Length 484;

Best Local Similarity 31.7%; Pred. No. 6.2e-14;

Matches 102; Conservative 46; Mismatches 129; Indels 45; Gaps 10;

QY 150 MRPECVPESTCKNKRKEAQRKDLPVSTTTVDHMPALMQCDPPPPPEAARHIEV-- 207

DB 203 MIAECLLTEIQCKSKRLKRVKQHADQ-----TVNEDD-----SEGRDLRQVTS 246

QY 208 VPRFLTEKLMQNRLKNVTPLSANQSLIARLVWYQEGYQPSBEDLKRVTQTWOLEEE 267

DB 247 TTKFCREK-----TELTADQQTLLDYIMDSYNKQRMPOE-----ITNKILKEEPS 291

QY 268 BEETDMPFRQITTEMTILTVQIVFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARRY 327

DB 292 AEEN---FLILTEMATSHVQILVEFTKKLPQFQTLHDHEDQIALLKGSVAEMFLSAEIP 348

QY 328 DAATDSVLFANNOAYTRDNYRKAGMS-YVIEDLLHFCRCMYSMDNVHYALLTAIVTFS 386

DB 349 ---NKKLPAGHADLLEERIRKSGISDEYITPMFSFYKSVGELKMTQEBEYALLTAIVLS 404

QY 387 -DRPGLQPLVEEIQRYVLTLYVILNQHSASPRCAVLFGKILGLVLTGLTQTSN 445

DB 405 PDQYIKNDREAVEKQLQEPFLDLVQLCKMYQEPNPQ---HFACLLGLRUTEIETFNHHA 461

QY 446 MCISLKLKNRKLPPPLEEIDV 467

DB 462 MLMSRWVNDHKTPLLCIWDV 483

RESULT 12

A56918

farnesoid x-activated receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004

C:Accession: A56918

R:Forman, B.M.; Goode, E.; Chen, J.; Oro, A.E.; Bradley, D.J.; Perlmann, T.; Noonan, D.J

A:Title: Identification of a nuclear receptor that is activated by farnesol metabolites

A:Reference number: A56918; MUID:95292336; PMID:7774010

A:Accession: A56918

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-469 <FOR>

A:Cross-references: UNIPROT:Q62735; GB:U18374; NID:G868031; PIDN:AAC52205.1; PID:G868032

C:Superfamily: unassigned erba-related proteins; erba transforming protein homology

C:Keywords: DNA binding; nucleus; zinc finger

F:122-390/Domain: erba transforming protein homology <ERBA>

Query Match 10.9%; Score 312; DB 2; Length 469;

Best Local Similarity 31.2%; Pred. No. 2.2e-13;

Matches 101; Conservative 47; Mismatches 126; Indels 50; Gaps 11;

QY 150 MRPECVPESTCKNKRKEAQRKDLPVSTTTVDHMPALMQCDPPPPPEAARHIEVVP 209

DB 189 MIAECLLTEIQCKSKRLKRVKQHADQ-----TVNE-----DSEGRDLRQVTS 231

QY 210 RFLTEKLMQNRLKNVTPLSANQSLIARLVWYQEGYQPSBEDLKRVTQTWOLEEEEEE 269

DB 232 ---TTKLCREK-----TELTVDQQTLLDYIMDSYSKQRMPOE-----ITNKILKEEPSAE 278

QY 270 ETDMPFRQITTEMTILTVQIVFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARRYDA 329

DB 279 EN---FLILTEMATSHVQILVEFTKRPGFQTLHDHEDQIALLKGSVAEMFLSAEIP-- 333

QY 330 ATDSVLFANNOAYTRDNYRKAGMS-YVIEDLLHFCRCMYSMDNVHYALLTAIVTFS-D 387

DB 334 ---NKKLPAGHADLLEERIRKSGISDEYITPMFSFYKSVGELKMTQEBEYALLTAIVLSPD 391

QY 388 RPLGELQPLVEEIQRYVLTLYVILNQHSASPRCAVLFGKILGLVLTGLTQTSN 443

DB 392 RQYIKNDREAVEKQLQEPFLDLVQLCKIY-----OPENPQHFACLLGLRUTEIETFNH 444

QY 444 SNMTCISLKLKNRKLPPPLEEIDV 467

DB 445 AEMLMSRWVNDHKTPLLCIWDV 468

RESULT 13

IXBE33

alpha trans-inducing protein - human herpesvirus 2 (strain 333)

N:Alternate names: virion transactivator protein Vmw65

C:Species: human herpesvirus 2

A>Note: host Homo sapiens (man)

Query Match	10.2%;	Score 290;	DB 2;	Length 448;
Best Local Similarity	22.2%;	Pred. No. 6.2e-12;		
Matches 117;	Conservative 86;	Mismatches 157;	Indels 166;	Gaps 19;

Qy	69	LLIFPREDLMLKMS	---LQD---IKALLTGLFVQDNVNKDAVTORLASVETMDPLTLR	123
		: : : :	: : : : :	: : :
Db	8	LAVSPAQMLDFYASPS	SCMLQEKALKACFSGL	45
		: : : :	-----AQTEW----	
Qy	124	QHRISATS	-----SSEE-----SSN-----KG----	140
		: : : :	-----	---
Db	46	QHRHSASQSVETQTS	SEBELVPSPPLPPRVYKPCFVCQDKSSGHHYGTACEGCKGFF	105
		: : : :	-----C-----	---
Qy	141	---QRQLTVSTRMR	PECVVPPEST	172
		: : : :	-----	---KNKREKEAQR
Db	106	RRSIQNMVYTC	HRDKNCVINKVTRNRCYCLQKCFEVMGSKESVRNDRNKKCKEPTKQ	165
		: : : :	-----	---
Qy	173	EKDQLPVSTTTVD	DHNPALMQCDPPPEAARITHEVVPRLFTKLMEQNRLKNVTPUSANQ	232
		: : : :	-----	---
Db	166	ESTENYEMTAELDD	-----LTKIRKA-----	187
		: : : :	-----	---
Qy	233	KSIIARLVNMQEY	QPSBEDLKRVYQTQWLEBEEBETDMPROJTEMILTIVQLIVER	292
		: : : :	-----	---
Db	188	-----HQETF--	PSICQKGYTNSADHRVRLDGL-WDKFSELATKCIIVBF	235
		: : : :	-----	---
Qy	293	AKGLPFKISOSDQIT	LLKASSEVMMLVARRVDAATDSVLFANNOAYTRDNYRKAGM	352
		: : : :	-----	---
Db	236	AKELPGFTSLTADQIT	LLKAACLDLIILIRICTRYTPEQDTWTFSDGLTNKTMQHNAGF	295
		: : : :	-----	---
Qy	353	SYVIEDLLHFCRC	WMSMDNVHYALLTAI-VIFSDRPGLEOPLAVEETQRYVYLKTRVY	411
		: : : :	-----	---
Db	296	GPLTDLVFTFANQLL	PLEMDDTETGLLSAICITCGDRQDLEBPMKVDLQEPLEALKIY	355
		: : : :	-----	---
Qy	412	ILNQHSASPRCAVL	FGKILGLVTELTTLGTQNSNCISILKL-NRKLPPFLSEIWDVAEV	470
		: : : :	-----	---
Db	356	IRKRPNKPH---M	PFKILMKITDLSRSKGAERVITLKMRIPOGSMPPILQEMLENSG	412
		: : : :	-----	---
Qy	471	STTKLAPPTDVS	LGBELHLDGSDVAMAHADALDDPDLMDLGGDSP	516

Db 413 H-----EPLPTNGN-----TAHSPSISPSVDNSVSQSP 445

Search completed: April 14, 2005, 12:20:32
Job time : 50 secs

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OM protein - protein search, using sw model

Run on: April 14, 2005, 12:19:35 ; Search time 184 Seconds
(without alignments)
1539.021 Million cell updates/sec

Title: US-10-087-167-105
Perfect score: 2856
Sequence: 1 MKLSSISBQACDICKLKLK.....ADFFEQMTDALGIDEYGG 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1673	58.6	556	1 ECR_MANSE	P49883 manduca sex
2	1518.5	53.2	518	2 Q8MYA7	Q8MYA7 chilo suppr
3	1518.5	53.2	547	2 Q8MYA6	Q8MYA6 chilo suppr
4	1497	52.4	541	2 Q6RVD3	Q6RVD3 plodia inte
5	1488.5	52.1	576	1 ECR_HBLVI	O18473 heliothis v
6	1458	51.1	339	2 Q9U0R9	Q9U0R9 junonia coe
7	1437	50.3	606	1 ECR_BOMMO	P49881 bombyx mori
8	1430	50.1	513	2 Q77240	O77240 choristoneu
9	1430	50.1	541	2 Q77255	O77255 choristoneu
10	1381	48.4	346	2 Q9U3U4	Q9U3U4 bicyclus an
11	1116	39.1	680	2 Q9U3Y4	Q9U3Y4 aedes albop
12	1113	39.0	675	1 ECR_ASDAE	P49880 aedes aegypt
13	1113	39.0	776	2 Q6VA69	Q6VA69 aedes aegypt
14	1029	36.0	536	1 ECR_CHITE	P49882 chironomus
15	1011	35.4	757	1 ECR_LUCCU	O18531 lucilia cup
16	1007	35.3	784	2 Q9GPH1	Q9GPH1 calliphora
17	992	34.7	673	2 Q76827	Q76827 ceratitis c
18	986.5	34.5	878	1 ECR_DROME	P34021 drosophila
19	983	34.4	520	2 Q7FVB2	Q7FVB2 anopheles g
20	849.5	29.7	541	2 Q70795	Q70795 locusta mig
21	838.5	29.4	491	2 O02035	O02035 tenebrio mo
22	764.5	26.8	881	1 GAL4_YEAST	P04386 saccharomyc
23	764.5	26.8	881	2 Q76NW9	Q76NW9 drosophila
24	748.5	26.2	518	2 Q76246	Q76246 uca pugilat
25	739	25.9	444	2 O44336	O44336 amblyomma a
26	739	25.9	560	2 O44337	O44337 amblyomma a
27	739	25.9	570	2 O44338	O44338 amblyomma a
28	711	24.9	336	2 Q6RIB4	Q6RIB4 carinus ma
29	683	23.9	403	2 Q8MRW2	Q8MRW2 scorpion
30	651	22.8	212	2 Q8MWR0	Q8MWR0 trichoplusi
31	481	16.8	182	2 Q8NGU6	Q8NGU6 sarcophaga

32	479	16.8	181	2	Q75ZW2	Q75ZW2 lucilia ser
33	456.5	16.0	402	2	Q81W13	Q81W13 homo sapien
34	456.5	16.0	447	1	NRH3_HUMAN	Q13133 homo sapien
35	456	16.0	207	2	Q9XYR8	Q9XYR8 bradyaia hy
36	453.5	15.9	445	2	Q91X41	Q91X41 mus musculu
37	452.5	15.8	445	1	NRH3_MOUSE	Q950Y9 mus musculu
38	451.5	15.8	445	1	NRH3_RAT	Q62685 rattus norv
39	438	15.3	443	2	Q8BP65	Q8BP65 mus musculu
40	438	15.3	446	1	NRH2_MOUSE	Q60644 mus musculu
41	436	15.3	446	1	NRH2_RAT	Q62755 rattus norv
42	434.5	15.2	409	2	Q8JHU1	Q8JHU1 gallus gall
43	431.5	15.1	409	2	Q8AXU8	Q8AXU8 gallus gall
44	428	15.0	441	2	Q6GMA2	Q6GMA2 xenopus lae
45	423	14.8	479	1	ATIN_HHVIF	P04486 human herpe

ALIGNMENTS

RESULT 1

ID	ECR_MANSE	STANDARD;	PRT;	556 AA.
AC	P49883;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone receptor) (20E receptor).			
DE	receptor) (20E receptor).			
GN	Name=ECR; Synonyms=NRH1;			
OS	Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditryaia; Sphingioidea;			
OC	Sphingidae; Sphinginae; Manduca.			
OX	NCBI_TaxID=7130;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95360028; PubMed=7633469; DOI=10.1016/0965-1748(95)00023-O;			
RA	Fujiwara H., Jindra M., Newitt R., Palli S.R., Hiruma K.,			
RA	Riddiford L.M.;			
RT	"Cloning of an ecdysone receptor homolog from Manduca sexta and the developmental profile of its mRNA in wings."			
RL	Insect Biochem. Mol. Biol. 25:845-856(1995).			
CC	-!- FUNCTION: Receptor for ecdysone. Binds to ecdysone response elements (ECRES).			
CC	-!- SUBCELLULAR LOCATION: Nuclear.			
CC	-!- TISSUE SPECIFICITY: It is found in both larval wing disks and pupal wings and in prothoracic glands. levels increase on day 2			
CC	-!- DEVELOPMENTAL STAGE: In the wing disks reaching a maximum on day 5, and then decrease sharply on day 6. In the prothoracic glands levels increase			
CC	sharply on day 6. then remain high throughout the larval-pupal transformation and after pupal ecdysis.			
CC	-!- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI subfamily.			
CC	-----			
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CC	-----			
CC	EMBL; U19812; AAA86699.1; -			
DR	HSSP; P20393; lA6Y.			
DR	InterPro; IPR000536; Hrmn_recept_lig.			
DR	InterPro; IPR001723; Stdhrmn_receptor.			
DR	InterPro; IPR008946; Str_ncl_receptor.			
DR	InterPro; IPR001628; Znf_C4steroid.			
DR	Pfam; PF00104; Hormone_recep; 1.			
DR	Pfam; PF00105; zf-C4; 1.			
DR	PRINTS; PR00398; STRDHORMONER.			
DR	PRINTS; PR00047; STROIDFINGER.			

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DR ProDom: PR000035; Znf_C4steroid; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
FT DOMAIN 1 146 Modulating (Potential).
FT FT DNA BIND 147 212 Nuclear receptor-type.
FT ZN_FING 147 167 C4-type.
FT ZN_FING 183 207 C4-type.
FT FT DOMAIN 305 528 Hormone-binding (Potential).
FT FT DOMAIN 75 84 Poly-Gln.
FT FT DOMAIN 258 261 Poly-Pro.
FT FT DOMAIN 326 332 Poly-Glu.
SQ SEQUENCE 556 AA; 62830 MW; 9AF83AA33D551EB1 CRC64;

Query Match 58.6%; Score 1673; DB 1; Length 556;
Best Local Similarity 99.1%; Pred. No. 1.7e-97;
Matches 325; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 150 MRPECVVPSTCKNKRREKEAQRKDKLPVSTTTVDDHMPAIMQCDPPPPPEAARIHEVVP 209
DB 212 MRPECVVPSTCKNKRREKEAQRKDKLPVSTTTVDDHMPAIMQCDPPPPPEAARIHEVVP 271

QY 210 RFLTEKLEQNRLKNVTPLSANQKSLIARLVYQEGYEQPSEEDLKRVTQTWQLEEEEEE 269
DB 272 RFLTEKLEQNRLKNVTPLSANQKSLIARLVYQEGYEQPSEEDLKRVTQTWQLEEEEEE 331

QY 270 ETDMPPFROITENTILTVQLIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARYDA 329
DB 332 ETDMPPFROITENTILTVQLIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARYDA 391

QY 330 ATDSVLFANNOAYTRDNYRKAGMSVVIEDLLHFCRCMYSMSMDNVHYALLTAIVIFSDRP 389
DB 392 ATDSVLFANNOAYTRDNYRKAGMSVVIEDLLHFCRCMYSMSMDNVHYALLTAIVIFSDRP 451

QY 390 GLEQPLLVVEEIQRYLYKTLRLVYLNQHSASPRCAVLFGKILGLVLTGLTQNSNMCIS 449
DB 452 GLEQPLLVVEEIQRYLYKTLRLVYLNQHSASPRCAVLFGKILGLVLTGLTQNSNMCIS 511

QY 450 LKLNKRLKLPPLLEEIWDVAEVSTTKLAP 477
DB 512 LKLNKRLKLPPLLEEIWDVAEVSTTKLAP 539

RESULT 2
Q8MYA7 PRELIMINARY; PRT; 518 AA.
AC Q8MYA7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ecdysone receptor A isoform.
GN Name=CBECR-A;
OS Chilo suppressalis.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
OC Pyralidae; Crambinae; Chilo.
OX NCBI_TaxID=168631;
RN [1] SEQUENCE FROM N.A.
RP TISSUE=Fat body;
RC MEDLINE=22202197; PubMed=12213236; DOI=10.1016/S0965-1748(02)00036-X;
RA Minakuchi C., Nakagawa Y., Kiuchi M., Tomita S., Kamimura M.;
RT "Molecular cloning, expression analysis and functional confirmation of
two ecdysone receptor isoforms from the rice stem borer Chilo
suppressalis.";
RL Insect Biochem. Mol. Biol. 32:999-1008(2002).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AB067811; BAC11713.1; -
DR HSSP; P34021; 1R00.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:0005496; F:steroid binding; IEA.

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DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003069; Ecdystd_receptor.
DR InterPro; IPR000536; Hrmn_recept_lig.
DR InterPro; IPR001723; Strhrmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR01283; ECDYSTEROIDE.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 518 AA; 58320 MW; 5E757803E248E118 CRC64;

Query Match 53.2%; Score 1518.5; DB 2; Length 518;
Best Local Similarity 86.7%; Pred. No. 9e-88;
Matches 293; Conservative 19; Mismatches 21; Indels 5; Gaps 1;

QY 150 MRPECVVPSTCKNKRREKEAQRKDKLPVSTTTVDDHMPAIMQCDPPPPPEAARI----- 204
DB 178 MRPECVVPSTCKNKRREKEAQRKDKLPVSTTTVDDHMPAIMQCDPPPPPEAARIIECLQ 237

QY 205 HEVVPRLTEKLEQNRLKNVTPLSANQKSLIARLVYQEGYEQPSEEDLKRVTQTWQLE 264
DB 238 HEVVPRLTEKLEQNRLKNVTPLSANQKSLIARLVYQEGYEQPSEEDLKRVTQTWQSN 297

QY 265 EEEEEETDMPPFROITENTILTVQLIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVA 324
DB 298 EDEEETDLPFRQITENTILTVQLIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVA 357

QY 325 RRYDAATDSVLFANNOAYTRDNYRKAGMSVVIEDLLHFCRCMYSMSMDNVHYALLTAIVI 384
DB 358 RRYDAASDSVLFANNOAYTRDNYRKAGMSVVIEDLLHFCRCMYSMSMDNVHYALLTAVI 417

QY 385 FSDRPGLEQPLLVVEEIQRYLYKTLRLVYLNQHSASPRCAVLFGKILGLVLTGLTQNS 444
DB 418 FSDRPGLEQPLLVVEEIQRYLYKTLRLVYLNQHSASPRCAVLFGKILGLVLTGLTQNS 477

QY 445 NMCISLKLKNRKLPPPLLEEIWDVAEVSTTKLAPPTDVS 482
DB 478 NMCISLKLKNRKLPPPLLEEIWDVAEVSAQAAPAIMDVA 515

RESULT 3
Q8MYA6 PRELIMINARY; PRT; 547 AA.
AC Q8MYA6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ecdysone receptor B1 isoform.
GN Name=CBECR-B1;
OS Chilo suppressalis.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
OC Pyralidae; Crambinae; Chilo.
OX NCBI_TaxID=168631;
RN [1] SEQUENCE FROM N.A.
RP TISSUE=Fat body;
RC MEDLINE=22202197; PubMed=12213236; DOI=10.1016/S0965-1748(02)00036-X;
RA Minakuchi C., Nakagawa Y., Kiuchi M., Tomita S., Kamimura M.;
RT "Molecular cloning, expression analysis and functional confirmation of
two ecdysone receptor isoforms from the rice stem borer Chilo
suppressalis.";
RL Insect Biochem. Mol. Biol. 32:999-1008(2002).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AB067811; BAC11713.1; -
DR HSSP; P34021; 1R00.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:0005496; F:steroid binding; IEA.

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DR EMBL; AB067812; BAC11714.1; --.
DR HSSP; P34021; IR00.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:0004894; F:steroid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003069; Ecdystd receptor.
DR InterPro; IPR001723; Strdhrn recept lig.
DR InterPro; IPR008946; Str ncl receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR01283; ECDYSTEROIDR.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 547 AA; 61815 MW; 335528572666256E CRC64;

Query Match 53.2%; Score 1518.5; DB 2; Length 547;
Best Local Similarity 86.7%; Pred. No. 9.7e-88;
Matches 293; Conservative 19; Mismatches 21; Indels 5; Gaps 1;

QY 150 MRPCVVPSTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPEAARI----- 204
DB 207 MRPCVVPSTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPEAARI----- 266

QY 205 HEVPRFTEKLEMEQRLKNVTPLSANOKSLIARLVWYQEGYQPSSEDLKRVTTOTWOLE 264
DB 267 HEVPRFTEKLEMEQRLKNVTPLSANOKSLIARLVWYQEGYQPSSEDLKRVTTOTWOLE 326

QY 265 EEEETDMPFRQITTEMTILTVQLIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVA 324
DB 327 EDEEBETDLPFRQITTEMTILTVQLIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVA 386

QY 325 RYDAATSVLFPANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMNDNVHALLTAIVI 384
DB 387 RYDAATSVLFPANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMNDNVHALLTAIVI 446

QY 385 FSDRGLEQPLVEIQRYLKTLRVYILNOHSASPRCAVLFGKILGVLTELRTLTGTONS 444
DB 447 FSDRGLEQPLVEIQRYLKTLRVYILNOHSASPRCAVLFGKILGVLTELRTLTGTONS 506

QY 445 NMCISLKNRKLPPPLEEINWDVAEVSTTKLAPPTDVS 482
DB 507 NMCISLKNRKLPPPLEEINWDVAEVSTTKLAPPTDVS 544

RESULT 4
Q6RVD3 PRELIMINARY; PRT; 541 AA.
AC Q6RVD3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Ecdysone receptor.
OS Plodia interpunctella (Indianmeal moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
OC Pyralidae; Phycitinae; Plodia.
OX NCBI_TaxID=58824;
RN [1]
RP SEQUENCE FROM N.A.
RA Slausasat D., Debernard S., Bozzolan F., Queguiner I., Porcheron P.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.

DR EMBL; AY489269; AAR84611.1; --.
DR HSSP; P20393; IAGY.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:0005496; F:steroid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003069; Ecdystd receptor.
DR InterPro; IPR001723; Strdhrn recept lig.
DR InterPro; IPR008946; Str ncl receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR01283; ECDYSTEROIDR.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 541 AA; 61030 MW; 145588BE2EFA07AD CRC64;

Query Match 52.4%; Score 1497; DB 2; Length 541;
Best Local Similarity 87.0%; Pred. No. 2.2e-86;
Matches 288; Conservative 20; Mismatches 21; Indels 2; Gaps 1;

QY 150 MRPCVVPSTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPEAARIHEVVP 209
DB 208 MRPCVVPSTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPEAARIHEVVP 267

QY 210 RFLTEKLEMEQRLKNVTPLSANOKSLIARLVWYQEGYQPSSEDLKRVTTOTWOLESEE 269
DB 268 RFLTEKLEMEQRLKNVTPLSANOKSLIARLVWYQEGYQPSSEDLKRVTTOTWOLESEE 327

QY 270 ETDMPFRQITTEMTILTVQLIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARRYDA 329
DB 328 --DMPFRQITTEMTILTVQLIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARRYDA 385

QY 330 ATDSVLFPANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMNDNVHALLTAIVIFSDRP 389
DB 386 ATDSVLFPANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMNDNVHALLTAIVIFSDRP 445

QY 390 GLEQPLVEIQRYLKTLRVYILNOHSASPRCAVLFGKILGVLTELRTLTGTONSNMCIS 449
DB 446 GLEQPLVEIQRYLKTLRVYILNOHSASPRCAVLFGKILGVLTELRTLTGTONSNMCIS 505

QY 450 LKLNKRLPPPLEEINWDVAEVSTTKLAPPTD 480
DB 506 LKLNKRLPPPLEEINWDVAEVSTTKLAPPTD 536

RESULT 5
ECR_HELVI STANDARD; PRT; 576 AA.
ID ECR_HELVI
AC O18473;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ecdysone receptor (Ecdysteroicd receptor) (20-hydroxy-ecdysone receptor) (20E receptor) (HvEcR).
GN Name=ECR; Synonyms=NR1H1;
OS Heliothis virescens (Noctuid moth) (Owllet moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Heliothis.
OX NCBI_TaxID=7102;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRC;
RX MEDLINE=99457718; PubMed=10528411; DOI=10.1016/S0965-1748(99)00067-3;

RA Martinez A., Scanlon D., Gross B., Perara S.C., Palli S.R.,
 RA Greenland A.J., Windass J., Pongs O., Broad P., Jepson I.;
 RT "Transcriptional activation of the cloned Heliothis virescens
 RT (Lepidoptera) ecdysone receptor (HVECR) by muristeroneA.";
 RL Insect Biochem. Mol. Biol. 29:915-930(1999).
 CC -!- FUNCTION: Receptor for ecdysone. Binds to ecdysone response
 CC elements (ECRES) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI
 CC subfamily.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Y09009; CAAY70212.1; -.
 DR PDB; 1R1K; X-ray; D:288-550.
 DR InterPro; IPR000536; Hrmn_recept_lig.
 DR InterPro; IPR001723; Strhmrn_receptor.
 DR InterPro; IPR008946; Str_ncl_receptor.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR Pfam; PF00104; Hormone_recep; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR00398; STRDHORMONER.
 DR PROSITE; PS00035; Znf_C4steroid; 1.
 DR PRODOM; PD000035; Znf_C4steroid; 1.
 DR SMART; SM00430; HOL1_1.
 DR SMART; SM00399; Znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 DR 3D-structure; DNA-binding; Nuclear protein; Receptor;
 KW Transcription regulation; Zinc-finger.
 FT DOMAIN 1 162 Modulating (Potential).
 FT DNA_BIND 163 228 Nuclear receptor-type.
 FT ZN_FING 163 183 C4-type.
 FT ZN_FING 199 223 C4-type.
 FT DOMAIN 326 545 Hormone-binding (Potential).
 SQ SEQUENCE 576 AA; 64638 MW; D13EF787BF263A8 CRC64;

Query Match 52.1%; Score 1488.5; DB 1; Length 576;
 Best Local Similarity 88.1%; Pred. No. 8.2e-86;
 Matches 290; Conservative 19; Mismatches 11; Indels 9; Gaps 2;
 QY 150 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPAAARI----- 204
 DB 228 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPAAARILECVQ 287
 QY 205 HEVVPRLTEKLMQNRLKNVTPLSANQKSLIARLVWYQEGYEQSPSEDLKRVTTQWOLE 264
 DB 288 HEVVPRLTEKLMQNRLKNVTPLSANQKSLIARLVWYQEGYEQSPSEDLKRVTTQWOLE 343
 QY 265 EEEETDMPFRQITTEMILTTLVQLIVEFAKGLPGFSGKISQSDQITLLKASSEVMMLRVA 324
 DB 344 DEDSDSDMPFRQITTEMILTTLVQLIVEFAKGLPGFSGKISQSDQITLLKASSEVMMLRVA 403
 QY 325 RRYDAATDSVLPANNOAYTRDNYRKAGMSYVIEDLLHFRCRCMYSMNDNVHALLTAIVI 384
 DB 404 RRYDAATDSVLPANNOAYTRDNYRKAGMSYVIEDLLHFRCRCMYSMNDNVHALLTAIVI 463
 QY 385 FSDRGLQPLVBEIQRYLTKLTVILNQHSASPRCAVLFGKILGVLTLRTLTGTONS 444
 DB 464 FSDRGLQPLVBEIQRYLTKLTVILNQHSASPRCAVLFGKILGVLTLRTLTGTONS 523
 QY 445 NNCISLKNRKLPPFLBEIWDVAEVSIT 473
 DB 524 NNCISLKNRKLPPFLBEIWDVAEVSIT 552

RESULT 6
 Q9U0R9

ID Q9U0R9 PRELIMINARY; PRT; 339 AA.
 AC Q9U0R9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Ecdysteroid receptor (Fragment).
 GN Name:ecr;
 OS Junonia coenia (Peacock butterfly) (Precis coenia).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Papilionoidea; Nymphalidae; Nymphalinae; Junonia.
 OX NCBI_TaxID=39708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Wing;
 RA Reinhardt R.K., Weber P., Koch P.B.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
 DR EMBL; AJ251809; CAB63485.1; -.
 DR HSP; P34021; IR00.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
 DR GO; GO:0005496; F:steroid binding; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003069; Ecdystd_receptor.
 DR InterPro; IPR000536; Hrmn_recept_lig.
 DR InterPro; IPR001723; Strhmrn_receptor.
 DR InterPro; IPR008946; Str_ncl_receptor.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR Pfam; PF00104; Hormone_recep; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR01283; ECDYSTEROIDR.
 DR PRINTS; PR00398; STRDHORMONER.
 DR SMART; SM00430; HOL1; 1.
 KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
 KW Transcription regulation; Zinc; Zinc-finger.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39363 MW; 3EC1C7AD294782EB CRC64;
 Query Match 51.1%; Score 1458; DB 2; Length 339;
 Best Local Similarity 87.7%; Pred. No. 3.4e-84;
 Matches 277; Conservative 23; Mismatches 16; Indels 0; Gaps 0;
 QY 150 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPAAARIHVVP 209
 DB 24 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPAAARIHVVP 83
 QY 210 RLTEKLMQNRLKNVTPLSANQKSLIARLVWYQEGYEQSPSEDLKRVTTQWOLEEEEE 269
 DB 84 RLTEKLMQNRLKNVTPLSANQKSLIARLVWYQEGYEQSPSEDLKRVTTQWOLEDEDE 143
 QY 270 ETDMPPFRQITTEMILTTLVQLIVEFAKGLPGFSGKISQSDQITLLKASSEVMMLRVARRIDA 329
 DB 144 ESDLPPFRQITTEMILTTLVQLIVEFAKGLPGFSGKISQSDQITLLKASSEVMMLRVARRIDA 203
 QY 330 ATDSVLPANNOAYTRDNYRKAGMSYVIEDLLHFRCRCMYSMNDNVHALLTAIVIFSDRP 389
 DB 204 TDSVLPANNOAYTRDNYRKAGMSYVIEDLLHFRCRCMYSMNDNVHALLTAIVIFSDRP 263
 QY 390 GLEOPLVBEIQRYLTKLTVILNQHSASPRCAVLFGKILGVLTLRTLTGTONSNMCIS 449
 DB 264 GLEOPLVBEIQRYLTKLTVILNQHSASPRCAVLFGKILGVLTLRTLTGTONSNMCIS 323
 QY 450 LKLNKRLPPFLBEIWDVAEVSIT 465
 DB 324 LKLNKRLPPFLBEIWDVAEVSIT 339

RESULT 7
 BCR_BOMMO

ID ECR_BOMMO STANDARD; PRT; 606 AA.
 AC P49881;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone receptor) (20E receptor).
 GN Name=ECR; Synonyms=NR1H1;
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Myse; TISSUE=Ovary;
 RX MEDLINE=95360029; PubMed=7633470; DOI=10.1016/0965-1748(95)00024-P;
 RA Swevers L., Drevet J.R., Lunke M.D., Iatrou K.;
 RT "The silkmoth homolog of the Drosophila ecdysone receptor (B1 isoform): cloning and analysis of expression during follicular cell differentiation.";
 RL Insect Biochem. Mol. Biol. 25:857-866(1995).
 RN [2]
 RP SEQUENCE OF 61-606 FROM N.A.
 RC STRAIN=Kinshu X Showa; TISSUE=Fat body;
 RA Kamimura M., Tomita S., Fujiwara H.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for ecdysone. Binds to ecdysone response elements (ECRES). May play a role in the implementation of the chorionic program at the end of vitellogenesis.
 CC -!- SUBUNIT: Heterodimer of ECR and Crf (potential).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Events=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P49881-1; Sequences=Displayed;
 CC Name=2;
 CC IsoId=P49881-2; Sequences=VSP 003663;
 CC -!- DEVELOPMENTAL STAGE: It is present in constant amounts in follicular cells throughout vitellogenesis but disappears transiently at the onset of choriogenesis and reappears during the later stages of choriogenesis.
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR1 subfamily.
 CC -!- CAUTION: It is uncertain whether Met-1 or Met-61 is the initiator.
 CC -----
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 CC -----
 CC EMBL; L35266; AAA87340.1; -;
 CC EMBL; L35266; AAA87340.1; -;
 CC EMBL; D43943; BAA07890.1; -;
 CC HSSP; P20393; IAGY.
 DR InterPro; IPR000536; Hrmn_recept_lig.
 DR InterPro; IPR001723; Strdhmn_receptor.
 DR InterPro; IPR008946; Str_ncl_receptor.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR Pfam; PF00104; Hormone_recep; 1.
 DR Pfam; PF00105; Zf-C4; 1.
 DR PRINTS; PR00398; STRDHMONER.
 DR PRINTS; PR00047; STROIDFINGER.
 DR ProDom; PD000035; Znf_C4steroid; 1.
 DR PROSITE; PS00031; NuclearRECEPTOR; 1.
 KW Alternative splicing; DNA-binding; Nuclear protein; Receptor;
 Transcription regulation; Zinc-finger.
 FT DOMAIN 1 206 Modulating (Potential).
 FT DNA_BIND 207 272 Nuclear receptor-type.
 FT ZN_FING 207 227 C4-type.

FT ZN_FING 243 267 C4-type.
 FT DOMAIN 364 586 Hormone-binding (Potential).
 FT DOMAIN 134 142 Poly-Gln.
 FT DOMAIN 317 320 Poly-Pro.
 FT VARSPLIC 380 382 Missing (in isoform 2).
 FT /FTID=VSP_003663.
 FT CONFLICT 67 67 N -> D (in Ref. 2).
 FT CONFLICT 81 81 S -> T (in Ref. 2).
 FT CONFLICT 108 108 R -> G (in Ref. 2).
 FT CONFLICT 469 470 QG -> KA (in Ref. 2).
 FT CONFLICT 591 591 A -> P (in Ref. 2).
 SQ SEQUENCE 606 AA; 68201 MW; 960EBB9A1E4F2202 CRC64;
 Query Match 50.3%; Score 1437; DB 1; Length 606;
 Best Local Similarity 83.3%; Pred. No. 1.6e-82;
 Matches 280; Conservative 31; Mismatches 15; Indels 10; Gaps 5;
 QY 150 MRPCVPESTCKNKRKEAQRKDK---LPVSTTTVDHMPAIMQCDPPPPPEAARIHE 206
 DB 272 MRPCVIQEPS-KNKDRQRQ---KKDKGILLPVSTTTVEDHMPPTMQCDPPPPPEAARIHE 327
 QY 207 VVPRFLTEKLEQNRLKNVTPLSANOKSLIARLVYQSGYEQPSEEDLKRVTTQTWQLEE 266
 DB 328 VVPRYLSKLEMEQNRQKNIPLSANQKSLIARLVYQSGYEQPSEEDLKRVTTQTWQ-SDE 386
 QY 267 EEEETDMPFRQITETITLTQLIVEFAKGLPGFKISQSDQITLLKASSSEVMMLRVARR 326
 DB 387 EDESDLPFRQITETITLTQLIVEFAKGLPGFKISQSDQITLLKASSSEVMMLRVARR 446
 QY 327 YDAATSDVLFANNOAYTRDNYRKAGMSYVIEDLHFCRCMYSMNDNVHYALLTAIVIFS 386
 DB 447 YDAASDSVLFANNAKAYTRDNYRQGMAYVIEDLHFCRCMFAMGNDNVHFALLTAIVIFS 506
 QY 387 DRPGLEQPLAVERIORYLKTLYVILNQHSAAPRCVLFCKILGLVLTGLTQNSNM 446
 DB 507 DRPGLEQPSLVEEIORYLYLNTLRIYINQNSASRCVAYIGRILSVLTGLTQNSNM 566
 QY 447 CISLKLNNRKLPPFLEEIWDVAEVSTT--KLAPPTD 480
 DB 567 CISLKLNNRKLPPFLEEIWDVAEVATHTPTVLPPTN 602
 RESULT 8
 O77240
 ID O77240 PRELIMINARY; PRT; 513 AA.
 AC O77240;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Ecdysone receptor isoform A.
 GN Name=ECR;
 OS Choristoneura fumiferana (Spruce budworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Tortricidae; Tortricinae; Choristoneura.
 OX NCBI_TaxID=7141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99359183; PubMed=10432225; DOI=10.1016/S0303-7207(99)00058-1;
 RA Perera S.C., Ladd T.R., Dhadialla T.S., Kreil P.J., Sohi S.S.,
 RA Retnakaran A., Palli S.R.;
 RT "Studies on two ecdysone receptor isoforms of the spruce budworm,
 Choristoneura fumiferana.";
 RL Mol. Cell. Endocrinol. 152:73-84(1999).
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
 DR EMBL; AF092030; AAC61596.2; -;
 DR HSSP; P34021; 1R0O.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
 DR GO; GO:0005496; F:steroid binding; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

```
DR InterPro; IPR003069; Ecdystd receptor.
DR InterPro; IPR000536; Hrmn_recept_lig.
DR InterPro; IPR001723; Stdhrmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR01283; ECDYSTEROIDR.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 513 AA; 57622 MW; F110540A3030E602 CRC64;

Query Match 50.1%; Score 1430; DB 2; Length 513;
Best Local Similarity 80.4%; Pred. No. 3.5e-82;
Matches 270; Conservative 36; Mismatches 26; Indels 4; Gaps 1;

QY 150 MRPECVPESTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPPEAAARIHEVVP 209
DB 150 MRPECVPESTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPPEAAARIHEVVP 209
QY 178 MRPECVPESTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPPEAAARIHEVVP 237
DB 178 MRPECVPESTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPPEAAARIHEVVP 237
QY 210 RFLTEKLEMEQNRLKNVTPLSANOKSLIARLVYQEGYEQSEEDLKRVTQTWOLEEEEEE 269
DB 210 RFLTEKLEMEQNRLKNVTPLSANOKSLIARLVYQEGYEQSEEDLKRVTQTWOLEEEEEE 269
QY 238 RFLSKLLETRQKNIPQLTANQOFLIARLIWYQGYEQSPDEDLKRITQTWQADADENE 297
DB 238 RFLSKLLETRQKNIPQLTANQOFLIARLIWYQGYEQSPDEDLKRITQTWQADADENE 297
QY 270 ETDMPFRQITMTILTTLVQVIVFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARYDA 329
DB 270 ETDMPFRQITMTILTTLVQVIVFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARYDA 329
QY 298 ESDTFRQITMTILTTLVQVIVFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARYDA 357
DB 298 ESDTFRQITMTILTTLVQVIVFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARYDA 357
QY 330 ATDSVLFANNQAYTRDNRKAGMSVIEDLLHFCRCMYSMNDNVHYALLTAIVIFSDRP 389
DB 330 ATDSVLFANNQAYTRDNRKAGMSVIEDLLHFCRCMYSMNDNVHYALLTAIVIFSDRP 389
QY 358 ASDSVLFANNQAYTRDNRKAGMAYVIEDLLHFCRCMYSMALDNIHYALLTAIVIFSDRP 417
DB 358 ASDSVLFANNQAYTRDNRKAGMAYVIEDLLHFCRCMYSMALDNIHYALLTAIVIFSDRP 417
QY 390 GLEQPLLVVEETORYVLTIRYILNQLSGSARSSVVIYKILSELRTLTGQNSNMCIIS 449
DB 390 GLEQPLLVVEETORYVLTIRYILNQLSGSARSSVVIYKILSELRTLTGQNSNMCIIS 449
QY 418 GLEQPLLVVEETORYVLTIRYILNQLSGSARSSVVIYKILSELRTLTGQNSNMCIIS 477
DB 418 GLEQPLLVVEETORYVLTIRYILNQLSGSARSSVVIYKILSELRTLTGQNSNMCIIS 477
QY 450 LKLNKRLPPFLEEIWDVAEVSSTTKLAP-PTDV 481
DB 450 LKLNKRLPPFLEEIWDVAEVSSTTKLAP-PTDV 481
QY 478 LKLNKRLPPFLEEIWDVAEVSSTTKLAP-PTDV 513
DB 478 LKLNKRLPPFLEEIWDVAEVSSTTKLAP-PTDV 513

RESULT 9
ID O77255 PRELIMINARY; PRT; 541 AA.
AC O77255;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ecdysteroide receptor Ecd-B.
OS Choristoneura fumiferana (Spruce budworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Tortricinae; Choristoneura.
OX NCBI_TaxID=7141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96191152; PubMed=8641050;
RA Kothapalli R., Palli S.R., Ladd T.R., Sohi S.S., Cress D.,
RA Dhadialla T.S., Izertinis G., Retnakaran A.;
RT "Cloning and developmental expression of the ecdysone receptor gene
RT from the spruce budworm, Choristoneura fumiferana.";
RL Dev. Genet. 17:319-330(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Kothapalli R., Palli S.R., Ladd T., Retnakaran A.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
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[1]
RN RP SEQUENCE FROM N.A.
RC RX MEDLINE=20112665; PubMed=10644973;
RA Reinhardt R.K., Weber P., Koch P.B.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -l- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -l- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AJ251810; CAB63236.1; -.
DR HSSP; P34021; 1R00.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:0005496; F:steroid binding; IEA.
DR GO; GO:0005700; F:transcription factor activity; IEA.
DR InterPro; IPR003355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003069; Ecdystd_receptor.
DR InterPro; IPR001723; Strdhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR PRINTS; PR01283; ECDYSTEROIDR.
DR PRINTS; PR00398; STRDHMONER.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
FT NON_TER 1
FT NON_TER 346
FT NON_TER 346
SQ SEQUENCE 346 AA; 40036 MW; 04323B79C2D055D2 CRC64;

Query Match 48.4%; Score 1381; DB 2; Length 346;
Best Local Similarity 82.4%; Pred. No. 2.6e-79;
Matches 266; Conservative 25; Mismatches 26; Indels 6; Gaps 2;

Qy 150 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPEAARI----- 204
Db 24 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPEAARILECLQ 83

Qy 205 HEVVPFRFTEKLEMEONRLKNVTPLSANOKSLIARLVWYQEGVEQSPSEDLKRVTTQTWOLE 264
Db 84 HEVVPFRFTEKLEMEONRLKNVTPLSANOKSLIARLVWYQEGVEQSPSEDLKRVTTQTWQAD 143

Qy 265 EEE--EEETDMPFRQITMTILTQVLIQVFAKGLPGFSKISQSDDITLLKASSEVMMLRV 323
Db 144 TEEIGEASDLPPRQITMTILTQVLIQVFAKGLPGFAXISQPDQITLLKACSEVMMLRV 203

Qy 324 ARRYDAATDSVLFANNQAYTRDNYRKAGMSVYIEDLLHFCRCMYSMDNVHYALLTAIV 383
Db 204 SRRYDMSTDSVYFANNQAYTREIYNKAGFGYVYIENLLHFCRCMYSMDNVHYALLTAV 263

Qy 384 IFSDRPGLEQPLVVEIQRYYLKTLLRVYLINQHSASPRCAVLFGKILGVLTELRTLTGTON 443
Db 264 IFSORPGLENQPLVVEIQRYYLKTLLRVYLINQHSASPRCAVLFGKILGVLTELRTLTGTON 323

Qy 444 SNWCISLKLKNRKLPPFLEEIWD 466
Db 324 SNWCISLKLKNRKLPPFLEEIWD 346

RESULT 11
Q9U3Y4 PRELIMINARY; PRT; 680 AA.
ID Q9U3Y4;
AC Q9U3Y4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ecdysteroid receptor.
GN Name=Ecr;
OS Aedes albopictus (Forest day mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7160;
RN [1]

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SEQUENCE FROM N.A.
RP RX MEDLINE=20112665; PubMed=10644973;
RX DOI=10.1002/(SICI)1520-6327(200002)43:2<87::AID-ARCH5>3.0.CO;2-0;
RA Jayachandran G., Fallon A.M.;
RT "Evidence for expression of Ecr and USP components of the 20-
hydroxyecdysone receptor by a mosquito cell line.";
RL Arch. Insect Biochem. Physiol. 43:87-96(2000).
CC -l- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -l- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AF210733; AAF19032.1; -.
DR HSSP; P34021; 1R00.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:0005496; F:steroid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003069; Ecdystd_receptor.
DR InterPro; IPR000536; Hrmn_recept_lig.
DR InterPro; IPR001723; Strdhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR01283; ECDYSTEROIDR.
DR PRINTS; PR00398; STRDHMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 680 AA; 74924 MW; 272C8E6AB1021C98 CRC64;

Query Match 39.1%; Score 1116; DB 2; Length 680;
Best Local Similarity 58.9%; Pred. No. 3.7e-62;
Matches 226; Conservative 59; Mismatches 71; Indels 28; Gaps 8;

Qy 150 MRPECVPESTCKNKRKEAQRKDKL-----PVSTTTV-----DDHMPAIMQCDPPPPPEAA 202
Db 255 MRPECVPESTCKNKRKEAQRKDKLKVQTNATVSTTSTYRSEILPILMKCDPPP----- 310

Qy 203 RIHEVVPFRFTEKLEMEONRLKNVTPLSANOKSLIARLVWYQEGVEQSPSEDLKRVTTQTWQ 262
Db 311 --HQAIIP-LLPEKLLQENLRNLNIPLLTANQMAVYIKLIWYQDGYEQSPSEDLKRI--MIG 365

Qy 263 LEEEEEETDMPFRQITMTILTQVLIQVFAKGLPGFSKISQSDDITLLKASSEVMMLR 322
Db 366 SPNEEDQDHDVHFHTEITLTQVLIQVFAKGLPAFTKIPQEDQITLLKACSEVMMLR 425

Qy 323 VARRYDAATDSVLFANNQAYTRDNYRKAGMSVYIEDLLHFCRCMYSMDNVHYALLTAI 382
Db 426 MARRYDAATDSVLFANNRSYTRDSYRMAGWADTIEDLLHFCRQMFSLTDVNDVYALLTAI 485

Qy 383 VIFSDRPGLEQPLVVEIQRYYLKTLLRVYLINQHSASPRCAVLFGKILGVLTELRTLTGTQ 442
Db 486 VIFSDRPGLEQAEVHEIQSYIIDTIRIYILNRHAGDPKCSVIPAKLLSILTLRTLTGNQ 545

Qy 443 NSNMCSISLKLKNRKLPPFLEEIWDVAVSTTKLAPPTDVSGLDELHLDG---EDVAMAH 499
Db 546 NSEMCFSKLKNRKLPPFLEEIWDVQDI-----PP---SMQAQMHSHGTQSSSSSSSS 596

Qy 500 DALDDFDLMDLGDGSPGPTFP 523
Db 597 SSSSSSSSSNGSSNGSSNGPFPHP 620

RESULT 12
ECR_AEDAE
ID ECR_AEDAE STANDARD; PRT; 675 AA.
AC P49880;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

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311 --HQAIP-LPEKLLQNRRLNPLLTANQNAVYIKLIWYQDGYEQSPSEBDLKRI--MIG 366

263 LEEEBEETDMPFRQITEMTILTVQLIVEFAKGLPGFSGKISQSDQITLLKASSSEVMMLR 322

366 SPNEEDQHDVHFRHITEITILTVQLIVEFAKGLPAFTKIPQEDQITLLKACSSSEVMMLR 425

323 VARRYDAATOSVLFANNOAYTRDNYRVKAGHSYVIEDLLHFCRCMYMSMDVHYALLTAI 382

426 MARRYDAATOSILFANNRSTRDYSRWAGMADTTIEDLLHFCRQMFSLTVDNVEYALLTAI 485

383 VIFSDRGLRQPLLVEBIOQRYVYLKTLAVYILNOHSASPRCAVLFGKILGVLTSLTGLTQ 442

486 VIFSDRGLRQAEVLVEHISQYVIDTLRIYILNRHAGPKCSVIFAKLSIITELTSLGNQ 545

443 NSNMCISLKNRKLPPFLBEEIWDVAEVSSTTKLAPPTDVSIGDELHLDGEDVAMAHADAL 502

546 NSEMCPSLKNRKLPRFLEEIWDVQDI-----PP---SMAQWHSHTQSSSSSSSS 596

503 DFDLMDLGDGSPGPGFTPHDSAPYG 529

597 SS-----SSNGSGNGSSNSNSQHG 618

RESULT 13

Q6VA69 PRELIMINARY; PRT; 776 AA.

ID Q6VA69 AC Q6VA69

05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE EGRA.

OS Aedes aegypti (Yellowfever mosquito).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.

ON NCBI_TaxID=17159;

RX SEQUENCE FROM N.A.

RP MEDLINE=2227472; PubMed=12385823; DOI=10.1016/S0303-7207(02)00225-3;

RA Wang S.F., Li C., Sun G., Zhu J., Raikhel A.S.;

CC -I- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -I- SIMILARITY: Belongs to the nuclear hormone receptor family.

DR EMBL; AY345989; AAQ23183.1; -.

DR HSP; P20393; IAGY

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.

DR GO; GO:0005496; F:steroid binding; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro; IPR0031069; Acdyatd_receptor.

DR InterPro; IPR000536; Hrmn_receptor.

DR InterPro; IPR001723; Strdhmn_receptor.

DR InterPro; IPR008946; Str_ncl_receptor.

DR InterPro; IPR001628; Znfc_C4steroid.

DR Pfam; PF00104; Hormone_recep; 1.

DR Pfam; PF00105; zf-C4; 1.

DR PRINTS; PR01283; ECDYSTEROIDS.

DR PRINTS; PR00398; STRDHMONER.

DR PRINTS; PR00047; STROIDFINGER.

DR ProDom; PD000035; Znfc_C4steroid; 1.

DR SMART; SM00430; HOLI; 1.

DR SMART; SM00399; ZnF_C4; 1.

DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.

KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;

KW Transcription regulation; Zinc; Zinc-finger.

SQ SEQUENCE 776 AA; 83645 MW; C9B1E893C08E0CAC CRC64;

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Query Match          39.0%; Score 1113; DB 2; Length 776;
Best Local Similarity 58.1%; Pred. No. 6.9e-62;
Matches 225; Conservative 61; Mismatches 71; Indels 30; Gaps 8;

QY 150 MRPECVVPESTCKNRRKEAQAQKDL-----PVSTTTV---DDHMPAIMQCDDPPPEAA 202
DB 356 MRPECVVPESTCKNRRKEAQAQKDLKVQTNATVSTNSTYSEILPILMKCDPPP----- 411
QY 203 RIHEVVPRFLTEKLMQNRLKNVTPLSANQSLIARLVWYQGYQPSSEEDLKRVYQTQW 262
DB 412 --HQAIP-LLPEKLLQENLRNIPLLTANQMAVIVKLIWYQGYQPSSEEDLKRI--MIG 466
QY 263 LEEBEEETDMPROITEITVTLVQVIFAFKGLGFSKISQSDQITLLKASSSEVMMLR 322
DB 467 SNEBEDQHDVFRHHTTEITLVQVIFAFKGLGFSKISQSDQITLLKASSSEVMMLR 526
QY 323 VARRYDAATSDVLFANNOAYTRDNRKAGMSVIEDLLHFCRCMYSMSDNVHYALLTAI 382
DB 527 MARRYDAATSDVLFANNOAYTRDNRKAGMSVIEDLLHFCRCMYSMSDNVHYALLTAI 586
QY 383 VIFSDRPGLEQPLVVEIQRYVYKTLRVVILNQHSASPRCAVLFKGLVLTFLTLGTQ 442
DB 587 VIFSDRPGLEQPLVVEIQRYVYKTLRVVILNQHSASPRCAVLFKGLVLTFLTLGTQ 646
QY 443 NSNMCLISLKNRKLPPFLLEIWDVAEVSITKLAPPTDVSGLDELHLDGEDVAMAHADAL 502
DB 647 NSNMCLISLKNRKLPPFLLEIWDVAEVSITKLAPPTDVSGLDELHLDGEDVAMAHADAL 597
QY 503 DDFDLDMLGDDSPGPGFTPHDSAPVG 529
DB 698 SS-----SSNGSSNGSSNSNSSQHG 719

RESULT 14
ECR CHITE
ID ECR CHITE STANDARD; PRT; 536 AA.
AC P49882;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone
DE receptor) (20E receptor) (ECRH).
GN Name=ECR; Synonyms=NRH1;
OS Chironomus tentans (Midge).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
OC Chironomidae; Chironominae; Chironomus.
OX NCBI_TaxID=7153;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93250857; PubMed=8485513; DOI=10.1016/0965-1748(93)90089-B;
RA Imhof M.O., Rusconi S., Lezzi M.;
RT "Cloning of a Chironomus tentans cDNA encoding a protein (cECRH)
RT homologous to the Drosophila melanogaster ecdysteroid receptor
RT (dECR).";
RL Insect Biochem. Mol. Biol. 23:115-124 (1993).
CC -!- FUNCTION: Receptor for ecdysone..Binds to ecdysone response
CC elements (ECRH).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI
CC subfamily.

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EMBL; S60739; AAC60500.1; -
PIR; A56590; A56590.
HSP; P20393; IAGY.
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DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR00536; Hrmn_recept_lig.
DR InterPro; IPR001723; Strdhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHOMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLJ_1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
FT DOMAIN 1 114 Modulating (Potential).
FT DNA_BIND 115 180 Nuclear receptor-type.
FT ZN_FING 115 135 C4-type.
FT ZN_FING 151 175 C4-type.
FT DOMAIN 290 511 Hormone-binding (Potential).
FT DOMAIN 216 219 Poly-Ser.
FT DOMAIN 307 312 Poly-Glu.
SQ SEQUENCE 536 AA; 61192 MW; 196B0C1CB8048CA7 CRC64;

Query Match          36.0%; Score 1029; DB 1; Length 536;
Best Local Similarity 52.0%; Pred. No. 8.5e-57;
Matches 210; Conservative 67; Mismatches 83; Indels 44; Gaps 5;

QY 97 FVQDNVKNDAVTDRLASVETDMLTLQHRISATSSSEESNKGQRQLTVSTRRPECV 156
DB 138 FFRSVTKNAVYCKFGHECEMDMYMR-----KQECRLKKCLAVGRPECV 186
QY 157 PESTCKNKRREKAQREKDKLP-----VSTTTV-----DDHMPAIM 192
DB 187 PENQCALKRKKAQKQKQKVGIVGNTSSSSLLNQSLNGSLKNLEISVRELLBQLM 246
QY 193 QCDPPPPPEAAIHEVVPFLTEKLMQNRLKNVTPLSANQSLIARLVWYQGYQPSSE 252
DB 247 KCDPPP-----HPMQQLLPKLLMENRAKGTQLTANQVAVIVKLIWYQGYQPSSE 299
QY 253 DLKRVDTQWLEBEESEETDMPFQITTEMILTQVIFAFKGLPGFSKISQSDQITLLK 312
DB 300 DLKRVDTQWLEBEESEETDMPFQITTEMILTQVIFAFKGLPGFSKISQSDQITLLK 357
QY 313 ASSEVVMMLRVARRYDAATSDVLFANNOAYTRDNRKAGMSVIEDLLHFCRCMYSMSMD 372
DB 358 ACSEVVMMLRVARRYDAATSDVLFANNOAYTRDNRKAGMSVIEDLLHFCRCMYSMSMD 417
QY 373 NVHYALLTAIVIFSDRPGLEQPLVVEIQRYVYKTLRVVILNQHSASPRCAVLFKGLV 432
DB 418 NVEYALLTAIVIFSDRPGLEQPLVVEIQRYVYKTLRVVILNQHSASPRCAVLFKGLV 477
QY 433 LTELRTIGTQNSNMCLISLKNRKLPPFLLEIWDVAEVSITKLAPPTDVSGLDELHLD 476
DB 478 LTELRTIGTQNSNMCLISLKNRKLPPFLLEIWDVAEVSITKLAPPTDVSGLDELHLD 521

RESULT 15
ECR LUCCU
ID ECR LUCCU STANDARD; PRT; 757 AA.
AC O18531;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone
DE receptor) (20E receptor).
GN Name=ECR; Synonyms=NRH1;
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Lucilia.
OX NCBI_TaxID=7375;
RN [1]
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Job time : 187 secs

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RP SEQUENCE FROM N.A.
RX MEDLINE=97449774; PubMed=9304790; DOI=10.1016/S0965-1748(97)00019-2;
RA Hannan G.N., Hill R.J.;
RT "Cloning and characterization of LcECR: a functional ecdysone receptor
RL from the sheep blowfly Lucilia cuprina.";
RL Insect Biochem. Mol. Biol. 27:479-488(1997).
CC -!- FUNCTION: Receptor for ecdysone. Binds to ecdysone response
CC elements (ECRES) (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR1
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U75355; AAB81130.1; -.
DR HSP; P20393; IAGY.
DR InterPro; IPR005336; Hrmn_recept_lig.
DR InterPro; IPR001723; Strdhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF0104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLI_1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW zinc-finger.
FT DOMAIN 1 300 Modulating (Potential).
FT DNA_BIND 301 366 Nuclear receptor-type.
FT ZN_FING 301 321 C4-type.
FT ZN_FING 337 361 C4-type.
FT DOMAIN 454 674 Hormone-binding (Potential).
SQ SEQUENCE 757 AA; 83075 MW; C1511452ED37D359 CRC64;

Query Match 35.4%; Score 1011; DB 1; Length 757;
Best Local Similarity 60.8%; Pred. No. 1.9e-55;
Matches 202; Conservative 43; Mismatches 69; Indels 18; Gaps 5;

QY 150 MRPECVPESTCKNRREKAEQREKDLFVS--TTTVDHMPAINQCDDPPPPPEAARIHEV 207
DQ 366 MRPECVVPENQCAMKREKKAQKDKIQTSVCAFEIKKEILDLMTCPPS-----HPT 419

QY 208 VPRFLTEKLMEQNRUKNVTPLSANQKSLIARLVWYQEGYQPSSEDLKRVTTQWLBEHE 267
DQ 420 CP-LLPEDILAKCQARNIPPLSYNQLAVIYKLIWYQDGYQPSSEDLKRIMSS---PDEN 475

QY 268 BEETDMPFROITEMILTQVLIVEFAKGLPGFSKISQSDQITLKASSEVMMLRVARRY 327
DQ 476 ESQHDASFHTEITILTQVLIVEFAKGLPAFTKIPQEDQITLLKACSEVMMLRMARRY 535

QY 328 DAATDSVLFPANQAYTRDNYRKAGMSYVIEDLLHFCRCMYGSMNDNVHYALLTAIVFSD 387
DQ 536 DHNSDSIFFANNRSYTRDSYKMGADNIEDLLHFCRCMYGSMKVDNVEYALLTAIVFSD 595

QY 388 RGLSQPLIVEIQRYLKLTVILNQHSASPRCAVLFGKILGVLTELRITLGTQNSNMC 447
DQ 596 RGLGEAEALVIAIQSYIDTLRIYILNRHCGDPMSLVFAKLLSLTELRITLGNQNAEMC 655

QY 448 ISLKLNRKLPFLEIWDVAEVSITKLAPPT 479
DQ 656 FSLKLNRKLPFLEIWDVHAI-----PPS 681
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Search completed: April 14, 2005, 12:26:43

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OM protein - protein search, using sw model

Run on: April 14, 2005, 12:19:39 ; Search time 44 Seconds
(without alignments)
938.203 Million cell updates/sec

Title: US-10-087-167-105
Perfect score: 2856
Sequence: 1 MKLSSIEQACDICRLKLLK.....ADFFEQMTDALGIDEYGG 553

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pdp.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pdp.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pdp.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pdp.*
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6: /cgn2_6/ptodata/1/iaa/backfiles.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1661	58.2	556	US-09-564-418-11	Sequence 11, Appl
2	1650.5	57.8	557	US-08-653-648A-12	Sequence 12, Appl
3	1507	52.8	546	US-09-393-839-2	Sequence 2, Appl
4	1479.5	51.8	575	US-08-653-648A-5	Sequence 5, Appl
5	1479.5	51.8	575	US-09-564-418-5	Sequence 5, Appl
6	1446	50.6	319	US-08-653-648A-7	Sequence 7, Appl
7	1446	50.6	319	US-09-564-418-13	Sequence 13, Appl
8	1437	50.3	606	US-08-891-298-3	Sequence 3, Appl
9	1425	49.9	606	US-08-653-648A-11	Sequence 11, Appl
10	1425	49.9	606	US-09-564-418-10	Sequence 10, Appl
11	1412.5	49.5	314	US-08-653-648A-16	Sequence 16, Appl
12	1412.5	49.5	314	US-09-564-418-7	Sequence 7, Appl
13	1113	39.0	674	US-08-653-648A-14	Sequence 14, Appl
14	1113	39.0	675	US-09-564-418-12	Sequence 12, Appl
15	1112.5	39.0	560	US-09-435-019-6	Sequence 6, Appl
16	1112.5	39.0	560	US-09-435-019-9	Sequence 9, Appl
17	1112.5	39.0	560	US-10-065-200A-6	Sequence 6, Appl
18	1112.5	39.0	560	US-10-065-200A-9	Sequence 9, Appl
19	1112.5	39.0	561	US-09-435-019-14	Sequence 14, Appl
20	1112.5	39.0	561	US-09-435-019-17	Sequence 17, Appl
21	1112.5	39.0	561	US-10-065-200A-14	Sequence 14, Appl
22	1112.5	39.0	561	US-10-065-200A-17	Sequence 17, Appl
23	1010	35.4	536	US-08-653-648A-13	Sequence 13, Appl
24	1010	35.4	536	US-09-564-418-9	Sequence 9, Appl
25	1000.5	35.0	226	US-09-133-321-2	Sequence 2, Appl
26	988.5	34.6	746	US-09-042-488B-5	Sequence 5, Appl
27	986.5	34.5	550	US-08-659-188-18	Sequence 18, Appl

28	986.5	34.5	550	3	US-08-655-227-18	Sequence 18, Appl
29	986.5	34.5	550	3	US-08-655-241-18	Sequence 18, Appl
30	986.5	34.5	550	3	US-09-398-326-18	Sequence 18, Appl
31	986.5	34.5	550	4	US-09-853-450-18	Sequence 18, Appl
32	986.5	34.5	746	4	US-03-042-488B-7	Sequence 7, Appl
33	986.5	34.5	1041	4	US-09-042-488B-9	Sequence 9, Appl
34	982.5	34.4	746	3	US-09-144-759-18	Sequence 18, Appl
35	982.5	34.4	746	3	US-09-570-267-18	Sequence 18, Appl
36	982.5	34.4	764	3	US-09-144-759-20	Sequence 20, Appl
37	982.5	34.4	764	4	US-09-570-267-20	Sequence 20, Appl
38	966	33.8	878	3	US-08-653-648A-15	Sequence 15, Appl
39	966	33.8	878	4	US-09-564-418-8	Sequence 8, Appl
40	876	30.7	231	4	US-09-324-258-20	Sequence 20, Appl
41	827.5	29.0	219	4	US-09-435-019-65	Sequence 65, Appl
42	827.5	29.0	219	4	US-09-435-019-67	Sequence 67, Appl
43	827.5	29.0	219	4	US-10-065-200A-65	Sequence 65, Appl
44	827.5	29.0	219	4	US-10-065-200A-67	Sequence 67, Appl
45	768	26.9	496	4	US-08-840-713-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-09-564-418-11
; Sequence 11, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jepsen, Ian
; APPLICANT: Martineez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Manduca sexta
US-09-564-418-11

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Best Local Similarity	98.8%	Pred. No.	1.1e-138;				
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Gaps	0;						
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Db	212	MRPCVVPESTCKNKRREKAQREKDKLPVSTTTTVDHMPAIMOCDDPPPPPAARITHEVVP	271				
Qy	210	RFLTEKLEQNRKLNVTPLSANQKSLIARLVYQEGYEQPSEEDLKRVTQTWLEEEEEE	269				
Db	272	RFLTEKLEQNRKLNVTPLSANQKSLIARLVYQEGYEQPSEEDLKRVTQTWLEEEEEE	331				
Qy	270	ETDMPFRQITETMTLTVOLIVEPAKGLPGFSGKISQSDQITLLKASSSVMMMLRVARRYDA	329				
Db	332	ETDMPFRQITETMTLTVOLIVEPAKGLPGFSGKISQSDQITLLKASSSVMMMLRVARRYDA	391				
Qy	330	ATDSVLFPANNOAYTRDNVRKAGMSYVIEDLHFCRCMYSMDNVHVALLTAVIFSDRP	389				
Db	392	ATDSVLFPANNOAYTRDNVRKAGMSYVIEDLHFCRCMYSMDNVHVALLTAVIFSDRP	451				
Qy	390	GLEQPLLVEEIQRYLKTLLRVYILNQHSASPRCAVLFGKILGVLTELTLGTQNSNMCS	449				
Db	452	GLEQPLLVEEIQRYLKTLLRVYILNQHSASPRCAVLFGKILGVLTELTLGTQNSNMCS	511				
Qy	450	LKLNKRLPPPLEBIWDVAEVSSTTKLAP	477				
Db	512	LKLNKRLPPPLEBIWDVAEVSSTTKLAP	539				

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RESULT 2
US-08-653-648A-12
; Sequence 12, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PFD50047/US
; CURRENT APPLICATION NUMBER: US/08/653.648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Manduca sexta
US-08-653-648A-12

Query Match          57.8%; Score 1650.5; DB 3; Length 557;
Best Local Similarity 98.5%; Pred. No. 9.6e-138;
Matches 324; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

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RESULT 4
US-08-653-648A-5
; Sequence 5, Application US/08653648A
; Patent No. 637945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653.648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65

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; LENGTH: 575
; TYPE: PRT
; ORGANISM: Heliothis virescens
US-08-853-648A-5

Query Match      51.8%; Score 1479.5; DB 3; Length 575;
Best Local Similarity 87.5%; Pred. No. 1.5e-122;
Matches 288; Conservative 20; Mismatches 12; Indels 9; Gaps 2

Qy      150 MRPECVVPESTCKNKRKEAQREKDKLPVSTTTTVDHHPAIMOCDDPPPPPEAARI----- 204
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Db      228 MRPECVVPEHQCAKMRKEKAQREKDKLPVSTTTTVDHHPIMQCDPPPPPEAARILECVQ 287
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy      205 HEVVPFELTEKLMFQNRLKNVTPISANQKSLIARLVWYQSEGYEQPSEBDLKRKVTQTWQLE 264
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Db 288 HEVPRFLNEKMEQNRLKNVPLTANQKSLIARLVWYQEGYEQSEEDLKRVTQS----- 343
Qy 265 EEEBETDMPFRQITTEMILTIVQLIVEFAKGLPGFSKISQSDQITLLKASSEVMMLRVA 324
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Qy 325 RRYDAATDSVLFANNAQYTRDNYRKAGMSYVIEDLLHFCRCMYSMSMDNVHYALLTAIVI 384
Db 404 RRYDAATDSVLFANNAQYTRDNYRKAGMAYVIEDLLHFCRCMYSMMMDNVHYALLTAIVI 463
Qy 385 FSDRGLQPLVEIQRYLKTLYILNQHSASPRCAVLFKGLVLTTELRTLTGQNS 444
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Db 524 NNCISLKLKRNKLPPLFLEIMDVAVT 552

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RESULT 5
US-09-564-418-5
; Sequence 5, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jenson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Heliothis virescens
US-09-564-418-5

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Query Match 51.8%; Score 1479.5; DB 4; Length 575;
Best Local Similarity 87.5%; Pred. No. 1.5e-122;
Matches 288; Conservative 20; Mismatches 12; Indels 9; Gaps 2;

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Db 228 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPEAARILECVQ 287
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Db 288 HEVPRFLNEKMEQNRLKNVPLTANQKSLIARLVWYQEGYEQSEEDLKRVTQS----- 343
Qy 265 EEEBETDMPFRQITTEMILTIVQLIVEFAKGLPGFSKISQSDQITLLKASSEVMMLRVA 324
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Db 404 RRYDAATDSVLFANNAQYTRDNYRKAGMAYVIEDLLHFCRCMYSMMMDNVHYALLTAIVI 463
Qy 385 FSDRGLQPLVEIQRYLKTLYILNQHSASPRCAVLFKGLVLTTELRTLTGQNS 444
Db 464 FSDRGLQPLVEIQRYLKTLYILNQHSASPRGAVIFGEILGILTEIRTLGQNS 523
Qy 445 NNCISLKLKRNKLPPLFLEIMDVAVSTT 473
Db 524 NNCISLKLKRNKLPPLFLEIMDVAVT 552

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RESULT 6

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US-08-653-648A-7
; Sequence 7, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jenson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Spodoptera exigua
US-08-653-648A-7

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Query Match 50.6%; Score 1446; DB 3; Length 319;
Best Local Similarity 87.9%; Pred. No. 5.8e-120;
Matches 284; Conservative 17; Mismatches 12; Indels 10; Gaps 3;

Qy 151 RPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPEAARI-----H 205
Db 1 RPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPEAARILECVQ 60
Qy 206 EVPRFLTEKLEMEQNRLKNVPLTANQKSLIARLVWYQEGYEQSEEDLKRVTQTWOLE 265
Db 61 EVPRFLNEKLEMEQNRLKNVPLTANQKSLIARLVWYQEGYEQSEEDLKRVTQS-----D 116
Qy 266 EEEBETDMPFRQITTEMILTIVQLIVEFAKGLPGFSKISQSDQITLLKASSEVMMLRVAR 325
Db 117 EDESDMPFRQITTEMILTIVQLIVEFAKGLPGFAKISQSDQITLLKACSEVMMLRVAR 176
Qy 326 RYDAATDSVLFANNAQYTRDNYRKAGMSYVIEDLLHFCRCMYSMSMDNVHYALLTAIVIF 385
Db 177 RYDAATDSVLFANNAQYTRDNYRKAGMAYVIEDLLHFCRCMYSMMMDNVHYALLTAIVIF 236
Qy 386 SDRGLQPLVEIQRYLKTLYILNQHSASPRCAVLFKGLVLTTELRTLTGQNS 445
Db 237 SDRGLQPLVEIQRYLKTLYILNQHSASPRGAVIFGEILGILTEIRTLGQNS 296
Qy 446 MCISLKLKRNKLPPLFLEIMDV 467
Db 297 MCISLKLKRNKLPPLFLEIMDV 319

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RESULT 7
US-09-564-418-13
; Sequence 13, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jenson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent in version 3.0

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; SEQ ID NO 13
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Heliothis virescens
US-09-564-418-13

Query Match      50.6%; Score 1446; DB 4; Length 319;
Best Local Similarity 87.9%; Pred. No. 5.8e-120; Indels 10; Gaps 3;
Matches 284; Conservative 17; Mismatches 12;

Qy 151 RPECVVPSTCKNKRREKAQREKDKLPVSTTTVDHMPAIMQCDPPPPPEAAARI-----H 205
Db 1 RPECVVPENQCAMKREKKAQREKDKLPVSTTTVDHMPIMQCDPPPPPEAAARILECVQH 60

Qy 206 EVVPRFLTEKMEQNRLKNVTPLSANQKSLIARLVWYQEGYEQSEEDLKRVTQTWOLEE 265
Db 61 EVVPRFLNEKMEQNRLKNVPLTANQKSLIARLVWYQEGYEQSEEDLKRVTQS----D 116

Qy 266 EEEETDMPFQITTEMILTTLVQLIVEFAKGLPGFSKISQSDQITLLKASSEVMMLRVAR 325
Db 117 EDEEDSDMPFQITTEMILTTLVQLIVEFAKGLPGFSKISQSDQITLLKASSEVMMLRVAR 176

Qy 326 RYDAATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMSMDNVHYALLTAIVIF 385
Db 177 RYDAATDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMMNDNVHYALLTAIVIF 236

Qy 386 SDRPGLQPLVVEIQRYLYKTLRVYILNQHSAPRCVLFPGKILGVLTUERTLTGTQNSN 445
Db 237 SDRPGLQPLVVEIQRYLYKTLRVYILNQHSAPRGAVIFGEILGILTEIRTLGMQNSN 296

Qy 446 MCISLKLKNRKLPPPLEEII-WDV 467
Db 297 MCISLKLKNRKLPPPLEEIDWDV 319

RESULT 8
US-08-891-298-3
; Sequence 3, Application US/08891298
; Patent No. 6300488
; GENERAL INFORMATION:
; APPLICANT: Gage, Frederick H.
; APPLICANT: Suhr, Steven T.
; TITLE OF INVENTION: Modified Lepidopteran Receptors
; TITLE OF INVENTION: and Hybrid Multi-Functional Proteins for Use in Transcription
; TITLE OF INVENTION: and Transgene Expression Regulation
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Gray Cary Ware & Freidenrich
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows DEMONSTRATION Version 2.0D
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,298
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; TBLEX:
```

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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 606 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-891-298-3

Query Match      50.3%; Score 1437; DB 3; Length 606;
Best Local Similarity 83.3%; Pred. No. 9.3e-119;
Matches 280; Conservative 31; Mismatches 15; Indels 10; Gaps 5;

Qy 150 MRPECVVPSTCKNKRREKAQREKDK---LPVSTTTVDHMPAIMQCDPPPPPEAAARIHE 206
Db 272 MRPECVIOEFS-KYKDRQHQ---KKDKGILLPVSTTTVEDHMPPIMQCDPPPPPEAAARIHE 327

Qy 207 VVPRFLTEKMEQNRLKNVTPLSANQKSLIARLVWYQEGYEQSEEDLKRVTQTWOLEE 266
Db 328 VVPRYLSEKMEQNRLKNVPLSANQKSLIARLVWYQEGYEQSEEDLKRVTQTWQ--SDE 386

Qy 267 EEEETDMPFQITTEMILTTLVQLIVEFAKGLPGFSKISQSDQITLLKASSEVMMLRVARR 326
Db 387 EDESDLPFQITTEMILTTLVQLIVEFAKGLPGFSKISQSDQITLLKASSEVMMLRVARR 446

Qy 327 YDAATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMSMDNVHYALLTAIVIFS 386
Db 447 YDAATDSVLFANNOAYTRDNYRQGGMAYVIEDLLHFCRCMFAMGMDNVHYALLTAIVIFS 506

Qy 387 DRPGLQPLVVEIQRYLYKTLRVYILNQHSAPRCVLFPGKILGVLTUERTLTGTQNSNM 446
Db 507 DRPGLQPLVVEIQRYLYKTLRVYILNQHSAPRCVAVIYGRILSVLTUERTLTGTQNSNM 566

Qy 447 CISLKLKNRKLPPPLEEIMDVAEVSTT--KLAPPTD 480
Db 567 CISLKLKNRKLPPPLEEIMDVAEVATHTPTVLPPTN 602

RESULT 9
US-08-653-648A-11
; Sequence 11, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 11
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Bombyx mori
US-08-653-648A-11

Query Match      49.9%; Score 1425; DB 3; Length 606;
Best Local Similarity 82.7%; Pred. No. 1.1e-117;
Matches 278; Conservative 31; Mismatches 17; Indels 10; Gaps 5;

Qy 150 MRPECVVPSTCKNKRREKAQREKDK---LPVSTTTVDHMPAIMQCDPPPPPEAAARIHE 206
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Db 272 MRPECVIQEPS-KNKDRQRQ---KKDKGILLPVSTTTVEDHMPPIMQCDPPPEAARIHE 327
Qy 207 VVPRFLEKMEQNRLKNVTPLSANQKSLIARLVWYQEGYQPSDEDLKRVTTQTWQLEEE 266
Db 328 VVPRYLSKMEQNQRKNIPLSANQKSLIARLVWYQEGYQPSDEDLKRVTTQTWQ-SDE 386
Qy 267 EEEETDMPFRQITTEMTILTQVLIIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARR 326
Db 387 EDEESDLPRQITTEMTILTQVLIIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARR 446
Qy 327 YDAATDSVLFANNOAYTRDNRKAGMSVYIEDLLHFCRCMYSMDNVHYALLTAIVIFS 386
Db 447 YDAASDSVLFANNOAYTRDNRKAGMSVYIEDLLHFCRCMYSMDNVHYALLTAIVIFS 506
Qy 387 DRPGLQPLLVEEIQRYVLTNRVILNQHSASPRCAVLFGKILGVLTELRTLTGQNSNM 446
Db 507 DRPGLQPLLVEEIQRYVLTNRVILNQHSASPRCAVLFGKILGVLTELRTLTGQNSNM 566
Qy 447 CISLKNRKLPPFLEEIWDVAEYST--TKLAPPTD 480
Db 567 CISLKNRKLPPFLEEIWDVAEYST--TKLAPPTD 602

RESULT 10

US-09-564-418-10
; Sequence 10, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jenson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US/09/564,418
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Bombyx mori
US-09-564-418-10

Query Match 49.9%; Score 1425; DB 4; Length 606;
Best Local Similarity 82.7%; Pred. No. 1.1e-117;
Matches 278; Conservative 31; Mismatches 17; Indels 10; Gaps 5;

Qy 150 MRPECVPESTCKNKRREKQREKDK--LPVSTTTVDDHMPAIMQCDPPPEAARIHE 206
Db 272 MRPECVIQEPS-KNKDRQRQ---KKDKGILLPVSTTTVEDHMPPIMQCDPPPEAARIHE 327
Qy 207 VVPRFLEKMEQNRLKNVTPLSANQKSLIARLVWYQEGYQPSDEDLKRVTTQTWQLEEE 266
Db 328 VVPRYLSKMEQNQRKNIPLSANQKSLIARLVWYQEGYQPSDEDLKRVTTQTWQ-SDE 386
Qy 267 EEEETDMPFRQITTEMTILTQVLIIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARR 326
Db 387 EDEESDLPRQITTEMTILTQVLIIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARR 446
Qy 327 YDAATDSVLFANNOAYTRDNRKAGMSVYIEDLLHFCRCMYSMDNVHYALLTAIVIFS 386
Db 447 YDAASDSVLFANNOAYTRDNRKAGMSVYIEDLLHFCRCMYSMDNVHYALLTAIVIFS 506
Qy 387 DRPGLQPLLVEEIQRYVLTNRVILNQHSASPRCAVLFGKILGVLTELRTLTGQNSNM 446
Db 507 DRPGLQPLLVEEIQRYVLTNRVILNQHSASPRCAVLFGKILGVLTELRTLTGQNSNM 566
Qy 447 CISLKNRKLPPFLEEIWDVAEYST--TKLAPPTD 480
Db 567 CISLKNRKLPPFLEEIWDVAEYST--TKLAPPTD 602

RESULT 11

US-08-653-648A-16
; Sequence 16, Application US/08653648A
; Patent No. 6379345
; GENERAL INFORMATION:
; APPLICANT: Jenson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; APPLICANT: A Gene Switch
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Spodoptera exigua
US-08-653-648A-16

Query Match 49.5%; Score 1412.5; DB 3; Length 314;
Best Local Similarity 86.5%; Pred. No. 5.3e-117;
Matches 275; Conservative 18; Mismatches 20; Indels 5; Gaps 2;

Qy 151 RPECVPESTCKNKRREKQREKDKLPVSTTTVDDHMPAIMQCDPPPEAARIHEVVPR 210
Db 1 RPECVPESTCKNKRREKQREKDKLPVSTTTVDDHMPAIMQCDPPPEAARIHEVVPR 60
Qy 211 FLTEKLEONRLKNVTPLSANQKSLIARLVWYQEGYQPSDEDLKRVTTQTWQLEEEEEE 270
Db 61 FLTEKLEONRLKNVTPLSANQKSLIARLVWYQEGYQPSDEDLKRVTTQTWQLEEEEEE 116
Qy 271 TDMPPFRQITTEMTILTQVLIIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARRYDAA 330
Db 117 SDMPFRQITTEMTILTQVLIIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLRVARRYDAA 176
Qy 331 TDSVLFANNOAYTRDNRKAGMSVYIEDLLHFCRCMYSMDNVHYALLTAIVIFSDDPPG 390
Db 177 TDSVLFANNOAYTRDNRKAGMSVYIEDLLHFCRCMYSMDNVHYALLTAIVIFSDDPPG 236
Qy 391 LEQPLAVEEIQRYVLTNRVILNQHSASPRCAVLFGKILGVLTELRTLTGQNSNMCI 450
Db 237 LEUTLLVEEIQRYVLTNRVILNQHSASPRCAVLFGKILGVLTELRTLTGQNSNMCI 296
Qy 451 KLKNRKLPPFLEEIWDV 467
Db 297 KLKNRKLPPFLEEIWDV 314

RESULT 12

US-09-564-418-7
; Sequence 7, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jenson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418

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; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Spodoptera exigua
US-09-564-418-7

Query Match          49.5%; Score 1412.5; DB 4; Length 314;
Best Local Similarity 86.5%; Pred. No. 5.3e-117;
Matches 275; Conservative 18; Mismatches 20; Indels 5; Gaps 2;

Qy 151 RPECVPESTCKNKRREKAEQDKLPSVSTTTVDHMPAIMQCDPPPEAAARTHEVVPR 210
Db 1 RPECVVPENQCAIKRREKAEQDKLPSVSTTTVDHMPAIMQCDPPPEAAARTHEVVPR 60

Qy 211 FLTEKLMQNRKLNKVTPLSANQKSLIARLVWYQEGYQPSSEDLKRVTTQWLEEEEEE 270
Db 61 FLNEKLMERTLRNVPLITANQKSLIARLVWYQEGYQPSSEDLKRVTTQWLEEEEEE 116

Qy 271 TDMFPRQITMTILTVQLIVFAKGLPGFSKISQSDQITLLKASSEVMMLRVARRYDAA 330
Db 117 SDMPFPRQITMTILTVQLIVFAKGLPAFAKISQSDQITLLKASSEVMMLRVARRYDAA 176

Qy 331 TDSVLFANNQAYTRDNYRKAGWSYVIEDLLHFCRCMYSMNDNVHYALLTAIVIFSDRPG 390
Db 177 TDSVLFANNQAYTRDNYRKAGWSYVIEDLLHFCRCMYSMNDNVHYALLTAIVIFSDRPG 236

Qy 391 LEQPLLVEEIQRYLYLKTIRVYILNQHSGASPRCAVLFGKILGLVLTGLTQNSNMCI 450
Db 237 LELTLVVEEIQRYLYLKTIRVYILNQHSGASPRCAVLFGKILGLVLTGLTQNSNMCI 296

Qy 451 KLNKRNKLPPLFEEI-WDV 467
Db 297 KLNKRNVPFPEDIDWDV 314

RESULT 13
US-08-653-648A-14
; Sequence 14, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; PRIOR FILING DATE: 1996-05-24
; PRIOR FILING DATE: 1995-05-26
; PRIOR FILING DATE: 1995-05-26
; PRIOR FILING DATE: 1996-03-18
; PRIOR FILING DATE: 1995-07-07
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 14
; TYPE: PRT
; ORGANISM: Aedes aegypti
US-08-653-648A-14

Query Match          39.0%; Score 1113; DB 3; Length 674;
Best Local Similarity 58.1%; Pred. No. 5.9e-90;
Matches 225; Conservative 61; Mismatches 71; Indels 30; Gaps 8;

Qy 150 MRPECVPESTCKNKRREKAEQDKL-----PVSTTTV-----DDHMPAIMQCDPPPEAA 202
Db 255 MRPECVVPENQCAIKRREKAEQDKLVQTNATVSTTNSYRSEILFILMKCDPPP----- 310

Qy 203 RIHEVVPRFELTEKLMQNRKLNKVTPLSANQKSLIARLVWYQEGYQPSSEDLKRVTTQW 262
Db 311 --HQALP--LLEKQLQENLRNIPLTANQMAVIYKLIWYQDGYEQPSSEDLKRI--MIG 365

Qy 263 LEBEEETDMPFPRQITMTILTVQLIVFAKGLPGFSKISQSDQITLLKASSEVMMLR 322
Db 366 SPNEEDQHDVHFRHTEITILTVQLIVFAKGLPAFTKIPQEDQITLLKACSEVMMLR 425

Qy 323 VARRYDAATDSVLFANNQAYTRDNYRKAGWSYVIEDLLHFCRCMYSMNDNVHYALLTAI 382
Db 426 MARRYDAATDSILFANNRSYTRDSYRMAGMADTIEDLLHFCRCQMFSLTVDNVYALLTAI 485

Qy 383 VIFSDRPGLEQPLVVEEIQRYLYLKTIRVYILNQHSGASPRCAVLFGKILGLVLTGLTQ 442
Db 486 VIFSDRPGLEQAEVHEIQSYIIDTLRIYILNHRAGDPKCSVIFAKLLSILTELRTLGNQ 545

RESULT 14
US-09-564-418-12
; Sequence 12, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jepson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 12
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Aedes aegypti
US-09-564-418-12

Query Match          39.0%; Score 1113; DB 4; Length 675;
Best Local Similarity 58.1%; Pred. No. 5.9e-90;
Matches 225; Conservative 61; Mismatches 71; Indels 30; Gaps 8;

Qy 150 MRPECVPESTCKNKRREKAEQDKL-----PVSTTTV-----DDHMPAIMQCDPPPEAA 202
Db 255 MRPECVVPENQCAIKRREKAEQDKLVQTNATVSTTNSYRSEILFILMKCDPPP----- 310

Qy 203 RIHEVVPRFELTEKLMQNRKLNKVTPLSANQKSLIARLVWYQEGYQPSSEDLKRVTTQW 262
Db 311 --HQALP--LLEKQLQENLRNIPLTANQMAVIYKLIWYQDGYEQPSSEDLKRI--MIG 365

Qy 263 LEBEEETDMPFPRQITMTILTVQLIVFAKGLPGFSKISQSDQITLLKASSEVMMLR 322
Db 366 SPNEEDQHDVHFRHTEITILTVQLIVFAKGLPAFTKIPQEDQITLLKACSEVMMLR 425

Qy 323 VARRYDAATDSVLFANNQAYTRDNYRKAGWSYVIEDLLHFCRCMYSMNDNVHYALLTAI 382
Db 426 MARRYDAATDSILFANNRSYTRDSYRMAGMADTIEDLLHFCRCQMFSLTVDNVYALLTAI 485

Qy 383 VIFSDRPGLEQPLVVEEIQRYLYLKTIRVYILNQHSGASPRCAVLFGKILGLVLTGLTQ 442
Db 486 VIFSDRPGLEQAEVHEIQSYIIDTLRIYILNHRAGDPKCSVIFAKLLSILTELRTLGNQ 545
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RESULT 15
US-09-435-019-6
; Sequence 6, Application US/09435019
; Patent No. 6489140
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Nancy
; APPLICANT: Becher, Anna M.
; APPLICANT: Jarvis, Eric
; TITLE OF INVENTION: NOVEL FLEA ECDYSONE AND ULTRASPIRACLE NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES, PROTEINS AND USES THEREOF
; FILE REFERENCE: FC-4
; CURRENT APPLICATION NUMBER: US/09/435,019
; CURRENT FILING DATE: 1999-11-05
; EARLIER APPLICATION NUMBER: 60/107,559
; EARLIER FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Ctеноcephalides felis
US-09-435-019-6

Search completed: April 14, 2005, 12:27:32
Job time : 46 secs

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1	2856	100.0	553	14	US-10-087-167-105	Sequence 105, App
2	2803	98.1	588	14	US-10-087-167-123	Sequence 123, App
3	2786.5	97.6	591	14	US-10-087-167-122	Sequence 127, App
4	2738.5	95.9	591	14	US-10-087-167-119	Sequence 119, App
5	2731	95.6	588	14	US-10-087-167-121	Sequence 121, App
6	2661.5	93.2	593	14	US-10-087-167-125	Sequence 125, App
7	2442.5	85.5	615	14	US-10-087-167-135	Sequence 135, App
8	2440	85.4	620	14	US-10-087-167-137	Sequence 137, App
9	2433	85.2	475	14	US-10-087-167-129	Sequence 129, App
10	2428	85.0	602	14	US-10-087-167-143	Sequence 143, App
11	2381.5	83.4	599	14	US-10-087-167-148	Sequence 148, App
12	2100	76.5	505	14	US-10-087-167-94	Sequence 94, App
13	2047	71.7	599	14	US-10-087-167-70	Sequence 70, App

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Qy 61 LERLEQLFLIIPREDLDMILKMSLODIKALLTGLFVQDNVKNDAVTDRLASVETDML 120
Db 61 LERLEQLFLIIPREDLDMILKMSLODIKALLTGLFVQDNVKNDAVTDRLASVETDML 120
Qy 121 TLQHRISATSSSESSNKGQRLTVSTRMRPECVWPSTCKNKRREKEAQREKDKLPVS 180
Db 121 TLQHRISATSSSESSNKGQRLTVSTRMRPECVWPSTCKNKRREKEAQREKDKLPVS 180
Qy 181 TTTVDDHMPAIMQCDPPPEAAARHEVVPRLTEKLMQNRKKNVTPLSANQKSLIARLV 240
Db 181 TTTVDDHMPAIMQCDPPPEAAARHEVVPRLTEKLMQNRKKNVTPLSANQKSLIARLV 240
Qy 241 WYQEGYQPSSEDLKRVYQWLESEEBEETDMPFRQITTEMILTVQLIIVEFAKGLPGFS 300
Db 241 WYQEGYQPSSEDLKRVYQWLESEEBEETDMPFRQITTEMILTVQLIIVEFAKGLPGFS 300
Qy 301 KISQSDQITLLKASSSEVMMLRVARRYDAATDSVLFANNQAYTRDNYRKAGMSYVIEDLL 360
Db 301 KISQSDQITLLKASSSEVMMLRVARRYDAATDSVLFANNQAYTRDNYRKAGMSYVIEDLL 360
Qy 361 HFCRCMYSMDNVHYALLTAIVIFSDRPGLEQPLLVVEIQRYYLKTLRVYILNQHSASP 420
Db 361 HFCRCMYSMDNVHYALLTAIVIFSDRPGLEQPLLVVEIQRYYLKTLRVYILNQHSASP 420
Qy 421 RCVLFGKILGVLTELRTLTGTONSNMCI SLKKNRKLPPFLEEIWDVAEYSTTKLAPPTD 480
Db 421 RCVLFGKILGVLTELRTLTGTONSNMCI SLKKNRKLPPFLEEIWDVAEYSTTKLAPPTD 480
Qy 481 VSLGDELHLGDEGVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDMADFEFEQ 540
Db 481 VSLGDELHLGDEGVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDMADFEFEQ 540
Qy 541 MFTDALGIDIEYGG 553
Db 541 MFTDALGIDIEYGG 553
```

RESULT 2

US-10-087-167-123
; Sequence 123, Application US/10087167
; Publication No. US20030154509A1

GENERAL INFORMATION:

; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Synthetic Construct

US-10-087-167-123

Query Match 98.1%; Score 2803; DB 14; Length 588;
Best Local Similarity 98.6%; Pred. No. 5,9e-225;
Matches 545; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

```
Qy 1 MKLLSSIEQACDICRLKCLKSKEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
Db 42 MKLLSSIEQACDICRLKCLKSKEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 101
Qy 61 LERLEQLFLIIPREDLDMILKMSLODIKALLTGLFVQDNVKNDAVTDRLASVETDML 120
Db 102 LERLEQLFLIIPREDLDMILKMSLODIKALLTGLFVQDNVKNDAVTDRLASVETDML 161
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```
Qy 121 TLQHRISATSSSESSNKGQRLTVSTRMRPECVWPSTCKNKRREKEAQREKDKLPVS 180
Db 121 TLQHRISATSSSESSNKGQRLTVSTRMRPECVWPSTCKNKRREKEAQREKDKLPVS 221
Qy 181 TTTVDDHMPAIMQCDPPPEAAARHEVVPRLTEKLMQNRKKNVTPLSANQKSLIARLV 240
Db 222 TTTVDDHMPAIMQCDPPPEAAARHEVVPRLTEKLMQNRKKNVTPLSANQKSLIARLV 281
Qy 241 WYQEGYQPSSEDLKRVYQWLESEEBEETDMPFRQITTEMILTVQLIIVEFAKGLPGFS 300
Db 282 WYQEGYQPSSEDLKRVYQWLESEEBEETDMPFRQITTEMILTVQLIIVEFAKGLPGFS 341
Qy 301 KISQSDQITLLKASSSEVMMLRVARRYDAATDSVLFANNQAYTRDNYRKAGMSYVIEDLL 360
Db 342 KISQSDQITLLKASSSEVMMLRVARRYDAATDSVLFANNQAYTRDNYRKAGMSYVIEDLL 401
Qy 361 HFCRCMYSMDNVHYALLTAIVIFSDRPGLEQPLLVVEIQRYYLKTLRVYILNQHSASP 420
Db 402 HFCRCMYSMDNVHYALLTAIVIFSDRPGLEQPLLVVEIQRYYLKTLRVYILNQHSASP 461
Qy 421 RCVLFGKILGVLTELRTLTGTONSNMCI SLKKNRKLPPFLEEIWDVAEYSTTKLAPPTD 480
Db 462 RCVLFGKILGVLTELRTLTGTONSNMCI SLKKNRKLPPFLEEIWDV-----KLAPPTD 515
Qy 481 VSLGDELHLGDEGVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDMADFEFEQ 540
Db 516 VSLGDELHLGDEGVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDMADFEFEQ 575
Qy 541 MFTDALGIDIEYGG 553
Db 576 MFTDALGIDIEYGG 588
```

RESULT 3

US-10-087-167-127
; Sequence 127, Application US/10087167
; Publication No. US20030154509A1

GENERAL INFORMATION:

; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Synthetic Construct

US-10-087-167-127

Query Match 97.6%; Score 2786.5; DB 14; Length 599;
Best Local Similarity 96.8%; Pred. No. 1.5e-223;
Matches 540; Conservative 7; Mismatches 6; Indels 5; Gaps 1;

```
Qy 1 MKLLSSIEQACDICRLKCLKSKEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
Db 42 MKLLSSIEQACDICRLKCLKSKEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 101
Qy 61 LERLEQLFLIIPREDLDMILKMSLODIKALLTGLFVQDNVKNDAVTDRLASVETDML 120
Db 102 LERLEQLFLIIPREDLDMILKMSLODIKALLTGLFVQDNVKNDAVTDRLASVETDML 161
Qy 121 TLQHRISATSSSESSNKGQRLTVSTRMRPECVWPSTCKNKRREKEAQREKDKLPVS 180
Db 162 TLQHRISATSSSESSNKGQRLTVSTRMRPECVWPSTCKNKRREKEAQREKDKLPVS 221
```

QY 181 TTTVDHMPAINQCDDPPPEAAARI-----HEVVPRLTEKLMQENRLKNVTPLSANQKSL 235
Db 222 TTTVDHMPAINQCDDPPPEAAARILECLQHEVVPRLSEKLMQENRLKNIPPLTANQOPL 281
QY 236 IARLVWYQEGYQOPSEEDLKRVTTQWLEEEEEEEDMPFROITTEMTILTVQLIVEFAK 295
Db 282 IARLVWYQEGYQOPSEEDLKRVTTQWLEEEEEEEDMPFROITTEMTILTVQLIVEFAK 341
QY 296 LFGFSKISQSDQITLLKASSSEVMMLRVARRYYDAATSDVLFANNOAYTRDNYRKAGMSV 355
Db 342 LFGFSKISQSDQITLLKASSSEVMMLRVARRYYDAATSDVLFANNOAYTRDNYRKAGMSV 401
QY 356 IEDLHFRCMYSMSMDNVHYALLTAIVIFSDRPGLEQPLIVEEIQRYVLTIRVYILNQ 415
Db 402 IEDLHFRCMYSMSMDNVHYALLTAIVIFSDRPGLEQPLIVEEIQRYVLTIRVYILNQ 461
QY 416 HSASPRCAVLFGKILGVLTTELRTLTGTONSNMNCISLKNRKLPPPLEEIDWVAEYSTTKL 475
Db 462 HSASPRCAVLFGKILGVLTTELRTLTGTONSNMNCISLKNRKLPPPLEEIDWVAEYSTTKL 521
QY 476 APTDVSIGDELHLDGEDVAMAHADALDDFDLMDLGDGSDPGPFTPHDSAPYGALDMAD 535
Db 522 APTDVSIGDELHLDGEDVAMAHADALDDFDLMDLGDGSDPGPFTPHDSAPYGALDMAD 581
QY 536 PFEQMTDALGIDEYGG 553
Db 582 PFEQMTDALGIDEYGG 599

RESULT 4

US-10-087-167-119
; Sequence 119, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian

; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 119
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Synthetic Construct

US-10-087-167-119

Query Match 95.9%; Score 2738.5; DB 14; Length 591;
Best Local Similarity 96.2%; Pred. No. 1.4e-219;
Matches 532; Conservative 8; Mismatches 10; Indels 3; Gaps 2;

QY 1 MKLSSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESR 60
Db 42 MKLSSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESR 101
QY 61 LERLEQLFLIIPREDLMDLKMDSLODIKALLTGLFVQDNVKNDAVTDRLASVETDML 120
Db 102 LERLEQLFLIIPREDLMDLKMDSLODIKALLTGLFVQDNVKNDAVTDRLASVETDML 161
QY 121 TLQHRISATSSSESSNKGQRLTVSTRMPECVPESTCKNKRKEAOREKDKLPVS 180
Db 162 TLQHRISATSSSESSNKGQRLTVSTRMPECVPESTCKNKRKEAOREKDKLPVS 221
QY 181 TTTVDHMPAINQCDDPPPEAAARIHEVVPRLTEKLMQENRLKNVTPLSANQKSLIARLV 240
Db 222 TTTVDHMPAINQCDDPPPEAAARILEVVPRLTEKLMQENRLKNVTPLSANQKSLIARLV 281

QY 241 WYQEGYQOPSEEDLKRVTTQWLEEEEEEEDMPFROITTEMTILTVQLIVEFAKGLPGFS 300
Db 282 WYQEGYQOPSEEDLKRVTTQW-SDEDESESDMPFROITTEMTILTVQLIVEFAKGLPGFA 340
QY 301 KISQSDQITLLKASSSEVMMLRVARRYYDAATSDVLFANNOAYTRDNYRKAGMSYVIEDLL 360
Db 341 KISQSDQITLLKASSSEVMMLRVARRYYDAATSDVLFANNOAYSRDNYRKAGMSYVIEDLL 400
QY 361 HFCRCMYSMSMDNVHYALLTAIVIFSDRPGLEQPLIVEEIQRYVLTIRVYILNOHSASP 420
Db 401 HFCRCMYSMSMDNVHYALLTAIVIFSDRPGLEQPLIVEEIQRYVLTIRVYILNOHSASP 460
QY 421 RCVLVFGKILGVLTTELRTLTGTONSNMNCISLKNRKLPPPLEEIDWVAEYSTTKLAPPTD 480
Db 461 RCVLVFGKILGVLTTELRTLTGTONSNMNCISLKNRKLPPPLEEIDWVE--SRGKLAPPTD 518
QY 481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSDPGPFTPHDSAPYGALDMADPFEQ 540
Db 519 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSDPGPFTPHDSAPYGALDMADPFEQ 578
QY 541 MFTDALGIDEYGG 553
Db 579 MFTDALGIDEYGG 591

RESULT 5

US-10-087-167-121
; Sequence 121, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian

; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 121
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Synthetic Construct

US-10-087-167-121

Query Match 95.6%; Score 2731; DB 14; Length 588;
Best Local Similarity 95.3%; Pred. No. 6.1e-219;
Matches 527; Conservative 10; Mismatches 10; Indels 6; Gaps 1;

QY 1 MKLSSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESR 60
Db 42 MKLSSIEQACDICRLKLLKCSKEPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESR 101
QY 61 LERLEQLFLIIPREDLMDLKMDSLODIKALLTGLFVQDNVKNDAVTDRLASVETDML 120
Db 102 LERLEQLFLIIPREDLMDLKMDSLODIKALLTGLFVQDNVKNDAVTDRLASVETDML 161
QY 121 TLQHRISATSSSESSNKGQRLTVSTRMPECVPESTCKNKRKEAOREKDKLPVS 180
Db 162 TLQHRISATSSSESSNKGQRLTVSTRMPECVPESTCKNKRKEAOREKDKLPVS 221
QY 181 TTTVDHMPAINQCDDPPPEAAARIHEVVPRLTEKLMQENRLKNVTPLSANQKSLIARLV 240
Db 222 TTTVDHMPAINQCDDPPPEAAARILEVVPRLTEKLMQENRLKNVTPLSANQKSLIARLV 281
QY 241 WYQEGYQOPSEEDLKRVTTQWLEEEEEEEDMPFROITTEMTILTVQLIVEFAKGLPGFS 300
Db 282 WYQEGYQOPSEEDLKRVTTQWQSADEDESDMPFROITTEMTILTVQLIVEFAKGLPGFS 341

QY 421 RCALVFGKILGVLTELRTGTQNSNMCISLKLKNRKLPPFLEEIWDVAEVSTTKLAPPTD 480
Db 462 RCALVFGKILGVLTELRTGTQNSNMCISLKLKNRKLPPFLEEIWDVAEVSTTKL--PKA 519
QY 481 VSLGDELHLDGEDVAMAHADALDDFDLMDLMDGDSFG 517
Db 520 VRCGTGLFFHRRDTPAHA---GETATPMAGGGGGG 553

RESULT 8
US-10-087-167-137
; Sequence 137, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 137
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Synthetic Construct
US-10-087-167-137

Query Match 85.4%; Score 2440; DB 14; Length 620;
Best Local Similarity 88.3%; Pred. No. 1.3e-194;
Matches 492; Conservative 7; Mismatches 34; Indels 24; Gaps 4;
QY 1 MKLLSSIEQACDICRLKCLKSKKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
Db 42 MKLLSSIEQACDICRLKCLKSKKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 101
QY 61 LERLEQLFLIFPREDLMDLMDSLQDIKALLTGLFVQDNNVNDVAVTDRLASVETDML 120
Db 102 LERLEQLFLIFPREDLMDLMDSLQDIKALLTGLFVQDNNVNDVAVTDRLASVETDML 161
QY 121 TLQRHRIATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRREKAEQKDKLPVS 180
Db 162 TLQRHRIATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRREKAEQKDKLPVS 221
QY 181 TTTVDHMPALMQCDPPPEAARIEHVVPFLTEKLMEQNRLKNVTPLSANQKSLIARLV 240
Db 222 TTTVDHMPALMQCDPPPEAARIEHVVPFLTEKLMEQNRLKNVTPLSANQKSLIARLV 281
QY 241 WYQEGYEQPSEEDLKRVTQTWOLEEEEEEDMPFRQITMTILTVQLIVFAKGLPGFS 300
Db 282 WYQEGYEQPSEEDLKRVTQTWOLEEEEEEDMPFRQITMTILTVQLIVFAKGLPGFS 341
QY 301 KISQSDQITLLKASSSEVMMLRVARYDAATDSVLFANNQAYTRDNYRKAGMSVYIEDLL 360
Db 342 KISQSDQITLLKASSSEVMMLRVARYDAATDSVLFANNQAYTRDNYRKAGMSVYIEDLL 401
QY 361 HFRCMYSMSMDNVHYALLTAIVFSDRPGLEQPLLVEEIOYYLKTURVILNQHSASP 420
Db 402 HFRCMYSMSMDNVHYALLTAIVFSDRPGLEQPLLVEEIOYYLKTURVILNQHSASP 461
QY 421 RCALVFGKILGVLTELRTGTQNSNMCISLKLKNRKLPPFLEEIWDVAEVSTTKLAPPTD 480
Db 462 RCALVFGKILGVLTELRTGTQNSNMCISLKLKNRKLPPFLEEIWDVAEVSTTKLELATA 521
QY 481 VSLGDEL-----HLGDGEDVAMAHADAL-----DFDLDMLDGG--DSRPGPFT 521
Db 522 ADPGKATATTTTTTSEITETGALESDSLAHLILQPGTDEAAVALGLGLSDFPSAGKA 581

QY 522 PHDSA-----PYGALDM 533
Db 582 VLDDDESGFWWPAASGFD 598
RESULT 9
US-10-087-167-129
; Sequence 129, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Synthetic Construct
US-10-087-167-129

Query Match 85.2%; Score 2433; DB 14; Length 475;
Best Local Similarity 100.0%; Pred. No. 3.3e-194;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLLSSIEQACDICRLKCLKSKKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
Db 1 MKLLSSIEQACDICRLKCLKSKKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
QY 61 LERLEQLFLIFPREDLMDLMDSLQDIKALLTGLFVQDNNVNDVAVTDRLASVETDML 120
Db 61 LERLEQLFLIFPREDLMDLMDSLQDIKALLTGLFVQDNNVNDVAVTDRLASVETDML 120
QY 121 TLQRHRIATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRREKAEQKDKLPVS 180
Db 121 TLQRHRIATSSSESSNKGQRLTVSTRMRPECVVPESTCKNKRREKAEQKDKLPVS 180
QY 181 TTTVDHMPALMQCDPPPEAARIEHVVPFLTEKLMEQNRLKNVTPLSANQKSLIARLV 240
Db 181 TTTVDHMPALMQCDPPPEAARIEHVVPFLTEKLMEQNRLKNVTPLSANQKSLIARLV 240
QY 241 WYQEGYEQPSEEDLKRVTQTWOLEEEEEEDMPFRQITMTILTVQLIVFAKGLPGFS 300
Db 241 WYQEGYEQPSEEDLKRVTQTWOLEEEEEEDMPFRQITMTILTVQLIVFAKGLPGFS 300
QY 301 KISQSDQITLLKASSSEVMMLRVARYDAATDSVLFANNQAYTRDNYRKAGMSVYIEDLL 360
Db 301 KISQSDQITLLKASSSEVMMLRVARYDAATDSVLFANNQAYTRDNYRKAGMSVYIEDLL 360
QY 361 HFRCMYSMSMDNVHYALLTAIVFSDRPGLEQPLLVEEIOYYLKTURVILNQHSASP 420
Db 361 HFRCMYSMSMDNVHYALLTAIVFSDRPGLEQPLLVEEIOYYLKTURVILNQHSASP 420
QY 421 RCALVFGKILGVLTELRTGTQNSNMCISLKLKNRKLPPFLEEIWDVAEVSTTKL 475
Db 421 RCALVFGKILGVLTELRTGTQNSNMCISLKLKNRKLPPFLEEIWDVAEVSTTKL 475
RESULT 10
US-10-087-167-143
; Sequence 143, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott

```
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 143
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Synthetic Construct
US-10-087-167-143

Query Match      85.0%; Score 2428; DB 14; Length 602;
Best Local Similarity 100.0%; Pred. No. 1.2e-193;
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KLLSSIEQACDICRLKLLKCSKEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESRL 61
Db 129 KLLSSIEQACDICRLKLLKCSKEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESRL 188
Qy 62 ERLEQLFLLIIPREDLDMILKWDLSQDIKALLTGTLFVQDNVKNDAVTDRLASVETDMLPT 121
Db 189 ERLEQLFLLIIPREDLDMILKWDLSQDIKALLTGTLFVQDNVKNDAVTDRLASVETDMLPT 248
Qy 122 LRQHRISATSSSESSNKGQRLTVSTRMRPECVVPSTCKNKRKEAQAQREKDKLPVST 181
Db 249 LRQHRISATSSSESSNKGQRLTVSTRMRPECVVPSTCKNKRKEAQAQREKDKLPVST 308
Qy 182 TTVDHMPAINQCDPPPEAARIHEVPRFTEKLEQNRLKNVTPISANQKSLIARLW 241
Db 309 TTVDHMPAINQCDPPPEAARIHEVPRFTEKLEQNRLKNVTPISANQKSLIARLW 368
Qy 242 YQEGYEQSEEDLKRVTQWOLEEBEETDMPFRQITMTILTVQLIVEFAKGLPGFSK 301
Db 369 YQEGYEQSEEDLKRVTQWOLEEBEETDMPFRQITMTILTVQLIVEFAKGLPGFSK 428
Qy 302 ISQSDQITLLKASSSEVMMLVARRYDAATSVLFPANNQATRDYRKAGMSYVIEDLLH 361
Db 429 ISQSDQITLLKASSSEVMMLVARRYDAATSVLFPANNQATRDYRKAGMSYVIEDLLH 488
Qy 362 FCRCMYSMDNVHYALLTAIVIFSDRPGLEQPLLVEIQRYLKTIRVYILNQHSASPR 421
Db 489 FCRCMYSMDNVHYALLTAIVIFSDRPGLEQPLLVEIQRYLKTIRVYILNQHSASPR 548
Qy 422 CAVLFGKILGVLTGTLTQNSNMCIISLKNRKLPPFLEEIWDVAEVSTTKL 475
Db 549 CAVLFGKILGVLTGTLTQNSNMCIISLKNRKLPPFLEEIWDVAEVSTTKL 602

RESULT 11
US-10-087-167-148
; Sequence 148, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 148

; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 148

; LENGTH: 599
; TYPE: PRT
; ORGANISM: Synthetic Construct
US-10-087-167-148

Query Match      83.4%; Score 2381.5; DB 14; Length 599;
Best Local Similarity 85.1%; Pred. No. 9.3e-190;
Matches 475; Conservative 0; Mismatches 0; Indels 83; Gaps 1;

Qy 1 MKLLSSIEQACDICRLKLLKCSKEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
Db 42 MKLLSSIEQACDICRLKLLKCSKEKPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 101
Qy 61 LERLEQLFLLIIPREDLDMILKWDLSQDIKALLTGTLFVQDNVKNDAVTDRLASVETDML 120
Db 102 LERLEQLFLLIIPREDLDMILKWDLSQDIKALLTGTLFVQDNVKNDAVTDRLASVETDML 161
Qy 121 TLRQHRISATSSSESSNKGQRLTVSTRMRPECVVPSTCKNKRKEAQAQREKDKLPVST 159
Db 162 TLRQHRISATSSSESSNKGQRLTVSTRMRPECVVPSTCKNKRKEAQAQREKDKLPVST 221
Qy 160 ----- 159
Db 222 DVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYGALDMADPEFEQMFMTDALGIDEYG 281
Qy 160 --TCKNKRKEAQAQREKDKLPVSTTTTVDHMPAINQCDPPPEAARIHEVPRFTEKLM 217
Db 282 GNTCKNKRKEAQAQREKDKLPVSTTTTVDHMPAINQCDPPPEAARIHEVPRFTEKLM 341
Qy 218 EQNRLKNVTPISANQKSLIARLWYQEGYEQSEEDLKRVTQWOLEEBEETDMPFRQ 277
Db 342 EQNRLKNVTPISANQKSLIARLWYQEGYEQSEEDLKRVTQWOLEEBEETDMPFRQ 401
Qy 278 ITEMILTITVQLIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLVARRYDAATSDVLFA 337
Db 402 ITEMILTITVQLIVEFAKGLPGFSKISQSDQITLLKASSSEVMMLVARRYDAATSDVLFA 461
Qy 338 NNQAYTRDNYRKAGMSYVIEDLLHFCRCMYSMDNVHYALLTAIVIFSDRPGLEQPLL 397
Db 462 NNQAYTRDNYRKAGMSYVIEDLLHFCRCMYSMDNVHYALLTAIVIFSDRPGLEQPLL 521
Qy 398 EETQRYLYKTLRVYILNQHSASPRCAVLFGKILGVLTGTLTQNSNMCIISLKNRKL 457
Db 522 EETQRYLYKTLRVYILNQHSASPRCAVLFGKILGVLTGTLTQNSNMCIISLKNRKL 581
Qy 458 PPFLLEEIWDVAEVSTTKL 475
Db 582 PPFLLEEIWDVAEVSTTKL 599

RESULT 12
US-10-087-167-94
; Sequence 94, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 94
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Synthetic construct
US-10-087-167-94
```

```
Query Match      73.5%; Score 2100; DB 14; Length 505;
Best Local Similarity 100.0%; Pred. No. 2.3e-166;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 150 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPAAARIHEVVP 209
Db 102 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPAAARIHEVVP 161

Qy 210 RFLTEKMEQNRKLNVTPLSANOKSLIARLVWYQEGYQPSSEEDLKRVTTQWOLEEBEES 269
Db 162 RFLTEKMEQNRKLNVTPLSANOKSLIARLVWYQEGYQPSSEEDLKRVTTQWOLEEBEES 221

Qy 270 ETDMPFRQITMTILTVQLIVFEFAKGLPGFSKISQSDQITLLKASSSVMMLRVARRYDA 329
Db 222 ETDMPFRQITMTILTVQLIVFEFAKGLPGFSKISQSDQITLLKASSSVMMLRVARRYDA 281

Qy 330 ATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFRCRCMYSMSMDNVHYALLTAIVIFSRRP 389
Db 282 ATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFRCRCMYSMSMDNVHYALLTAIVIFSRRP 341

Qy 390 GLEOPLIVVEEIQRYLTKLRVYILNQHSASPRCAVLFGKILGVLTGLTGTQNSNMCIS 449
Db 342 GLEOPLIVVEEIQRYLTKLRVYILNQHSASPRCAVLFGKILGVLTGLTGTQNSNMCIS 401

Qy 450 LKLNKRKLPPLEEBIWDVAEVSTTKLAPPTDVSIGDELHLDGEDVAMAHADALDDFDLDM 509
Db 402 LKLNKRKLPPLEEBIWDVAEVSTTKLAPPTDVSIGDELHLDGEDVAMAHADALDDFDLDM 455

Qy 510 LGDGSPPGPTPHDSAPYGALDMADFEFEQMTDALGIDEYGG 553
Db 456 LGDGSPPGPTPHDSAPYGALDMADFEFEQMTDALGIDEYGG 499

RESULT 14
US-10-087-167-80
; Sequence 80, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 80
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Synthetic construct
US-10-087-167-80

Query Match      71.1%; Score 2030.5; DB 14; Length 510;
Best Local Similarity 95.6%; Pred. No. 1.5e-160;
Matches 391; Conservative 7; Mismatches 6; Indels 5; Gaps 1;

Qy 150 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPAAARI----- 204
Db 102 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPAAARI----- 161

Qy 205 HEVVPREFLTKLMEQNRKLNVTPLSANOKSLIARLVWYQEGYQPSSEEDLKRVTTQWOLE 264
Db 162 HEVVPREFLTKLMEQNRKLNVTPLSANOKSLIARLVWYQEGYQPSSEEDLKRVTTQWOLE 221

Qy 265 EEEEEEDMPFRQITMTILTVQLIVFEFAKGLPGFSKISQSDQITLLKASSSVMMLRVA 324
Db 222 EEEEEEDMPFRQITMTILTVQLIVFEFAKGLPGFSKISQSDQITLLKASSSVMMLRVA 281

Qy 325 RRYDAATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFRCRCMYSMSMDNVHYALLTAIVI 384
Db 282 RRYDAATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFRCRCMYSMSMDNVHYALLTAIVI 341

Qy 385 PSDRPGLVEQPLLEEBIQRVYLKLRVYILNQHSASPRCAVLFGKILGVLTGLTGTQNS 444
Db 342 PSDRPGLVEQPLLEEBIQRVYLKLRVYILNQHSASPRCAVLFGKILGVLTGLTGTQNS 401

Qy 445 NMCISLKLKLRKLPPLLEEBIWDVAEVSTTKLAPPTDVSIGDELHLDGEDVAMAHADALDD 504
Db 402 NMCISLKLKLRKLPPLLEEBIWDVAEVSTTKLAPPTDVSIGDELHLDGEDVAMAHADALDD 461

Qy 505 FDLMLGDGSPGPGFTPHDSAPYGALDMADFEFEQMTDALGIDEYGG 553
Db 462 FDLMLGDGSPGPGFTPHDSAPYGALDMADFEFEQMTDALGIDEYGG 510

Query Match      71.7%; Score 2047; DB 14; Length 499;
Best Local Similarity 98.0%; Pred. No. 5.9e-162;
Matches 396; Conservative 1; Mismatches 1; Indels 6; Gaps 1;

Qy 150 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPAAARIHEVVP 209
Db 102 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPAAARIHEVVP 161

Qy 210 RFLTEKMEQNRKLNVTPLSANOKSLIARLVWYQEGYQPSSEEDLKRVTTQWOLEEBEES 269
Db 162 RFLTEKMEQNRKLNVTPLSANOKSLIARLVWYQEGYQPSSEEDLKRVTTQWOLEEBEES 221

Qy 270 ETDMPFRQITMTILTVQLIVFEFAKGLPGFSKISQSDQITLLKASSSVMMLRVARRYDA 329
Db 222 ETDMPFRQITMTILTVQLIVFEFAKGLPGFSKISQSDQITLLKASSSVMMLRVARRYDA 281
```

```
RESULT 15
US-10-087-167-66
; Sequence 66, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Synthetic construct
US-10-087-167-66

Query Match      69.4%; Score 1982.5; DB 14; Length 502;
Best Local Similarity 94.8%; Pred. No. 1.5e-156;
Matches 383; Conservative 8; Mismatches 10; Indels 3; Gaps 2;

QY 150 MRPECVPESTCKNKRREKEAQREKDLPSVSTTTVDDHMPAIMQCDDPPPEAAARIHEVVP 209
Db 102 MRPECVPESTCKNKRREKEAQREKDLPSVSTTTVDDHMPAIMQCDDPPPEAAARIHEVVP 161

QY 210 RFLTEKLEQNRLKNVTPLSANQKSLIARLVWYQEGYQPSSEDLKRVTTQTWQLEEEEEE 269
Db 162 RFLTEKLEQNRLKNVTPLSANQKSLIARLVWYQEGYQPSSEDLKRVTTQTWQ-SDEDEE 220

QY 270 ETDMPFRQITENTILTVQLIVFEFAGLPGFSKISOSDOITLLKASSSEVMMLRVARRYDA 329
Db 221 ESDMPFRQITENTILTVQLIVFEFAGLPGFSKISOSDOITLLKACSEVMMLRVARRYDA 280

QY 330 ATDSVLFANNQAYTRDNYRKAGMSYVIEDLLHFCRCMYSMSMDNVHYALLTAIVIFSDRP 389
Db 281 ATDSVLFANNQAYSRDNYRKAGMSYVIEDLLHFCRCMYSMMDNVHYALLTAIVIFSDRP 340

QY 390 GLEQPLLVEEIQRYYLKLTVYILNQHSAPRCVLFGLKILGLVLTGLTQNSNMCIS 449
Db 341 GLEQPLLVEEIQRYYLNTLRVYILNQHSAPRCVYVFAKILGLTGLTQNSNMCIS 400

QY 450 LKLNKRLPPPLEETDVAEYSTTKLAPPTDVSGLDELHLDGEDVAMAHADALDDFDLDM 509
Db 401 LKLNKRLPPPLEETDVAEYSTTKLAPPTDVSGLDELHLDGEDVAMAHADALDDFDLDM 458

QY 510 LGDGDSPGPGFTPHDSPA PYGALDMADFEQMFDTALGIDEYGG 553
Db 459 LGDGDSPGPGFTPHDSPA PYGALDMADFEQMFDTALGIDEYGG 502
```

Search completed: April 14, 2005, 12:29:56
Job time : 139 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2005, 14:36:55 ; Search time 79 Seconds
(without alignments)
2878.672 Million cell updates/sec

Title: US-10-087-167-121

Perfect score: 3072

Sequence: 1 MQQLYVDFSPAFIRYLPFW.....ADFFEQMTDALGIDEGG 588

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3072	100.0	588	5	Abj05373 Chimeric
2	3072	100.0	588	7	Adf49193 Ecdysone
3	3002.5	97.7	593	5	Abj05375 Chimeric
4	3002.5	97.7	593	7	Adf49197 Ecdysone
5	2968.5	96.6	591	5	Abj05372 Chimeric
6	2968.5	96.6	591	7	Adf49191 Ecdysone
7	2965	96.5	588	5	Abj05374 Chimeric
8	2965	96.5	588	7	Adf49195 Ecdysone
9	2895.5	94.3	599	5	Abj05376 Chimeric
10	2895.5	94.3	599	7	Adf49199 Ecdysone
11	2731	88.9	553	5	Abj05371 Ecdysone
12	2731	88.9	553	7	Adf49177 Ecdysone
13	2552	83.1	620	5	Abj05379 Chimeric
14	2552	83.1	620	7	Adf49209 Ecdysone
15	2551.5	83.1	615	5	Abj05378 Chimeric
16	2551.5	83.1	615	7	Adf49207 Ecdysone
17	2494.5	81.2	599	5	Abj05381 Chimeric
18	2494.5	81.2	599	7	Adf49220 Ecdysone
19	2493	81.2	602	5	Abj05380 Chimeric
20	2493	81.2	602	7	Adf49215 Ecdysone
21	2312	75.3	475	5	Abj05377 Chimeric
22	2312	75.3	475	7	Adf49201 Ecdysone
23	2082	67.8	499	5	Abj05356 Chimeric
24	2082	67.8	499	7	Adf49140 Ecdysone
25	2012.5	65.5	504	5	Abj05360 Chimeric

26	2012.5	65.5	504	7	Adf49148	Ecdysone
27	1978.5	64.4	502	5	Abj05355	Chimeric
28	1978.5	64.4	502	7	Adf49138	Ecdysone
29	1975	64.3	499	5	Abj05357	Chimeric
30	1975	64.3	499	7	Adf49142	Ecdysone
31	1975	64.3	505	5	Abj05369	Chimeric
32	1975	64.3	505	7	Adf49166	Ecdysone
33	1909	62.1	507	5	Abj05361	Chimeric
34	1909	62.1	507	7	Adf49150	Ecdysone
35	1905.5	62.0	510	5	Abj05362	Chimeric
36	1905.5	62.0	510	7	Adf49152	Ecdysone
37	1741	56.7	501	5	Abj05354	Chimeric
38	1741	56.7	501	7	Adf49136	Ecdysone
39	1716.5	55.9	500	5	Abj05368	Chimeric
40	1716.5	55.9	500	7	Adf49164	Ecdysone
41	1691	55.0	521	5	Abj05367	Chimeric
42	1691	55.0	521	7	Adf49162	Ecdysone
43	1670	54.4	513	5	Abj05359	Chimeric
44	1670	54.4	513	7	Adf49146	Ecdysone
45	1666.5	54.2	516	5	Abj05358	Chimeric

ALIGNMENTS

RESULT 1

ABJ05373
ID ABJ05373 standard; protein; 588 AA.

XX AC ABJ05373;

XX XX

DT 29-AUG-2003 (revised)

DT 07-NOV-2002 (first entry)

XX Chimeric ecdysone receptor SEQ ID NO: 121.

DE Plant; gene expression control; insect; hormone receptor; fertility;
KW ecdysone receptor.

XX Manduca sexta.

OS Ostrinia nubilalis.

OS Chimeric.

XX WO200261102-A2.

XX 08-AUG-2002.

PD 24-OCT-2001; 2001WO-US051417.

XX 24-OCT-2000; 2000US-0242969P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

XX WPI; 2002-619259/66.

XX N-PSDB; ABT07367.

XX New receptor cassette encoding a chimeric receptor polypeptide, useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility.

XX Claim 6; Page 273-275; 319pp; English.

XX The present invention relates to a receptor cassette encoding a chimeric receptor polypeptide comprising at least one DNA binding domain, a hinge domain of an ecdysone receptor (EcR) of an insect, a ligand binding domain of an insect EcR, where the ligand binding domain is heterologous with respect to the hinge domain and an activation domain. The chimeric insect hormone receptors and receptor cassettes are useful in regulating expression of target polypeptides in plants in the presence of appropriate ligands that may be used in controlling plant fertility. The method is useful for decreasing or increasing plant gene expression. The

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CC present sequence is a protein described in the exemplification of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 588 AA;

Query Match      100.0%; Score 3072; DB 5; Length 588;
Best Local Similarity 100.0%; Pred. No. 3.6e-250;
Matches 588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQQLYVDFSPAFIRYLFAMYCFCRCSPCLVLLQGSATMKLLSSIEQACDICRLKKL 60
DB 1 MQQLYVDFSPAFIRYLFAMYCFCRCSPCLVLLQGSATMKLLSSIEQACDICRLKKL 60

QY 61 KCSKEPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLIIPREDLM 120
DB 61 KCSKEPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLIIPREDLM 120

QY 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180
DB 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180

QY 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180
DB 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180

QY 181 GORQLTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPP 240
DB 181 GORQLTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPP 240

QY 241 EAARIHEVVRPRFTEKLMQNRLKNVTPLSANOKSLIARLVWYQDGYEQPSEEDLKRVTQ 300
DB 241 EAARIHEVVRPRFTEKLMQNRLKNVTPLSANOKSLIARLVWYQDGYEQPSEEDLKRVTQ 300

QY 241 EAARIHEVVRPRFTEKLMQNRLKNVTPLSANOKSLIARLVWYQDGYEQPSEEDLKRVTQ 300
DB 241 EAARIHEVVRPRFTEKLMQNRLKNVTPLSANOKSLIARLVWYQDGYEQPSEEDLKRVTQ 300

QY 301 TWSADEDESDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVM 360
DB 301 TWSADEDESDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVM 360

QY 301 TWSADEDESDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVM 360
DB 301 TWSADEDESDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVM 360

QY 361 MLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMDNVHYALL 420
DB 361 MLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMDNVHYALL 420

QY 421 TAIIVFSDRPGLEQPOLVEBIQRYIYLNTRVYIMNQHSPRCAVIYAKILSVLTELRTL 480
DB 421 TAIIVFSDRPGLEQPOLVEBIQRYIYLNTRVYIMNQHSPRCAVIYAKILSVLTELRTL 480

QY 481 GNQNSNMICISLKNRKLPPFLEEIWDVKLAPPTDVSIGDELHLDGEDVAMAHADALDDF 540
DB 481 GNQNSNMICISLKNRKLPPFLEEIWDVKLAPPTDVSIGDELHLDGEDVAMAHADALDDF 540

QY 541 DLDMLGDSGSPGFTPHDSAPYGALDMADFEFEQMTDALGIDEYGG 588
DB 541 DLDMLGDSGSPGFTPHDSAPYGALDMADFEFEQMTDALGIDEYGG 588

RESULT 2
ADF49193
ID ADF49193 standard; protein; 588 AA.
XX
AC ADF49193;
XX
DT 12-FEB-2004 (first entry)
XX
DE Ecdysone receptor/VP16 transactivation domain seq id 121.
XX
KW receptor cassette; chimeric receptor polypeptide; DNA binding domain;
KW hinge domain; ecdysone receptor; Ecr; ligand binding domain;
KW activation domain; transgenic seed; transgenic plant; plant line;
KW herbicide; pesticide; chimeric ecdysone receptor; Ecr;
KW yeast GAL4 DNA binding domain; VP16 transactivation domain.
XX
OS Synthetic.
OS Manduca sexta.
OS Ascomycota.
OS Ostrinia nubilalis.
OS Herpes simplex virus unknown type.
XX
PN US2003154509-A1.
```

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XX
PD 14-AUG-2003.
XX
PF 24-OCT-2001; 2001US-00087167.
XX
PR 24-OCT-2001; 2001US-00087167.
XX
PA (PASC/) PASCAL E J.
PA (VALE/) VALENTINE S A.
PA (BROW/) BROWN J A.
PA (COCK/) COCKRELL A S.
PA (JOHN/) JOHNSON B D.
XX
PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
XX WPI; 2003-897756/82.
XX
DR N-PSDB; ADF49192.
XX
XX New receptor cassette encoding a chimeric receptor polypeptide, useful
XX for regulating the expression of target polypeptides in plants in the
XX presence of appropriate chemical ligands.
XX
XX Example 23; SEQ ID NO 121; 186pp; English.
XX
XX The invention describes a receptor cassette encoding a chimeric receptor
XX polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
XX (D) domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
XX (E) domain that is heterologous with respect to the D domain, and an
XX activation domain. The receptor cassette and method are useful in
XX regulating the expression of target polypeptides in plants in the
XX presence of appropriate chemical ligands. The transgenic seeds and plants
XX can be used for the breeding of improved plant lines that, for e.g.
XX increase the effectiveness of conventional methods such as herbicide or
XX pesticide treatment. This is the amino acid sequence of an ecdysone
XX receptor-VP16 transactivation domain fusion protein.
XX
XX Sequence 588 AA;

Query Match      100.0%; Score 3072; DB 7; Length 588;
Best Local Similarity 100.0%; Pred. No. 3.6e-250;
Matches 588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQQLYVDFSPAFIRYLFAMYCFCRCSPCLVLLQGSATMKLLSSIEQACDICRLKKL 60
DB 1 MQQLYVDFSPAFIRYLFAMYCFCRCSPCLVLLQGSATMKLLSSIEQACDICRLKKL 60

QY 61 KCSKEPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLIIPREDLM 120
DB 61 KCSKEPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLIIPREDLM 120

QY 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180
DB 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180

QY 181 GORQLTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPP 240
DB 181 GORQLTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPP 240

QY 241 EAARIHEVVRPRFTEKLMQNRLKNVTPLSANOKSLIARLVWYQDGYEQPSEEDLKRVTQ 300
DB 241 EAARIHEVVRPRFTEKLMQNRLKNVTPLSANOKSLIARLVWYQDGYEQPSEEDLKRVTQ 300

QY 241 EAARIHEVVRPRFTEKLMQNRLKNVTPLSANOKSLIARLVWYQDGYEQPSEEDLKRVTQ 300
DB 241 EAARIHEVVRPRFTEKLMQNRLKNVTPLSANOKSLIARLVWYQDGYEQPSEEDLKRVTQ 300

QY 301 TWSADEDESDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVM 360
DB 301 TWSADEDESDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVM 360

QY 301 TWSADEDESDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVM 360
DB 301 TWSADEDESDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVM 360

QY 361 MLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMDNVHYALL 420
DB 361 MLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMDNVHYALL 420

QY 421 TAIIVFSDRPGLEQPOLVEBIQRYIYLNTRVYIMNQHSPRCAVIYAKILSVLTELRTL 480
DB 421 TAIIVFSDRPGLEQPOLVEBIQRYIYLNTRVYIMNQHSPRCAVIYAKILSVLTELRTL 480

QY 421 TAIIVFSDRPGLEQPOLVEBIQRYIYLNTRVYIMNQHSPRCAVIYAKILSVLTELRTL 480
DB 421 TAIIVFSDRPGLEQPOLVEBIQRYIYLNTRVYIMNQHSPRCAVIYAKILSVLTELRTL 480
```


Db 301 TWQS-DEDEESDMPFRQITMTVQLIIVEFAKGLPGFAKISQSDQITLLKACSEVM 359
 Qy 361 MLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHYALL 420
 Db 360 MLRVARRYDAATSDSVLFANNOAYSNDNYRKAGMSVIEDLLHFCRCMYSMSMDNVHYALL 419
 Qy 421 TAIVIFSDRPGLEOPOLVEEIQRYVYLNTRVYIMNQHSAASPCAVIYAKILSVLTELRTL 480
 Db 420 TAIVIFSDRPGLEOPOLVEEIQRYVYLNTRVYIMNQHSAASPCAVIYAKILSVLTELRTL 479
 Qy 481 GQNSNMCMISLKLKRNKLPPLFEEIWDV- ---KLAPPTDVSIGDELHLDGEDVAMAHADA 536
 Db 480 GQNSNMCMISLKLKRNKLPPLFEEIWDV- ---KLAPPTDVSIGDELHLDGEDVAMAHADA 539
 Qy 537 LDDFDLMDLGDSPGPGFTPHDSAPYCALDMADFEFEQMTDALGIDEYGG 588
 Db 540 LDDFDLMDLGDSPGPGFTPHDSAPYCALDMADFEFEQMTDALGIDEYGG 591

RESULT 6

ID ADF49191 standard; protein; 591 AA.
 XX ADF49191;

DT 12-FEB-2004 (first entry)

DE Ecdysone receptor/VP16 transactivation domain seq id 119.

XX receptor cassette; chimeric receptor polypeptide; DNA binding domain;
 KW hinge domain; ecdysone receptor; ECR; ligand binding domain;
 KW activation domain; transgenic seed; transgenic plant; plant line;
 KW herbicide; pesticide; chimeric ecdysone receptor; ECR;
 KW yeast GAL4 DNA binding domain; VP16 transactivation domain.

XX Synthetic.

OS Manduca sexta.

OS Ascomycota.

OS Agrotis ipsilon.

OS Herpes simplex virus unknown type.

XX US2003154509-A1.

PN 14-AUG-2003.

PD 24-OCT-2001; 2001US-00087167.

PF 24-OCT-2001; 2001US-00087167.

PR 24-OCT-2001; 2001US-00087167.

PA (PASC/) PASCAL E J.

PA (VALE/) VALENTINE S A.

PA (BROW/) BROWN J A.

PA (COCK/) COCKRELL A S.

PA (JOHN/) JOHNSON B D.

PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

XX WPI, 2003-897756/82.

DR N-FSDB; ADF49190.

XX New receptor cassette encoding a chimeric receptor polypeptide, useful
 PT for regulating the expression of target polypeptides in plants in the
 PT presence of appropriate chemical ligands.

XX Example 23; SEQ ID NO 119; 186pp; English.

XX The invention describes a receptor cassette encoding a chimeric receptor
 CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
 CC (D) domain of an ecdysone receptor (ECR) of an insect, a ligand binding
 CC (E) domain that is heterologous with respect to the D domain, and an
 CC activation domain. The receptor cassette and method are useful in
 CC regulating the expression of target polypeptides in plants in the
 CC presence of appropriate chemical ligands. The transgenic seeds and plants

CC can be used for the breeding of improved plant lines that, for e.g.
 CC increase the effectiveness of conventional methods such as herbicide or
 CC pesticide treatment. This is the amino acid sequence of an ecdysone
 CC receptor-VP16 transactivation domain fusion protein.

XX Sequence 591 AA;

Query Match 96.6%; Score 2968.5; DB 7; Length 591;
 Best Local Similarity 95.9%; Pred. No. 2e-241;
 Matches 568; Conservative 13; Mismatches 6; Indels 5; Gaps 2;

Qy 1 MQQLYVDFPFPAPFIRYLFAMCYFCRCSPCLVLLQGSATMKLLSSIEQACDCLRLKKL 60

Db 1 MQQLYVDFPFPAPFIRYLFAMCYFCRCSPCLVLLQGSATMKLLSSIEQACDCLRLKKL 60

Qy 61 KCSKEKPKCAKCLKNNECRYSPTKRSPLTRAHLEVESLERLEQLFLIFPREDLDM 120

Db 61 KCSKEKPKCAKCLKNNECRYSPTKRSPLTRAHLEVESLERLEQLFLIFPREDLDM 120

Qy 121 ILKMSLQDILKALLTGLFVQDNVKNDAVTRLASVETDMLTLRQHRISATSSSESSNK 180

Db 121 ILKMSLQDILKALLTGLFVQDNVKNDAVTRLASVETDMLTLRQHRISATSSSESSNK 180

Qy 181 GORQLTVSTRMRPECVVPPESTCKNKRKEKAQREKDKLPVSTTTVDHMPAIMQCDDPPP 240

Db 181 GORQLTVSTRMRPECVVPPESTCKNKRKEKAQREKDKLPVSTTTVDHMPAIMQCDDPPP 240

Qy 241 EAARIHEVVPFLTEKLMQENRNLKNTPLSANOKSLIARLVYQDGYEQPSEEDLKRYTQ 300

Db 241 EAARIHEVVPFLTEKLMQENRNLKNTPLSANOKSLIARLVYQDGYEQPSEEDLKRYTQ 300

Qy 301 TWQSADBEDSDMPFRQITMTVQLIIVEFAKGLPGFSKISQPDQITLLKACSEVM 360

Db 301 TWQS-DEDEESDMPFRQITMTVQLIIVEFAKGLPGPAKISQSDQITLLKACSEVM 359

Qy 361 MLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHYALL 420

Db 360 MLRVARRYDAATSDSVLFANNOAYSNDNYRKAGMSVIEDLLHFCRCMYSMSMDNVHYALL 419

Qy 421 TAIVIFSDRPGLEOPOLVEEIQRYVYLNTRVYIMNQHSAASPCAVIYAKILSVLTELRTL 480

Db 420 TAIVIFSDRPGLEOPOLVEEIQRYVYLNTRVYIMNQHSAASPCAVIYAKILSVLTELRTL 479

Qy 481 GQNSNMCMISLKLKRNKLPPLFEEIWDV- ---KLAPPTDVSIGDELHLDGEDVAMAHADA 536

Db 480 GQNSNMCMISLKLKRNKLPPLFEEIWDV- ---KLAPPTDVSIGDELHLDGEDVAMAHADA 539

Qy 537 LDDFDLMDLGDSPGPGFTPHDSAPYCALDMADFEFEQMTDALGIDEYGG 588

Db 540 LDDFDLMDLGDSPGPGFTPHDSAPYCALDMADFEFEQMTDALGIDEYGG 591

RESULT 7

ABJ05374

ID ABJ05374 standard; protein; 588 AA.

XX ABJ05374;

XX 29-AUG-2003 (revised)

DT 07-NOV-2002 (first entry)

XX Chimeric ecdysone receptor SEQ ID NO: 123.

XX Plant; gene expression control; insect; hormone receptor; fertility;
 KW ecdysone receptor.

XX Manduca sexta.

OS Spodoptera frugiperda.

XX Chimeric.

PN WO200261102-A2.

XX 08-AUG-2002.

XX PF 24-OCT-2001; 2001WO-US051417.
 XX PR 24-OCT-2000; 2000US-0242969P.
 XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 XX DR WPI; 2002-619259/66.
 XX DR N-PSDB; ABT07368.
 XX PT New receptor cassette encoding a chimeric receptor polypeptide, useful in
 PT regulating expression of target polypeptides in plants in the presence of
 PT appropriate ligands that may be used in controlling plant fertility.
 XX PS Example 23; Page 278-280; 319pp; English.
 XX CC The present invention relates to a receptor cassette encoding a chimeric
 CC receptor polypeptide comprising at least one DNA binding domain, a hinge
 CC domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
 CC domain of an insect Ecr, where the ligand binding domain is heterologous
 CC with respect to the hinge domain and an activation domain. The chimeric
 CC insect hormone receptors and receptor cassettes are useful in regulating
 CC expression of target polypeptides in plants in the presence of
 CC appropriate ligands that may be used in controlling plant fertility. The
 CC method is useful for decreasing or increasing plant gene expression. The
 CC present sequence is a protein described in the exemplification of the
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)
 XX SQ Sequence 588 AA;

Query Match 96.5%; Score 2965; DB 5; Length 588;
 Best Local Similarity 96.3%; Pred. No. 3.9e-241;
 Matches 566; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 1 MQQLYVDFSPAFIRYLFANWCFRCSPCLVLLQGSATMKLLSSIEQACDICRLKKL 60
 DB 1 MQQLYVDFSPAFIRYLFANWCFRCSPCLVLLQGSATMKLLSSIEQACDICRLKKL 60

QY 61 KCSKEKPKCAKCKNNWECRYSPKTRSPKTRAHLEVESESLERLEQLFLIFPREDLDM 120
 DB 61 KCSKEKPKCAKCKNNWECRYSPKTRSPKTRAHLEVESESLERLEQLFLIFPREDLDM 120

QY 121 ILKMDSLQDIKALLTGLFQDQNVNKAQVTDRLASVETDPLTLQHRISATSSSESSNK 180
 DB 121 ILKMDSLQDIKALLTGLFQDQNVNKAQVTDRLASVETDPLTLQHRISATSSSESSNK 180

QY 181 GORQLTVSTRMRPECVPESTCKNKRREKQREKDKLPVSTTTVDHMPAIMQCDPPPP 240
 DB 181 GORQLTVSTRMRPECVPESTCKNKRREKQREKDKLPVSTTTVDHMPAIMQCDPPPP 240

QY 241 EAARHEVVPFLTEKLEMEQNLKNTVPLSANQKSLIARLVYQGYQPSSEEDLKRVTQ 300
 DB 241 EAARHEVVPFLTEKLEMEQNLKNTVPLSANQKSLIARLVYQGYQPSSEEDLKRVTQ 300

QY 301 TWQSADEDESDMPFOITETILTTLVOLIVEFAGLPGFSKISOPDQITLLKACSSVM 360
 DB 301 TWQSADEDESDMPFOITETILTTLVOLIVEFAGLPGFSKISOPDQITLLKACSSVM 360

QY 361 MLRVARRYDAVSDSVLFANNAQYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHYALL 420
 DB 361 MLRVARRYDAVSDSVLFANNAQYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHYALL 420

QY 421 TAIVIFSDRPGLEQPOLVEETORYLNTLRVYIMNQHSAASPCAVIYAKILSVLTELTL 480
 DB 421 TAIVIFSDRPGLEQPOLVEETORYLNTLRVYIMNQHSAASPCAVIYAKILSVLTELTL 480

QY 481 GQNSNMCIISLKNRKLPPFLEEVDVKLAPPTDVSIGDELHLDGEDVMAHADALDDF 540
 DB 481 GQNSNMCIISLKNRKLPPFLEEVDVKLAPPTDVSIGDELHLDGEDVMAHADALDDF 540

QY 541 DLDMLGDSGPGFTPHDSAPYGALDMADFEFEQMFDTALGIDYGG 588

DB 541 DLDMLGDSGPGFTPHDSAPYGALDMADFEFEQMFDTALGIDYGG 588

RESULT 8
 ADF49195
 ID ADF49195 standard; protein; 588 AA.
 XX AC ADF49195;
 XX DT 12-FEB-2004 (first entry)
 XX DE Ecdysone receptor/VP16 transactivation domain seq id 123.
 XX KW receptor cassette; chimeric receptor polypeptide; DNA binding domain;
 KW hinge domain; ecdysone receptor; Ecr; ligand binding domain;
 KW activation domain; transgenic seed; transgenic plant; line;
 KW herbicide; pesticide; chimeric ecdysone receptor; ECR;
 KW yeast GAL4 DNA binding domain; VP16 transactivation domain.
 XX OS Synthetic.
 OS Manduca sexta.
 OS Ascomycota.
 OS Spodoptera frugiperda.
 OS Herpes simplex virus unknown type.
 XX US2003154509-A1.
 XX 14-AUG-2003.
 XX 24-OCT-2001; 2001US-00087167.
 XX 24-OCT-2001; 2001US-00087167.
 XX (PASC/) PASCAL B J.
 XX (VALE/) VALENTINE S A.
 XX (BROW/) BROWN J A.
 XX (COCK/) COCKRELL A S.
 XX (JOHN/) JOHNSON B D.
 XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
 XX WPI; 2003-897756/82.
 XX N-PSDB; ADF49194.
 XX New receptor cassette encoding a chimeric receptor polypeptide, useful
 PT for regulating the expression of target polypeptides in plants in the
 PT presence of appropriate chemical ligands.
 XX Example 23; SEQ ID NO 123; 186pp; English.
 XX The invention describes a receptor cassette encoding a chimeric receptor
 CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
 CC (D) domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
 CC (E) domain that is heterologous with respect to the D domain, and an
 CC activation domain. The receptor cassette and method are useful in
 CC regulating the expression of target polypeptides in plants in the
 CC presence of appropriate chemical ligands. The transgenic seeds and plants
 CC can be used for the breeding of improved plant lines that, for e.g.,
 CC increase the effectiveness of conventional methods such as herbicide or
 CC pesticide treatment. This is the amino acid sequence of an ecdysone
 CC receptor-VP16 transactivation domain fusion protein.
 XX Sequence 588 AA;

Query Match 96.5%; Score 2965; DB 7; Length 588;
 Best Local Similarity 96.3%; Pred. No. 3.9e-241;
 Matches 566; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 1 MQQLYVDFSPAFIRYLFANWCFRCSPCLVLLQGSATMKLLSSIEQACDICRLKKL 60
 DB 1 MQQLYVDFSPAFIRYLFANWCFRCSPCLVLLQGSATMKLLSSIEQACDICRLKKL 60

hinge domain; ecdysone receptor; ECR; ligand binding domain;
activation domain; transgenic seed; transgenic plant; plant line;
herbicide; pesticide; chimeric ecdysone receptor; ECR;
yeast GAL4 DNA binding domain; VP16 transactivation domain.

Synthetic.
Ostrinia nubilalis.
Ascomycota.
Manduca sexta.
Herpes simplex virus unknown type.
US2003154509-A1.
14-AUG-2003.
24-OCT-2001; 2001US-00087167.
24-OCT-2001; 2001US-00087167.
(PASC/) PASCAL E J.
(VALE/) VALENTINE S A.
(BROW/) BROWN J A.
(COCK/) COCKRELL A S.
(JOHN/) JOHNSON B D.

Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
WPI; 2003-897756/82.
N-PSDB; ADF49198.

New receptor cassette encoding a chimeric receptor polypeptide, useful
for regulating the expression of target polypeptides in plants in the
presence of appropriate chemical ligands.

Example 23; SEQ ID NO 127; 186pp; English.

The invention describes a receptor cassette encoding a chimeric receptor
polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
(D) domain of an ecdysone receptor (ECR) of an insect, a ligand binding
(E) domain that is heterologous with respect to the D domain, and an
activation domain. The receptor cassette and method are useful in
regulating the expression of target polypeptides in plants in the
presence of appropriate chemical ligands. The transgenic seeds and plants
can be used for the breeding of improved plant lines that, for e.g.
increase the effectiveness of conventional methods such as herbicide or
pesticide treatment. This is the amino acid sequence of an ecdysone
receptor-VP16 transactivation domain fusion protein.

Sequence 599 AA;

Query Match
Best Local Similarity 94.3%; Score 2895.5; DB 7; Length 599;
Matches 555; Conservative 17; Mismatches 16; Indels 11; Gaps 2;

QY 1 MQQLYVDFSPAFIRYLFAMWYFFRCRSPCCVLVLLQGSATMKLSSIEQACDICKLKL 60
DB 1 MQQLYVDFSPAFIRYLFAMWYFFRCRSPCCVLVLLQGSATMKLSSIEQACDICKLKL 60

QY 61 KCSKEKPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLIPREDLDM 120
DB 61 KCSKEKPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESRLERLEQLFLIPREDLDM 120

QY 121 ILKMDSLQDIKALLTGLFQDNNVNDKAVTDRLASVETDPLTLRQHRISATSSSESSNK 180
DB 121 ILKMDSLQDIKALLTGLFQDNNVNDKAVTDRLASVETDPLTLRQHRISATSSSESSNK 180

QY 181 GORQLTVSTRMRPECVPESTCKNKRKEAQRXDKLPVSTTTVDHMPAIMQCDPPPP 240
DB 181 GORQLTVSTRMRPECVPESTCKNKRKEAQRXDKLPVSTTTVDHMPAIMQCDPPPP 240

QY 241 EAARI-----HVVPRFLTEKMEQNRLKNVTPLSANQKSLIARLVWYQDGEQSEEDL 295
DB 241 EAARILECLQHEVVPFRFLSEKLEMEQNRLKNIPPLTANQOFLIARLVWYQGEYQSEEDL 300

QY 296 KRYVTQWQADBEDESDMPFROITMTILTQVLIVEFAKGLPGFSKISQPDQITLLKAC 355
DB 301 KRYVTQWQLEEBEEBETDMPFROITMTILTQVLIVEFAKGLPGFSKISQSDQITLLKAS 360

QY 356 SSEVMMLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNV 415
DB 361 SSEVMMLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMSMDNV 420

QY 416 HYALLTAIVFSDRPGLEQPOLVEETORYVNTLRVYIMNQHSHASPRCAVIYAKILSVLT 475
DB 421 HYALLTAIVFSDRPGLEQPOLVEETORYVNTLRVYIMNQHSHASPRCAVLFKILGVLT 480

QY 476 ELRTLGMQNSMCISLKNRKLPPFLEEIWV-----KLAPPTDVSLGDELHLHGEDV 529
DB 481 ELRTLGMQNSMCISLKNRKLPPFLEEIWVAEVSTTKLAPPTDVSLGDELHLHGEDV 540

QY 530 AMAHADALDDFDLMDLGDGSPGFTPHDSAPYGALDMADFEFQMTDALGIDEYGG 588
DB 541 AMAHADALDDFDLMDLGDGSPGFTPHDSAPYGALDMADFEFQMTDALGIDEYGG 599

RESULT 11
ABJ05371

ID ABJ05371 standard; protein; 553 AA.

AC ABJ05371;

XX 07-NOV-2002 (first entry)

DE Bcdysone receptor encoded by vector pCGS202 SEQ ID NO: 105.

XX Plant; gene expression control; insect; hormone receptor; fertility;
ecdysonic receptor.

OS Synthetic.

PN WO200261102-A2.

PD 08-AUG-2002.

XX 24-OCT-2001; 2001WO-US051417.

XX 24-OCT-2000; 2000US-0242969P.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

DR WPI; 2002-619259/66.

DR N-PSDB; ABT07353.

XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
regulating expression of target polypeptides in plants in the presence of
appropriate ligands that may be used in controlling plant fertility.

PS Claim 27; Page 258-261; 319pp; English.

CC The present invention relates to a receptor cassette encoding a chimeric
receptor polypeptide comprising at least one DNA binding domain, a hinge
domain of an ecdysone receptor (ECR) of an insect, a ligand binding
domain of an insect ECR, where the ligand binding domain is heterologous
with respect to the hinge domain and an activation domain. The chimeric
insect hormone receptors and receptor cassettes are useful in regulating
expression of target polypeptides in plants in the presence of
appropriate ligands that may be used in controlling plant fertility. The
method is useful for decreasing or increasing plant gene expression. The
present sequence is a protein described in the exemplification of the
invention

XX Sequence 553 AA;

Query Match 88.9%; Score 2731; DB 5; Length 553;

```
Best Local Similarity 95.3%; Pred. No. 2e-221;
Matches 527; Conservative 10; Mismatches 10; Indels 6; Gaps 1;

QY 42 MKLLSSIEQACDICRLKKLCKSKPKCAKCLKNWECRYSPKTRSPTRAHLTEVERSR 101
Db 1 MKLLSSIEQACDICRLKKLCKSKPKCAKCLKNWECRYSPKTRSPTRAHLTEVERSR 60
QY 102 LERLEQLFLIIPREDLMILKMSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDML 161
Db 61 LERLEQLFLIIPREDLMILKMSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDML 120
QY 162 TLROHRISATSSSESSNGKQRLTVSTRMRPECVPESTCKNKRKEAQRKDLPLVS 221
Db 121 TLROHRISATSSSESSNGKQRLTVSTRMRPECVPESTCKNKRKEAQRKDLPLVS 180
QY 222 TTTVDHMPAIMQCDDPPPEAARIHEVVPRPLTEKLMQNRLKNVTPLSANQSLIARLV 281
Db 181 TTTVDHMPAIMQCDDPPPEAARIHEVVPRPLTEKLMQNRLKNVTPLSANQSLIARLV 240
QY 282 WYQGYEQPSEEDLKRVTQWQSADEEDSDMPFRQITMTILTQVLIQVFAKGLPGFS 341
Db 241 WYQGYEQPSEEDLKRVTQWQSADEEDSDMPFRQITMTILTQVLIQVFAKGLPGFS 300
QY 342 KISQPDQITLLKACSEVMMLRVARYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLL 401
Db 301 KISQPDQITLLKACSEVMMLRVARYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLL 360
QY 402 HFCRCWYMSMDNVHYALLTAIVIFSDRPGLEQPOLVEEIQRYVLTNRVYIMNQHSA 461
Db 361 HFCRCWYMSMDNVHYALLTAIVIFSDRPGLEQPOLVEEIQRYVLTNRVYIMNQHSA 420
QY 462 RCVIYAKILSVLTELRTGLMNSNMCIKLNKRLPPFLEEIWDAVETDML 515
Db 421 RCVIYAKILSVLTELRTGLMNSNMCIKLNKRLPPFLEEIWDAVETDML 480
QY 516 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYCALDMADFEFEQ 575
Db 481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYCALDMADFEFEQ 540
QY 576 MFTDALGIDEYGG 588
Db 541 MFTDALGIDEYGG 553

RESULT 12
ADF49177
ID ADF49177 standard; protein; 553 AA.
XX AC ADF49177;
XX DT 12-FEB-2004 (first entry)
XX DE Ecdysone receptor/VPL6 transactivation domain seq id 105.
KW receptor cassette; chimeric receptor polypeptide; DNA binding domain;
KW hinge domain; ecdysone receptor; ECR; ligand binding domain;
KW activation domain; transgenic seed; transgenic plant; plant line;
KW herbicide; pesticide; chimeric ecdysone receptor; ECR;
KW yeast GAL4 DNA binding domain; VPL6 transactivation domain.
XX OS Synthetic.
OS Manduca sexta.
OS Ascomycota.
OS Herpes simplex virus unknown type.
XX PN US2003154509-A1.
XX PP 14-AUG-2003.
XX PR 24-OCT-2001; 2001US-00087167.
XX PR 24-OCT-2001; 2001US-00087167.
XX PR 24-OCT-2001; 2001US-00087167.
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(PASC/) PASCAL E. J.
PA (VALE/) VALENTINE S. A.
PA (BROW/) BROWN J. A.
PA (COCK/) COCKRELL A. S.
XX (JOHN/) JOHNSON B. D.

Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
WPI; 2003-897756/82.

New receptor cassette encoding a chimeric receptor polypeptide, useful
for regulating the expression of target polypeptides in plants in the
presence of appropriate chemical ligands.

Example 11; SEQ ID NO 105; 186pp; English.

The invention describes a receptor cassette encoding a chimeric receptor
polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
(D) domain of an ecdysone receptor (EcR) of an insect, a ligand binding
(E) domain that is heterologous with respect to the D domain, and an
activation domain. The receptor cassette and method are useful in
regulating the expression of target polypeptides in plants in the
presence of appropriate chemical ligands. The transgenic seeds and plants
can be used for the breeding of improved plant lines that, for e.g.
increase the effectiveness of conventional methods such as herbicide or
pesticide treatment. This is the amino acid sequence of an ecdysone
receptor-VPL6 transactivation domain fusion protein.

XX Sequence 553 AA;
QY Query Match 88.9%; Score 2731; DB 7; Length 553;
Db Best Local Similarity 95.3%; Pred. No. 2e-221;
Matches 527; Conservative 10; Mismatches 10; Indels 6; Gaps 1;

QY 42 MKLLSSIEQACDICRLKKLCKSKPKCAKCLKNWECRYSPKTRSPTRAHLTEVERSR 101
Db 1 MKLLSSIEQACDICRLKKLCKSKPKCAKCLKNWECRYSPKTRSPTRAHLTEVERSR 60
QY 102 LERLEQLFLIIPREDLMILKMSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDML 161
Db 61 LERLEQLFLIIPREDLMILKMSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDML 120
QY 162 TLROHRISATSSSESSNGKQRLTVSTRMRPECVPESTCKNKRKEAQRKDLPLVS 221
Db 121 TLROHRISATSSSESSNGKQRLTVSTRMRPECVPESTCKNKRKEAQRKDLPLVS 180
QY 222 TTTVDHMPAIMQCDDPPPEAARIHEVVPRPLTEKLMQNRLKNVTPLSANQSLIARLV 281
Db 181 TTTVDHMPAIMQCDDPPPEAARIHEVVPRPLTEKLMQNRLKNVTPLSANQSLIARLV 240
QY 282 WYQGYEQPSEEDLKRVTQWQSADEEDSDMPFRQITMTILTQVLIQVFAKGLPGFS 341
Db 241 WYQGYEQPSEEDLKRVTQWQSADEEDSDMPFRQITMTILTQVLIQVFAKGLPGFS 300
QY 342 KISQPDQITLLKACSEVMMLRVARYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLL 401
Db 301 KISQPDQITLLKACSEVMMLRVARYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLL 360
QY 402 HFCRCWYMSMDNVHYALLTAIVIFSDRPGLEQPOLVEEIQRYVLTNRVYIMNQHSA 461
Db 361 HFCRCWYMSMDNVHYALLTAIVIFSDRPGLEQPOLVEEIQRYVLTNRVYIMNQHSA 420
QY 462 RCVIYAKILSVLTELRTGLMNSNMCIKLNKRLPPFLEEIWDAVETDML 515
Db 421 RCVIYAKILSVLTELRTGLMNSNMCIKLNKRLPPFLEEIWDAVETDML 480
QY 516 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYCALDMADFEFEQ 575
Db 481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYCALDMADFEFEQ 540
QY 576 MFTDALGIDEYGG 588
Db 541 MFTDALGIDEYGG 553
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RESULT 13
ABJ05379
ID ABJ05379 standard; protein; 620 AA.
XX
XX AC ABJ05379;
XX
XX DT 29-AUG-2003 (revised)
XX DT 07-NOV-2002 (first entry)
XX
XX DE Chimeric ecdysone receptor SEQ ID NO: 137.
XX
XX KW Plant; gene expression control; insect; hormone receptor; fertility;
XX KW ecdysone receptor.
XX
XX OS Manduca sexta.
XX OS Chimeric.
XX
XX PN WO200261102-A2.
XX
XX PD 08-AUG-2002.
XX
XX PF 24-OCT-2001; 2001WO-US051417.
XX
XX PR 24-OCT-2000; 2000US-0242969P.
XX
XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
XX DR WPI; 2002-619259/66.
XX DR N-PSDB; ABT07377.
XX
XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
XX regulating expression of target polypeptides in plants in the presence of
XX appropriate ligands that may be used in controlling plant fertility.
XX
XX Example 25; Page 304-306; 319pp; English.
XX
XX The present invention relates to a receptor cassette encoding a chimeric
XX receptor polypeptide comprising at least one DNA binding domain, a hinge
XX domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
XX domain with respect to the hinge domain and an activation domain. The chimeric
XX insect hormone receptors and receptor cassettes are useful in regulating
XX expression of target polypeptides in plants in the presence of
XX appropriate ligands that may be used in controlling plant fertility. The
XX method is useful for decreasing or increasing plant gene expression. The
XX present sequence is a protein described in the exemplification of the
XX invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 620 AA;
XX
XX Query Match 83.1%; Score 2552; DB 5; Length 620;
XX Best Local Similarity 84.4%; Pred. No. 3.1e-206;
XX Matches 505; Conservative 18; Mismatches 45; Indels 30; Gaps 4;
XX
XX 1 MQQLYVDFSPAFIRYLFAMWYCFRCRSPCLVLLQGSATMKLLSSIEQACDICRLKKL 60
XX
XX 1 MQQLYVDFSPAFIRYLFAMWYCFRCRSPCLVLLQGSATMKLLSSIEQACDICRLKKL 60
XX
XX 61 KCSKEKPKCAKCKNNWECRSPKTRSPFRAHLTEVESRLERLEQLFLIFPREDLDM 120
XX
XX 61 KCSKEKPKCAKCKNNWECRSPKTRSPFRAHLTEVESRLERLEQLFLIFPREDLDM 120
XX
XX 121 ILKMDSLQDIKALLTGLFVQDNVNDKDAVTDRLASVETDMPITLQHRISATSSSESSNK 180
XX
XX 121 ILKMDSLQDIKALLTGLFVQDNVNDKDAVTDRLASVETDMPITLQHRISATSSSESSNK 180
XX
XX 181 GORQLTVSTRMRPECVPESTCKNKRKEKAQREKDKLPVSTTTTVDHHPAIMQCDPPPP 240

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Db 181 GORQLTVSTRMRPECVPESTCKNKRKEKAQREKDKLPVSTTTTVDHHPAIMQCDPPPP 240
Qy 241 EAARIHEVVPRFLTEKLMQNRLKNYTPLSANOKSLIARLVWYODGYEQSPSEEDLKRVTQ 300
Db 241 EAARIHEVVPRFLTEKLMQNRLKNYTPLSANOKSLIARLVWYODGYEQSPSEEDLKRVTQ 300
Qy 301 TWQSADEDEDSMPFRQITEMTILTVQLIVEPAKGLPGFSKISQPDQITLLKACSEVM 360
Db 301 TWQLEEBEETDMPFRQITEMTILTVQLIVEPAKGLPGFSKISQSDQITLLKACSEVM 360
Qy 361 MLRVARRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCWYMSMDNVHYALL 420
Db 361 MLRVARRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCWYMSMDNVHYALL 420
Qy 421 TAIVIFSDRPLGLEPOLVVEIQRYLYLNTLRVYIMNQHSA SPRCAVIYAKILSVLTERTL 480
Db 421 TAIVIFSDRPLGLEPOLVVEIQRYLYLNTLRVYIMNQHSA SPRCAVIYAKILSVLTERTL 480
Qy 481 GMQNSNMCI SLKLNKRLPPFLEEIWDVKLAPPTDVSIGDEL-----HLDG 526
Db 481 GTQNSNMCI SLKLNKRLPPFLEEIWDVAEVSTTKLELATAADPGKTATTTTITSEITT 540
Qy 527 EDVAMAHADAL-----DDFDLMLDGG--DSPGPGFTPHDSA-----PYGALDM 568
Db 541 ETGALEDSLSLAHLQLQPGTDEAEVALGGLGSLDFPSAGKAVLDDEDSFYWPAASFDM 598

RESULT 14
ADF49209
ID ADF49209 standard; protein; 620 AA.
XX
XX AC ADF49209;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX DE Ecdysone receptor/Dof1 transactivation domain seq id 137.
XX
XX KW receptor cassette; chimeric receptor polypeptide; DNA binding domain;
XX KW hinge domain; ecdysone receptor; Ecr; ligand binding domain;
XX KW activation domain; transgenic seed; transgenic plant; plant line;
XX KW herbicide; pesticide; chimeric ecdysone receptor; Ecr;
XX KW yeast GAL4 DNA binding domain; Dof1 transactivation domain.
XX
XX OS Synthetic.
XX OS Manduca sexta.
XX OS Ascomycota.
XX OS Zea mays.
XX
XX PN US2003154509-A1.
XX
XX PD 14-AUG-2003.
XX
XX PF 24-OCT-2001; 2001US-00087167.
XX
XX PR 24-OCT-2001; 2001US-00087167.
XX
XX PA (PASC/) PASCAL E J.
XX PA (VALE/) VALENTINE S A.
XX PA (BROW/) BROWN J A.
XX PA (COCK/) COCKRELL A S.
XX PA (JOHN/) JOHNSON B D.
XX
XX PI Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;
XX
XX WPI; 2003-897756/82.
XX
XX New receptor cassette encoding a chimeric receptor polypeptide, useful
XX for regulating the expression of target polypeptides in plants in the
XX presence of appropriate chemical ligands.
XX
XX Example 25; SEQ ID NO 137; 186pp; English.
XX
XX The invention describes a receptor cassette encoding a chimeric receptor
XX

```

CC polypeptide. The polypeptide comprises a DNA binding (C) domain, a hinge
 CC (D) domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
 CC (E) domain that is heterologous with respect to the D domain, and an
 CC activation domain. The receptor cassette and method are useful in
 CC regulating the expression of target polypeptides in plants in the
 CC presence of appropriate chemical ligands. The transgenic seeds and plants
 CC can be used for the breeding of improved plant lines that, for e.g.,
 CC increase the effectiveness of conventional methods such as herbicide or
 CC pesticide treatment. This is the amino acid sequence of an ecdysone
 CC receptor-Dof1 transactivation domain fusion protein.

XX Sequence 620 AA;

Query Match 83.1%; Score 2552; DB 7; Length 620;
 Best Local Similarity 84.4%; Pred. No. 3.1e-206;
 Matches 505; Conservative 18; Mismatches 45; Indels 30; Gaps 4;

Qy 1 MQQLYVDFSPAFIRYLFAMCYFCRCSPCCVLVLLQGSATMKLLSSIEQACDLCRLKL 60
 Db 1 MQQLYVDFSPAFIRYLFAMCYFCRCSPCCVLVLLQGSATMKLLSSIEQACDLCRLKL 60

Qy 61 KCSKEKPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESLERLEQLFLIFPREDLDM 120
 Db 61 KCSKEKPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESLERLEQLFLIFPREDLDM 120

Qy 121 ILKMDSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDPLTLRQHRISATSSSESSNK 180
 Db 121 ILKMDSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDPLTLRQHRISATSSSESSNK 180

Qy 181 GORQLTVSTRMRPECVVPSTCKNKRKEAQREKDKLPVSTTTVDDHMPAIMQCDPPPP 240
 Db 181 GORQLTVSTRMRPECVVPSTCKNKRKEAQREKDKLPVSTTTVDDHMPAIMQCDPPPP 240

Qy 241 EAARLHEVVPFLTEKLMQNRKNVTPLSANOKSLIARLVYQDGYEQPSEEDLKRVTQ 300
 Db 241 EAARLHEVVPFLTEKLMQNRKNVTPLSANOKSLIARLVYQDGYEQPSEEDLKRVTQ 300

Qy 301 TWQSADEDESDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVM 360
 Db 301 TWQLEEESEETDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVM 360

Qy 361 MLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMDNVHYALL 420
 Db 361 MLRVARRYDAATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMDNVHYALL 420

Qy 421 TAIIVFSRDRPGLEQPOLVEEIQRYLYLTLRVYIMNHSASPRCAVIYAKILSVLTETL 480
 Db 421 TAIIVFSRDRPGLEQPOLVEEIQRYLYLTLRVYIMNHSASPRCAVIFGKILGVLTETL 480

Qy 481 GQNSNMCSLKNRKLPPFLIEIWDVVKLAPPTDVSIGDEL-----HLDG 526
 Db 481 GTQNSNMCSLKNRKLPPFLIEIWDVAEVSSTKLELATAADPGKTATTTTITSEITT 540

Qy 527 EDVAHAHADAL-----DDFDLMDLGDG--DSPGPGFTPHDSA-----PYGALDM 568
 Db 541 ETGALESDSLAHLQLQPGTDEAAEVALGLSLDPPSAGKAVLDDSDSFVWPAASFD 598

RESULT 15

ID ABJ05378 standard; protein; 615 AA.

XX AC ABJ05378;

XX DT 29-AUG-2003 (revised)

XX DT 07-NOV-2002 (first entry)

XX DE Chimeric ecdysone receptor SEQ ID NO: 135.

KW Plant; gene expression control; insect; hormone receptor; fertility;

KW ecdysone receptor.

XX OS Manduca sexta.

OS Manduca sexta.
 OS Chimeric.

PN WO200361102-A2.

XX 08-AUG-2002.

XX 24-OCT-2001; 2001WO-US051417.

XX 24-OCT-2000; 2000US-0242969P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Pascal EJ, Valentine SA, Brown JA, Cockrell AS, Johnson BD;

XX WPI; 2002-619259/66.

XX N-PSDB; ABT07376.

XX New receptor cassette encoding a chimeric receptor polypeptide, useful in
 PT regulating expression of target polypeptides in plants in the presence of
 PT appropriate ligands that may be used in controlling plant fertility.

XX Example 25; Page 299-301; 319pp; English.

XX The present invention relates to a receptor cassette encoding a chimeric
 CC receptor polypeptide comprising at least one DNA binding domain, a hinge
 CC domain of an ecdysone receptor (Ecr) of an insect, a ligand binding
 CC domain of an insect Ecr, where the ligand binding domain is heterologous
 CC with respect to the hinge domain and an activation domain. The chimeric
 CC insect hormone receptors and receptor cassettes are useful in regulating
 CC expression of target polypeptides in plants in the presence of
 CC appropriate ligands that may be used in controlling plant fertility. The
 CC method is useful for decreasing or increasing plant gene expression. The
 CC present sequence is a protein described in the exemplification of the
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 615 AA;

Query Match 83.1%; Score 2551.5; DB 5; Length 615;
 Best Local Similarity 89.8%; Pred. No. 3.3e-206;
 Matches 501; Conservative 11; Mismatches 35; Indels 11; Gaps 3;

Qy 1 MQQLYVDFSPAFIRYLFAMCYFCRCSPCCVLVLLQGSATMKLLSSIEQACDLCRLKL 60

Db 1 MQQLYVDFSPAFIRYLFAMCYFCRCSPCCVLVLLQGSATMKLLSSIEQACDLCRLKL 60

Qy 61 KCSKEKPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESLERLEQLFLIFPREDLDM 120

Db 61 KCSKEKPKCAKCLKNWECRYSPTKRSPLTRAHLTEVESLERLEQLFLIFPREDLDM 120

Qy 121 ILKMDSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDPLTLRQHRISATSSSESSNK 180

Db 121 ILKMDSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDPLTLRQHRISATSSSESSNK 180

Qy 181 GORQLTVSTRMRPECVVPSTCKNKRKEAQREKDKLPVSTTTVDDHMPAIMQCDPPPP 240

Db 181 GORQLTVSTRMRPECVVPSTCKNKRKEAQREKDKLPVSTTTVDDHMPAIMQCDPPPP 240

Qy 241 EAARLHEVVPFLTEKLMQNRKNVTPLSANOKSLIARLVYQDGYEQPSEEDLKRVTQ 300

Db 241 EAARLHEVVPFLTEKLMQNRKNVTPLSANOKSLIARLVYQDGYEQPSEEDLKRVTQ 300

Qy 301 TWQSADEDESDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVM 360

Db 301 TWQLEEESEETDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVM 360

Qy 361 MLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMDNVHYALL 420

Db 361 MLRVARRYDAATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMDNVHYALL 420

Qy 421 TAIIVFSRDRPGLEQPOLVEEIQRYLYLTLRVYIMNHSASPRCAVIYAKILSVLTETL 480

Db 421 TAIIVFSRDRPGLEQPOLVEEIQRYLYLTLRVYIMNHSASPRCAVIFGKILGVLTETL 480

```
Qy 481 GWOHNMCIISLKNRKLPPFLEEIWDV-----KLAPPTDVSLGDEIHLHDGEDVANAH 534
Db 481 GTQNSNMCIISLKNRKLPPFLEEIWDVAEVSTTKL--PKAVRCTGGLFFHRTTTPAHA 538
Qy 535 DALDDFDLMDLGDGDS PG 552
Db 539 ---GETATPMAGGGGGG 553
```

Search completed: April 15, 2005, 14:49:22
Job time : 81 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2005, 14:36:55 ; Search time 47 Seconds
(without alignments)
1203.733 Million cell updates/sec

Title: US-10-087-167-121
Perfect score: 3072
Sequence: 1 MQLLVDFSPAFIRYLPFW.....ADBFQEQMTDALGIDEYGG 588
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1025.5	33.4	878	2 A41055	ecdysone receptor
2	1018	33.1	536	2 A56590	ecdysteroid recept
3	754	24.5	881	1 R8YGA	regulatory protein
4	425.5	14.0	447	2 I38975	nuclear orphan rec
5	426.5	13.9	445	2 A56043	steroid hormone re
6	425	13.8	446	2 I49021	retinoid X recepto
7	423	13.8	446	2 I59354	orphan nuclear rec
8	423	13.8	479	1 IXBELF	alpha trans-induci
9	423	13.8	490	1 IXBEL7	alpha trans-induci
10	406	13.2	461	2 J40114	steroid hormone-nu
11	316.5	10.3	484	2 I49018	retinoid X recepto
12	307	10.0	469	2 A56918	farnesoid x-activa
13	298.5	9.7	490	1 IXBEL33	alpha trans-induci
14	298.5	9.7	490	2 J50689	vitron protein 16
15	284	9.2	448	2 A43786	retinoic acid rece
16	283.5	9.2	448	2 B56558	retinoic acid rece
17	283.5	9.2	459	2 A41977	retinoic acid rece
18	283.5	9.2	464	2 A56558	retinoic acid rece
19	281.5	9.2	448	2 S02827	retinoic acid rece
20	281	9.1	455	2 S13512	retinoic acid rece
21	281	9.1	462	2 S05050	retinoic acid rece
22	280.5	9.1	452	2 S78481	retinoic acid rece
23	280.5	9.1	458	2 S06123	retinoic acid rece
24	280.5	9.1	462	1 A29491	retinoic acid rece
25	280.5	9.1	955	4 C40045	probable transcrip
26	280	9.1	448	2 S05051	retinoic acid rece
27	279.5	9.1	453	2 I50674	retinoic acid rece
28	274.5	8.9	454	2 S06124	retinoic acid rece
29	273.5	8.9	373	2 C36067	thyroid hormone re

ALIGNMENTS

RESULT 1

A41055
ecdysone receptor - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
A:Accession: A41055

R:Koelle, M.R.; Talbot, W.S.; Segraves, W.A.; Bender, M.T.; Cherbas, P.; Hogness, D.S.
Cell 67, 59-77, 1991

A:Title: The Drosophila Ecr gene encodes an ecdysone receptor, a new member of the steroid hormone receptor superfamily

A:Reference number: A41055; MUID:92005697; PMID:1913820
A:Accession: A41055
A:Molecule type: mRNA

A:Residues: 1-878 <KOE>

A:Cross-references: UNIPROT:P34021; GB:M74078; NID:g157317; PIDN:AAA28498.1; PID:g157318

A:Note: The authors also sequenced genomic exon boundaries

C:Comment: mRNA for this receptor is heavily expressed at the end of the third larval in

C:Genetics:

A:Gene: FlyBase:Ecr

A:Cross-references: FlyBase:FBgn0000546

A:Introns: 227/1; 398/3; 446/3; 497/3

C:Superfamily: unassigned erba-related proteins; erba transforming protein homology

C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; zi

F:262-572/Domain: erba transforming protein homology <ERBA>

Query Match 33.4%; Score 1025.5; DB 2; Length 878;
Best Local Similarity 57.9%; Pred. No. 1.6e-61;
Matches 205; Conservative 50; Mismatches 70; Indels 29; Gaps 5;

Qy	191	MRPECVVPSTCKNKRREKAEQREKDLPVSTTT-----VDDHMPALMQ	234
Db	329	MRPECVVPENQCAMKRREKKAQKEKDKNTTSPSSQHGNGSLASGGGQDFVKKEILDLMT	388
Qy	235	CDPPPEBAARIEHVVPFLTEKLMQNRKLNVTPLSANQKSLIARLVWYQGYQPSSEED	294
Db	389	CEPQ-----HATIP-LLPDEILAKQARNIPSLTNQLAVIKLIWYQGYEQPSSEED	441
Qy	295	LKRYTQTWQSDEDESDMPFROIETMTLTVLIVFAKGLPGFKSPKISQPDQITLKA	354
Db	442	LRRL---MSOPDENESQTDVSFRHITITLTVLIVFAKGLPAFTKIPQEDQITLKA	498
Qy	355	CSSEWMLRVARRVDVSDSVLPANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMMDN	414
Db	499	CSSEWMLRVARRVDHSDSIFPANNRSYRDSYKMGAGMADNIEDLLHFCRCMSMKVDN	558
Qy	415	VHYALLTAIVFSDRPGLEQPLVEEIQRYVLTNLTLYVIMNQHSASPRCAVIYAKILSVL	474
Db	559	VEYALLTAIVFSDRPGLEQPLVEEIQRYVLTNLTLYVIMNQHSASPRCAVIYAKILSVL	618
Qy	475	TELTILGQNSMCMISIKLNKRLPPLEETWYKLPAPTDVSLGDELHGDGED	528
Db	619	TELTILGQNSMCMISIKLNKRLPPLEETWYKLPAPTDVSLGDELHGDGED	669

RESULT 2

A56590
ecdysteroid receptor homolog cERH - midge (*Chironomus tentans*)
C:Species: *Chironomus tentans*
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C:Accession: A56590
R:Imhof, M.O.; Rusconi, S.; Lezzi, M.
Insect Biochem. Mol. Biol. 23, 115-124, 1993
A:Title: Cloning of a *Chironomus tentans* cDNA encoding a protein (cERH) homologous to b
A:Reference number: A56590; MUID:93250857; PMID:8485513
A:Accession: A56590
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-536 <IMH>
A:Cross-references: UNIPROT:P49882; GB:S60739; NID:g385893; PID:AA60500.1; PID:g385894
A:Note: Sequence extracted from NCBI backbone (NCBIN:132124, NCBI:P132127)
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; steroid hormone receptor; zinc finger
F:113-432/Domain: erba transforming protein homology <ERBA>

Query Match 33.1%; Score 1018; DB 2; Length 536;
Best Local Similarity 52.4%; Pred. No. 2.6e-61;
Matches 207; Conservative 65; Mismatches 79; Indels 44; Gaps 5;
Qy 138 FQVDNVKDAVTDRLASVETDMLTLRQHRISATSSSESSNKGQRLTVSTRMRPCVV 197
Db 138 FFRSVTKNAVYCKFGHECEMDYMR-----KQECRLKKCLAVGMRPCVV 186
Qy 198 PESTCKNRRKEAQRDKLP-----VSTTV-----DDHMPAIM 233
Db 187 PENCAIKRKEKAKQEKDKVPGIVGNTSSSLLNQSLNGLKNLEISYRELLSQLM 246
Qy 234 QCDPPPEAARIHEVPRFLTEKMEQNLKNVTPLSANQKSLIARLVWYQDGEQSEE 293
Db 247 KCDPPP-----HPMQLLPEKLMENRAGTPTOLTANQVAVIKLIWYQDGEQSEE 299
Qy 294 DLKRVQTQWQSADEDESDMPFRQITWTLTVQVIVFAKGLPGESKIQPDITLLK 353
Db 300 DLKRIT--ELEEEEDQHEANFRYITETILTQVIVFAKGLPAFIPQEDQITLLK 357
Qy 354 ACSSEVMMLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVEDLLHFCRCMYMSMD 413
Db 358 ACSSEVMMLRVARRYDHDSDSILFANNYATYKQTYQLAGMEETIDDLHFCRQYALSID 417
Qy 414 NVHYALLTAIVFSDRPGLEQPOLVEIQRYVNTLRVYINQHSASPRCAVIYAKILSV 473
Db 418 NVEYALLTAIVFSDRPGLEAKEMVDIIQSYVTETLKVIYVNRHGGESRCSQVAKLGI 477
Qy 474 LTELRTLGQNSNMCISLKNRKLPPLEIWDV 508
Db 478 LTELRTMGNKSEMCFSKLNRKLPRFLEWDV 512

RESULT 3

REGYG4
regulatory protein GAL4 - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein P1021; protein YP248C
C:Species: *Saccharomyces cerevisiae*
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: A05022; S61016; S65277; S12977
R:Laughon, A.; Gesteland, R.F.
Mol. Cell. Biol. 4, 260-267, 1984
A:Title: Primary structure of the *Saccharomyces cerevisiae* GAL4 gene.
A:Reference number: A05022; MUID:84141879; PMID:6366516
A:Accession: A05022
A:Molecule type: DNA
A:Residues: 1-881 <LAU>
A:Cross-references: UNIPROT:P04386; EMBL:K01486; NID:g171557; PID:AAA34626.1; PID:g1715
R:Gadnavi, P.L.; Raine, A.R.C.; Alefounder, P.R.; Laue, E.D.
FEBS Lett. 276, 49-53, 1990
A:Title: Complete assignment of the (1)H NMR spectrum and secondary structure of the DNA
A:Reference number: S12977; MUID:91092433; PMID:2265711

A:Contents: annotation; zinc finger

R:Pohl, T.M.

Submitted to the EMBL Data Library, November 1995

A:Reference number: S61010

A:Accession: S61016

A:Molecule type: DNA

A:Residues: 1-881 <POH>

A:Cross-references: EMBL:Z67751; NID:g1061234; PIDN:CAA91596.1; PID:g1061241

R:Pohl, T.M.

Submitted to the Protein Sequence Database, May 1996

A:Reference number: S64899

A:Accession: S65277

A:Molecule type: DNA

A:Residues: 1-881 <POW>

A:Cross-references: EMBL:Z73604; NID:g1370510; PIDN:CAA97969.1; PID:g1370511; GSPDB:GN00

A:Experimental source: strain S288C (AB972)

C:Comment: This protein is a positive regulator for the gene expression of the galactose

C:Genetics:

A:Gene: SGD:YPL248C

A:Cross-references: SGD:S0006169; MIPS:YPL248C

A:Map position: 16L

C:Superfamily: regulatory protein GAL4; GAL4 zinc binuclear cluster homology

C:Keywords: DNA binding; galactose utilization; transcription regulation; zinc finger

F:6-43/Domain: GAL4 zinc binuclear cluster homology <GAL4>

F:11-38/Region: zinc finger CCCC motif

Query Match 24.5%; Score 754; DB 1; Length 881;
Best Local Similarity 38.0%; Pred. No. 3.8e-43;
Matches 208; Conservative 58; Mismatches 129; Indels 152; Gaps 18;
Qy 42 MKLLSIEQAQDCIRLKKLCKSKPKCAKCLKNNECRYSPKTKRSPTRAHLTEVESR 101
Db 1 MKLLSIEQAQDCIRLKKLCKSKPKCAKCLKNNECRYSPKTKRSPTRAHLTEVESR 60
Qy 102 LERLEQLFLIFREDLMLKMDSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDML 161
Db 61 LERLEQLFLIFREDLMLKMDSLQDIKALLTGLFVQDNVKNDAVTDRLASVETDML 120
Qy 162 TLQRHSATSSSESSNKGQRLTVSTRMRPCVVPESTCKNKRKEAQRDKLPVS 221
Db 121 TLQRHSATSSSESSNKGQRLTVSI-----DSAAHNDSTIPLD 162
Qy 222 TTTVD-----DHMPAIMQCDPP----- 238
Db 163 FMRDALHGFDSSEDDMSDGLP-FLKTDNNNGFFGDSLLCLIRSIGKPENYNSNV 221
Qy 239 ---PPEAARIHEVPRFLTEKMEQNLKNVTPLS--ANOKSLIARLVWYQDGEQSEE 293
Db 222 NRLFPTMITDRYTLASRSTTSRL--QSYLNNFHPYCPVHSPTL---MMLYNNQIEIASK 277
Qy 294 DLKRVQTQW-----SADDEDESDMPFRQITWTLTVQVIVFAKGLPGFS 341
Db 278 Q-----WQLFNCLIAIGAWCIEGSTIDIVFYQNAKSHLT-----S 315
Qy 342 KISQPDQITLLKACSEVMMLRVAR-----RYDAVSDSVLFANNOAYTRDNYRKAGMA 394
Db 316 KVPESGSIILVTALH---LLSRVTVQWQKNTSNPHSFIRMAISLGLNRDLPSFSFSDS 372
Qy 395 YVIEDLLHFCRCMYMSMDNVHYALLTAIVFSDRPGLEQPOLVEIQRYVNTLRVYIM 454
Db 373 SILEQRRRIWMSVYSW---EIQLSLTVGRSIQTSQNTISFSSVDDVOR----- 418
Qy 455 NQHSASPRCAVIY-----AKILSVLTTEL---RTLGMQNSNMCI-----SLKKNR 496
Db 419 --TTTGP---TIVHGIETARLLQVFTKIYELDKVTVAEKSPICAKKCLMCNIEEVS 473
Qy 497 KLPPPLE 503
Db 474 QAPKFLQ 480

RESULT 4
138975

nuclear orphan receptor LXR-alpha - human
 C:Species: Homo sapiens (man)
 C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 16-Aug-2004
 C:Accession: U138975
 R:Willy, P.J.; Umesono, K.; Ong, E.S.; Evans, R.M.; Heyman, R.A.; Mangelsdorf, D.J.
 Genes Dev. 9, 1033-1045, 1995
 A:Title: LXR, a nuclear receptor that defines a distinct retinoid response pathway.
 A:Reference number: U138975; MUID:95262897; PMID:7744246
 A:Accession: U138975
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-447 <RES>
 A:CROSS-references: UNIPROT:Q13133; EMBL:U22662; NID:G726512; PID:AAA85856.1; PID:G7265
 C:Superfamily: erba transforming protein homology
 C:Keywords: zinc finger
 F:96-367/Domain: erba transforming protein homology <ERBA>

Query Match 14.0%; Score 429.5; DB 2; Length 447;
 Best Local Similarity 33.6%; Pred. No. 1.4e-21;
 Matches 109; Conservative 56; Mismatches 112; Indels 47; Gaps 9;
 QY 191 MRPECVPESTCKNK--RREKAEQKDKLPVSTTTTVDHMPAINQCDDPPPEAARIHEV 248
 DB 163 MRECVLSEEQIRLKKLRQEEQAHATSLPPRRS-----PP-----QI 202
 QY 249 VPRFTEKLMQNRLKNVTPLSANQKSLIARLVYQDGYEQPSEEDLKRVTQTWQSADE- 307
 DB 203 LPQ-----LSPEQLGMIEKLVAAQOCNRRSFSRDLRVT-PWPAPDP 244
 QY 308 -EDESMPFRQITMTILTVQILVEFAKGLPGFSKISQPDQITLLKACSEVMMRLVAR 366
 DB 245 HSREARQORFAHFTLAIIVSQEIVDFAKLPGFLQSLREDQIALKTSIEVMMLETSR 304
 QY 367 RYDVSDFVFNANQAYTRDNYRKAGM-AVYIEDLLHFCRCMYSMNDNVHALLTAIVI 425
 DB 305 RYNGSEITFLKDFSYNREDFAKAGLQVEFINPFEFSRAMELQNDABFALLIAISI 364
 QY 426 FS-DRPGLQEPOLVEEIQRYLNTLVYIMNQHSAPRCACAVIYAKILSVLTSLRTLGNQ 484
 DB 365 FSADRPNVQDQOVERLQHTYVEALHAYVSIHH---PHDRLMFPRLMKLVSLRTLSVH 421
 QY 485 SNMCISLKNRKLPPPLEEINDV 508
 DB 422 SEQVFAIRLQDKKLPPLLEINDV 445

RESULT 5
 A56043
 steroid hormone receptor-like protein RLD-1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
 C:Accession: A56043
 R:Apfel, R.; Benbrook, D.; Lernhardt, E.; Ortiz, M.A.; Salbert, G.; Pfahl, M.
 Mol. Cell. Biol. 14, 7025-7035, 1994
 A:Title: A novel orphan receptor specific for a subset of thyroid hormone-responsive ele
 A:Reference number: A56043; MUID:95021230; PMID:7935418
 A:Accession: A56043
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-445 <APP>
 A:CROSS-references: UNIPROT:Q62685; GB:U11685; NID:G555751; PID:AAA53633.1; PID:G555752
 A>Note: authors translated the codon GAG for residue 73 as Ser
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: steroid hormone receptor; zinc finger
 F:94-365/Domain: erba transforming protein homology <ERBA>

Query Match 13.9%; Score 426.5; DB 2; Length 445;
 Best Local Similarity 32.9%; Pred. No. 2.3e-21;
 Matches 106; Conservative 57; Mismatches 116; Indels 43; Gaps 7;
 QY 191 MRPECVPESTCKNKREKAEQKDKLPVSTTTTVDHMPAINQCDDPPPEAARIHEV 250
 DB 161 MRECVLSEEQIRLKKLRQEEQAHATSLPPRRS-----PPVSSPPQVLP 202

QY 251 RFLTEKLMQNRLKNVTPLSANQKSLIARLVYQDGYEQPSEEDLKRVTQTWQSADEBD- 309
 DB 203 Q-----LSPEQLGMIEKLVAAQOCNRRSFSRDLRVT-PWPIAPDPQS 244
 QY 310 -EDESMPFRQITMTILTVQILVEFAKGLPGFSKISQPDQITLLKACSEVMMRLVAR 368
 DB 245 REARQORFAHFTLAIIVSQEIVDFAKLPGFLQSLREDQIALKTSIEVMMLETSSRY 304
 QY 369 DAVSDSVLFANQAYTRDNYRKAGM-AVYIEDLLHFCRCMYSMNDNVHALLTAIVIFS 427
 DB 305 NPGSESITFLKDFSYNREDFAKAGLQVEFINPFEFSRAMELQNDABFALLIAISIFS 364
 QY 428 -DRPGLQEPOLVEEIQRYLNTLVYIMNQHSAPRCACAVIYAKILSVLTSLRTLGNQSN 486
 DB 365 ADRENVQDQOVERLQHTYVEALHAYVSIHH---PHDRLMFPRLMKLVSLRTLSVHSE 421
 QY 487 MCISLKNRKLPPPLEEINDV 508
 DB 422 QVFAIRLQDKKLPPLLEINDV 443

RESULT 6
 I49021
 retinoid X receptor interacting protein No.15 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
 C:Accession: I49021
 R:Seol, W.; Choi, H.S.; Moore, D.D.
 Mol. Endocrinol. 9, 72-85, 1995
 A:Title: Isolation of proteins that interact specifically with the retinoid X receptor:
 A:Reference number: A57664; MUID:95280959; PMID:7760852
 A:Accession: I49021
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-446 <RES>
 A:CROSS-references: UNIPROT:Q60644; EMBL:U09419; NID:G691713; PID:AA52164.1; PID:G6917
 C:Genetics:
 A:Gene: RIP15
 C:Superfamily: erba transforming protein homology
 C:Keywords: zinc finger
 F:76-366/Domain: erba transforming protein homology <ERBA>

Query Match 13.8%; Score 425; DB 2; Length 446;
 Best Local Similarity 33.0%; Pred. No. 2.9e-21;
 Matches 107; Conservative 62; Mismatches 125; Indels 30; Gaps 6;
 QY 191 MRPECVPESTCKNKREKAEQKDKLPVSTTTTVDHMPAINQCDDPPPEAARIHEV 250
 DB 145 MRECVLSEEQIRKRIKQKQKQ-----PPPPSEPAASSSGRP 183
 QY 251 RF---LTEKLMQNRLKNVTPLSANQKSLIARLVYQDGYEQPSEEDLKRVTQTWQSADE 307
 DB 184 AASPGTSEASSGSGEGEGITLTAQAQQLVAAQOCNRRSFSQDQKVTTPMLGADP 243
 QY 308 EDEDS-DMPFRQITMTILTVQILVEFAKGLPGFSKISQPDQITLLKACSEVMMRLVAR 366
 DB 244 QSRDARQORFAHFTLAIIVSQEIVDFAKVPGFLQGREQIALKASTIEIMLETAR 303
 QY 367 RYDVSDFVFNANQAYTRDNYRKAGM-AVYIEDLLHFCRCMYSMNDNVHALLTAIVI 425
 DB 304 RYNHETECITFLKDFSYNREDFAKAGLQVEFINPFEFSRAMELQNDABFALLIAINI 363
 QY 426 FS-DRPGLQEPOLVEEIQRYLNTLVYIMNQHSAPRCACAVIYAKILSVLTSLRTLGNQ 484
 DB 364 FSADRPNVQDQOVERLQHTYVEALHAYVSIHH---PHDRLMFPRLMKLVSLRTLSVH 420
 QY 485 SNMCISLKNRKLPPPLEEINDV 508
 DB 421 SEQVFAIRLQDKKLPPLLEINDV 444

RESULT 7

Db 247 TTKCREK-----TELTAQOQTLL---LDYIMDSYNKQRMPOEITNKKLKEEFSAE 293
 Qy 307 EEDSDMPFRQITEMTILTVQLIVFAKGLPGFSKISQPPQITLLKKACSEVMMLRVAR 366
 Db 294 EN-----FLILTEMATSHVQILVEPTKKLPGFQTLDHEDQIALLKGSAAVEAMFLRSAE 346
 Qy 367 RYDAVSDSVLFANNOAYTRDNYRKAGMA-YVIEDLLHFCRCMYSMGMDNVHVALTAIVI 425
 Db 347 ----IFNKKLPAGHADLLERIKSGISDEYITPMFSFYKSGVGLKMTQEEVALLTAIVI 402
 Qy 426 FS-DRPGLQPOLVEEIQRYLYNTLRVYIMNHQSASPRCAVIYAKILSVLTLERTLGMQN 484
 Db 403 LSPDRQYIKDREAVEKIQEPLLDVLQKLCKMYQENPQ---HFACLLGRLTLELRTFNHHH 459
 Qy 485 SNMCISLKLKNRKLPPLPFEIWDVK 509
 Db 460 AEMLSMRVNDHKFTPLLCIWDVQ 484

 RESULT 12
 A:56918
 C:farnesoid x-activated receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
 C:Accession: A56918
 E:Forman, B.M.; Goode, E.; Chen, J.; Oro, A.E.; Bradley, D.J.; Perlmann, T.; Nien
 Cell 81, 687-695, 1995
 A:Title: Identification of a nuclear receptor that is activated by farnesol me
 A:Reference number: A56918; MUID:95292336; PMID:7774010
 A:Accession: A56918
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-469 <FOR>
 A:Cross-references: UNIPROT:Q62735; GB:U18374; NID:g868031; PIDN:AAC52205.1; P
 C:Superfamily: unassigned erba-related proteins; erba transforming protein hom
 C:Keywords: DNA binding; nucleus; zinc finger
 F:122-390/Domain: erba transforming protein homology <ERBA>

 Query Match 10.0%; Score 307; DB 2; Length 469;
 Best Local Similarity 30.0%; Pred. No. 3e-13; Gaps 12
 Matches 98; Conservative 56; Mismatches 119; Indels 54; Gaps 12

 Qy 191 MRPECVVPSTCKNKRKEAQRKDKLPVSTTTVDDHMPALMQCDPPPEAARIHEVVP 250
 Db 189 MIAECLLTETQCKSKRLRNKVKQHADQ-----TVNE-----DSEGRDLRQVTS 231
 Qy 251 RFLTEKLMEQNRLKNVTPLSANQKSLIARLVVYQDGY--EOPSEBDLKRVTOTWQSADBE 308
 Db 232 ---TTKLCREK-----TELTVDQOQTLL---LDYIMDSYSKQRMPOEITNKKLKEEFSAEEN 280
 Qy 309 DEDSDMPFRQITEMTILTVQLIVFAKGLPGFSKISQPPQITLLKACSEVMMLRVARY 368
 Db 281 ----FLILTEMATSHVQILVEPTKKLPGFQTLDHEDQIALLKGSAAVEAMFLRSAB--- 331
 Qy 369 DAVSDSVLFANNOAYTRDNYRKAGMA-YVIEDLLHFCRCMYSMGMDNVHVALTAIVTFS 427
 Db 332 --IFNKKLPAGHADLLERIKSGISDEYITPMFSFYKSGVGLKMTQEEVALLTAIVILS 389
 Qy 428 -DRGLQPOLVEEIQRYLYNTL-----RVYIMNHQSASPRCAVIYAKILSVLTLERTLGM 482
 Db 390 PDROYIKDREAVEKIQEPLLDVLQKLCKIY-----OPENPQHFACLGRLTLELRTFNH 442

```

DB      463 HHAEMLNSWRVNDHKFTPLLCEIWDVQ   469
          *::|:::|||||
RESULT 13
IXB833
alpha trans-acting protein - human herpesvirus 2 (strain 333)
N;Alternate names: virion transactivator protein Vmw65
C;Species: human herpesvirus 2
A;Note: host Homo sapiens (man)
```

C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 16-Feb-1997

A:Accession: A41562
R:Greaves, R.F.; O'Hare, P.
J. Virol. 65, 6705-6713, 1991
A:Title: Sequence, function, and regulation of the Vmw65 gene of herpes simplex virus type 1
A:Reference number: A41562; MUID:92046332; PMID:1658370
A:Accession: A41562
A:Molecule type: DNA
A:Residues: 1-490 <R>
A:Cross-references: GB:M75098
A:Superfamily: herpesvirus alpha trans-inducing protein
C:Keywords: DNA binding; trans-inducing protein; transcription

Query Match 9.7%; Score 298.5; DB 1; Length 490;
Best Local Similarity 74.4%; Pred. No. 1.2e-12;
Matches 58; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

Qy 511 APPTDVSIGDLHLDGEDVAMAHADALDDFDLMLGDSGSPGFTPHDSAPYCALDMAD 570

Db 414 APITDVSIGDELRLDGEEDVMTPADALDDFLEMLGDVESPSPGWT-HDPVSYGALDVDD 472

Qy 571 FEFQMFTDALGIDYGG 588

Db 473 FEFQMFTDAMGIDDFGG 490

RESULT 14

JS0689
virion protein 16 - human herpesvirus 2
C:Species: human herpesvirus 2
C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 26-Aug-1999
A:Accession: JS0689
R:Crass, A.; Triesenberg, S.J.
Gene 103, 235-238, 1991
A:Title: Nucleotide and deduced amino acid sequences of the gene encoding virion protein 16
A:Reference number: JS0689; MUID:91365250; PMID:1653757
A:Accession: JS0689
A:Molecule type: DNA
A:Residues: 1-490 <R>
A:Cross-references: GB:M60050; NID:G330317; PIDN:AAA45863.1; PID:G330318
A:Experimental source: strain HG52
C:Superfamily: herpesvirus alpha trans-inducing protein
C:Keywords: DNA binding; transcription regulation

Query Match 9.7%; Score 298.5; DB 2; Length 490;
Best Local Similarity 74.4%; Pred. No. 1.2e-12;
Matches 58; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

Qy 511 APPTDVSIGDLHLDGEDVAMAHADALDDFDLMLGDSGSPGFTPHDSAPYCALDMAD 570

Db 414 APITDVSIGDELRLDGEEDVMTPADALDDFLEMLGDVESPSPGWT-HDPVSYGALDVDD 472

Qy 571 FEFQMFTDALGIDYGG 588

Db 473 FEFQMFTDAMGIDDFGG 490

RESULT 15

A43786
retinoic acid receptor beta-4 - chicken
C:Species: Gallus gallus (chicken)
C>Date: 11-Dec-1992 #sequence_revision 30-Jan-1993 #text_change 09-Jul-2004
A:Accession: A43786; S14291; A60129; S17072; S16243
R:Smith, S.M.; Eichele, G.
Development 111, 245-252, 1991
A:Title: Temporal and regional differences in the expression pattern of distinct retinoic acid receptors
A:Reference number: A43786; MUID:91199956; PMID:1849811
A:Accession: A43786
A:Molecule type: mRNA
A:Residues: 1-448 <SMI>
A:Cross-references: UNIPROT:P22448; GB:X59473; NID:G63753; PIDN:CAA42077.1; PID:G63754
A>Note: the authors translated the codon ACT for residue 96 as Ser, TCC for residue 167
R:Noji, S.; Nohno, T.; Koyama, E.; Muto, K.; Ohya, K.; Aoki, Y.; Tamura, K.; Ohnogi, K.

Nature 350, 83-86, 1991

A:Title: Retinoic acid induces polarizing activity but is unlikely to be a morphogen in the chicken embryo
A:Reference number: S14291; MUID:91163640; PMID:1848357
A:Accession: S14291
A:Molecule type: mRNA
A:Residues: 1-95; 'S', '97-448 <NOJ>
A:Cross-references: EMBL:X57340; NID:G62976; PIDN:CAA40616.1; PID:G62977
R:Rowe, A.; Richman, J.M.; Brickell, P.M.
Development 111, 1007-1016, 1991
A:Title: Retinoic acid treatment alters the distribution of retinoic acid receptor-beta
A:Reference number: A60129; MUID:91347912; PMID:1652423
A:Accession: A60129
A:Molecule type: mRNA
A:Residues: 23-24, 26-95; 'S', '97-165; 'D', '167-448 <ROW>
A:Cross-references: GB:563196; NID:G234370; PIDN:AAB19628.1; PID:G234371
R:Nohno, T.
submitted to the EMBL Data Library, January 1991
A:Reference number: S17072
A:Accession: S17072
A:Molecule type: mRNA
A:Residues: 15-95; 'S', '97-434 <NOH1>
A:Cross-references: EMBL:X57339
R:Nohno, T.; Muto, K.; Noji, S.; Saito, T.; Taniguchi, S.
Biochim. Biophys. Acta 1089, 273-275, 1991
A:Title: Isoforms of retinoic acid receptor beta expressed in the chicken embryo.
A:Reference number: S16243; MUID:91274365; PMID:1647216
A:Accession: S16243
A:Molecule type: mRNA
A:Residues: 15-60 <NOH2>
A:Cross-references: EMBL:X57339
C:Superfamily: retinoic acid receptor alpha; erba transforming protein homology
C:Keywords: alternative splicing; DNA binding; zinc finger
F:79-330/Domain: erba transforming protein homology <ERBA>
F:81-101/Region: zinc finger
F:117-141/Region: zinc finger

Query Match 9.2%; Score 284; DB 2; Length 448;

Best Local Similarity 22.8%; Pred. No. 1e-11;

Matches 119; Conservative 80; Mismatches 159; Indels 164; Gaps 19;

Qy 110 LLIFPREDDMLKMDPS---LQD--IKALITGLFVQDNVNKDAVTDRLASVETDMLTLR 164

Db 8 LAVSPAQMLEDFTATSPSSCMLQKALKACFSGL-----AQTEW----- 45

Qy 165 QHRISATS-----SSEE-----SSN-----KG-- 181

Db 46 QHRHSAQSVETQSTSEELVPSPPPLPPRVKPCVCQDKSGSYHYGVTAECGCKGFF 105

Qy 182 ---QRLTVSTRMRPECVVPEST-----C-----KNKREKEAQR 213

Db 106 RRSIQKNWVYTCRDKNVCINKVTRNCQYCRLOKCEVGSKESVENDRNKKKKEPTKQ 165

Qy 214 EKDKLPVSTTTVDHMPAIMQCDDPPPEAAAIHEVVRFLTEKLMQNRLKNVTPLSANQ 273

Db 166 ESTENYEMTAELDD-----LTKIRK-----AQTEW-----AHQ 189

Qy 274 KSLLIARLVWYQDGYEQPSEEDLKRVTQTWOSADEDESDMPFRQITMTILTTLVQLIVEP 333

Db 190 ETF-----PSCQLGKYT--TNSADHRVRLDLGLWDFSELATKCIKIVEF 235

Qy 334 AKGLPGFSKISQPDQITLLKACSVVMMLRVARRYDAVSDVLFANNQAVTRDNRKAGM 393

Db 236 AKLPGFSTLTADQITLLKAACDLILILICITRYTPEQDTMTFSDGLTLNRTQMHNAGF 295

Qy 394 AYVIEDLLHFCRCMYMSMDNVHALLTAI-VTFSDRPGLEQPOLVBEIQRYYINTURVY 452

Db 296 GPLTDLVFTFANQLLPLEMDDTETGLLSAICLCIGDRQDLEEPKVKDKLQEPLEALKIY 355

Qy 453 IMNQHSNPRCAVIYAKILSVLTETRLTGLNQSNMWCISLKL-NRKLPPFLEEINWVLA 511

Db 356 IRKRERNPKPH---MFPKILMKITDLRSISAKGAERVTLLKQWIPGSMPLIQEMLNSEG 412

Qy 512 --PPTDVSIGDELHLDGEDVAMAHADALDDFDLMLGDSGDS 551

Db 413 HEPLTPTSGN-----TAHSPSISPSVDNSSVSQSP 445

Search completed: April 15, 2005, 14:47:56
Job time : 48 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2005, 14:36:56 ; Search time 77 Seconds
(without alignments)
3910.423 Million cell updates/sec

Title: US-10-087-167-121
Perfect score: 3072
Sequence: 1 MQLYVDFSPAFIRYLPFW.....ADFFEQMTDALGIDYGG 588

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1557	50.7	556	1 ECR MANSE	P49883 manduca sex
2	1552.5	50.5	518	2 Q8MYA7	Q8MYA7 chilo suppr
3	1552.5	50.5	547	2 Q8MYA6	Q8MYA6 chilo suppr
4	1525.5	49.7	541	2 Q6RVD3	Q6RVD3 plodia inte
5	1504	49.0	339	2 Q9U0R9	Q9U0R9 junonia coe
6	1470.5	47.9	576	1 ECR HELVI	O18473 heliothis v
7	1467	47.8	513	2 Q77240	O77240 choriostoneu
8	1467	47.8	541	2 Q77255	O77255 choriostoneu
9	1418	46.2	346	2 Q9U3U4	Q9U3U4 bicyclus an
10	1416	46.1	606	1 ECR BOMMO	P49881 bombyx mori
11	1142	37.2	680	2 Q9U3Y4	Q9U3Y4 aedes albop
12	1139	37.1	675	1 ECR ASDAE	P49880 aedes aegypt
13	1139	37.1	776	2 Q6VA69	Q6VA69 aedes aegypt
14	1050	34.2	757	1 ECR LUCCU	O18531 lucilia cup
15	1046	34.0	784	2 Q9GPH1	Q9GPH1 calliphora
16	1033	33.6	673	2 Q76827	Q76827 ceratitis c
17	1025.5	33.4	878	1 ECR DROME	P34021 drosophila
18	1018	33.1	536	1 ECR CHITE	P49882 chironomus
19	1003	32.6	520	2 Q7PVB2	Q7PVB2 anopheles g
20	867.5	28.2	541	2 Q97095	Q97095 locusta mig
21	864.5	28.1	491	2 Q02035	Q02035 tenebrio mo
22	754	24.5	881	1 GAL4 YEAST	P04386 saccharomyc
23	754	24.5	881	2 Q76MW9	Q76MW9 drosophila
24	753.5	24.5	518	2 Q76246	Q76246 uca pugilat
25	749	24.4	444	2 Q44336	Q44336 amblyomma a
26	749	24.4	560	2 Q44337	Q44337 amblyomma a
27	749	24.4	570	2 Q44338	Q44338 amblyomma a
28	732	23.8	336	2 Q6RIB4	Q6RIB4 carcinus ma
29	685	22.3	403	2 Q8MWR2	Q8MWR2 trichoptera
30	663	21.6	212	2 Q8MWR0	Q8MWR0 trichoptera
31	497	16.2	182	2 Q8NGU6	Q8NGU6 sarcophaga

32	495	16.1	181	2	Q75ZW2	Q75ZW2 lucilia ser
33	463	15.1	207	2	Q9XYR8	Q9XYR8 bradyzia hy
34	433.5	14.1	402	2	Q8IWI3	Q8IWI3 homo sapien
35	433.5	14.1	447	1	NRH3 HUMAN	Q13133 homo sapien
36	428.5	13.9	445	2	Q91X41	Q91X41 mus musculu
37	427.5	13.9	445	1	NRH3 MOUSE	Q940Y9 mus musculu
38	426.5	13.9	445	1	NRH3 RAT	Q62685 ratu mus norv
39	425	13.8	443	2	Q8BP65	Q8BP65 mus musculu
40	425	13.8	446	1	NRH2 MOUSE	Q60644 mus musculu
41	423	13.8	446	1	NRH2 RAT	Q62755 ratu mus norv
42	423	13.8	479	1	ATIN_HHVL	P04486 human herpe
43	423	13.8	490	1	ATIN_HHVL	P04492 human herpe
44	418.5	13.6	409	2	Q8JHUI	Q8JHUI gallus gall
45	416.5	13.6	409	2	Q8AXU8	Q8AXU8 gallus gall

ALIGNMENTS

RESULT 1

ID	ECR MANSE	STANDARD	PRT	556 AA
AC	P49883			
DT	01-OCT-1996	(Rel. 34, Created)		
DT	01-OCT-1996	(Rel. 34, Last sequence update)		
DT	05-JUL-2004	(Rel. 44, Last annotation update)		
DE	Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone receptor) (20E receptor).			
DE	receptor) (20E receptor).			
GN	Name=ECR; Synonyms=NR1H1;			
OS	Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;			
OX	Sphingidae; Sphinginae; Manduca.			
OX	NCBI_TaxID=7130;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95360028; PubMed=7633469; DOI=10.1016/0965-1748(95)00023-O;			
RA	Fujiwara H., Jindra M., Newitt R., Palli S.R., Hiruma K.,			
RA	Riddiford L.M.;			
RT	"Cloning of an ecdysone receptor homolog from Manduca sexta and the developmental profile of its mRNA in wings."			
RL	Insect Biochem. Mol. Biol. 25:845-856(1995).			
CC	-!- FUNCTION: Receptor for ecdysone. Binds to ecdysone response elements (ECRES).			
CC	-!- SUBCELLULAR LOCATION: Nuclear.			
CC	-!- TISSUE SPECIFICITY: It is found in both larval wing disks and pupal wings and in prothoracic glands.			
CC	-!- DEVELOPMENTAL STAGE: In the wing disks levels increase on day 2 sharply on day 6. In the prothoracic glands levels increase sharply on day 2 then remain high throughout the larval-pupal transformation and after pupal ecdysis.			
CC	-!- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI subfamily.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U19812; AAA86699.1; -			
DR	HSPF; P20393; IAGY.			
DR	InterPro; IPR000536; Hrmn_recept_lig.			
DR	InterPro; IPR001723; Stdhrmn_recept.			
DR	InterPro; IPR008946; Str_ncl_receptor.			
DR	InterPro; IPR001628; Znf_C4steroid.			
DR	Pfam; PF00104; Hormone_recep; 1.			
DR	Pfam; PF00105; zf-C4; 1.			
DR	PRINTS; PR00398; STRDHORMONER.			
DR	PRINTS; PR00047; STROIDFINGER.			

```

DR ProDom; PD000035; Znf C4steroid; 1.
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
FT DOMAIN 1 146 Modulating (Potential).
FT DNA BIND 147 212 Nuclear receptor-type.
FT ZN_FING 147 207 C4-type.
FT ZN_FING 183 207 C4-type.
FT DOMAIN 305 528 Hormone-binding (Potential).
FT DOMAIN 75 84 Poly-Gln.
FT DOMAIN 258 261 Poly-Pro.
FT DOMAIN 326 332 Poly-Glu.
SQ SEQUENCE 556 AA; 62830 MW; 9AF83AA33D551EB1 CRC64;

Query Match 50.7%; Score 1557; DB 1; Length 556;
Best Local Similarity 91.2%; Pred. No. 2.4e-92;
Matches 300; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 191 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPPEAARIHEVVP 250
DB 212 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPPEAARIHEVVP 271

QY 251 RFLTEKLEQNRLKNVTPLSANQSLIARLVYQGYEQPSEEDLKRVTTQWQSADEDE 310
DB 272 RFLTEKLEQNRLKNVTPLSANQSLIARLVYQGYEQPSEEDLKRVTTQWQLEEEEEE 331

QY 311 DSDMPFRQITMTILTVLIQVEFAKGLPGFSKISQPDQITLLKACSSVMMRLVARYDA 370
DB 332 ETDMPFRQITMTILTVLIQVEFAKGLPGFSKISQSDQITLLKACSSVMMRLVARYDA 391

QY 371 VSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHYALLTAIVIFSDRP 430
DB 392 ATDSVLFANNOAYTRDNYRKAGMSVIEDLLHFCRCMYSMSMDNVHYALLTAIVIFSDRP 451

QY 431 GLEQQLVEEQRYLYNLTRVYIMNQHSAPRCVAVIYAKILSVLTSLTELTLGQNSMNCIS 490
DB 452 GLEQQLVEEQRYLYNLTRVYIMNQHSAPRCVAVLFGKILGVLTELTLGTONSMNCIS 511

QY 491 LKLNKRLPPPLEEIIWDVYKLAPPTDVSIG 519
DB 512 LKLNKRLPPPLEEIIWDVAEVSTTQPTFG 540

RESULT 2
Q8MYA7 PRELIMINARY; PRT; 518 AA.
AC Q8MYA7;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Ecdysone receptor A isoform.
GN Name=C8EcR-A;
OS Chilo suppressalis.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
OC Pyralidae; Crambinae; Chilo.
OX NCBI_TaxID=168631;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fat body;
RX MEDLINE=2202197; PubMed=12213236; DOI=10.1016/S0965-1748(02)00036-X;
RA Minakuchi C., Nakagawa Y., Kiuchi M., Tomita S., Kamimura M.;
RT "Molecular cloning, expression analysis and functional confirmation of
two ecdysone receptor isoforms from the rice stem borer Chilo
suppressalis.";
RL Insect Biochem. Mol. Biol. 32:999-1008(2002).
CC -|- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -|- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AB067811; BAC11713.1; -.
DR HSSP; P34021; 1R00.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:0005496; F:steroid binding; IEA.

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DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003069; Ecdystd receptor.
DR InterPro; IPR00536; Hrmn_recept_lig.
DR InterPro; IPR001723; Strdhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR01283; ECDYSTEROIDR.
DR PRINTS; PR00398; STRDHOMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SMO0430; HOLI; 1.
DR SMART; SMO0399; Znf C4; 1.
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 518 AA; 58320 MW; 5E757803E248E118 CRC64;

Query Match 50.5%; Score 1552.5; DB 2; Length 518;
Best Local Similarity 85.0%; Pred. No. 4.3e-92;
Matches 301; Conservative 18; Mismatches 12; Indels 23; Gaps 2;

QY 191 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPPEAARI----- 245
DB 178 MRPECVPETTCARKEKKAQRKDKLPVSTTTVDHMPPIQCDDPPPPPEAARILECLQ 237

QY 246 HEVVPFLTEKLEQNRLKNVTPLSANQSLIARLVYQGYEQPSEEDLKRVTTQWQSA 305
DB 238 HEVVPFLSEKLEQNRLKNIPLTANQQILARLVYQGYEQPSEEDLKRVTTQWQSN 297

QY 306 DEDESDMPFRQITMTILTVLIQVEFAKGLPGFSKISQPDQITLLKACSSVMMRLVA 365
DB 298 EDEEETDLFPRQITMTILTVLIQVEFAKGLPGFSKISQPDQITLLKACSSVMMRLVA 357

QY 366 RRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHYALLTAIVI 425
DB 358 RRYDAASDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSLSMDNVHYALLTAVVI 417

QY 426 FSDRPGLEQPOLVEEQRYLYNLTRVYIMNQHSAPRCVAVIYAKILSVLTSLTELTLGQNS 485
DB 418 FSDRPGLEQPOLVEEQRYLYNLTRVYIMNQHSAPRCVAVIYAKILSVLTSLTELTLGQNS 477

QY 486 NMCISLKNRKLPPPLEEIIWDVYKLAPPTDVSIGDELHLDGEDVMAHADALDD 539
DB 478 NMCISLKNRKLPPPLEEIIWDV-----ADVSAAQAAPIMD 513

RESULT 3
Q8MYA6 PRELIMINARY; PRT; 547 AA.
AC Q8MYA6;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Ecdysone receptor B1 isoform.
GN Name=C8EcR-B1;
OS Chilo suppressalis.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
OC Pyralidae; Crambinae; Chilo.
OX NCBI_TaxID=168631;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fat body;
RX MEDLINE=2202197; PubMed=12213236; DOI=10.1016/S0965-1748(02)00036-X;
RA Minakuchi C., Nakagawa Y., Kiuchi M., Tomita S., Kamimura M.;
RT "Molecular cloning, expression analysis and functional confirmation of
two ecdysone receptor isoforms from the rice stem borer Chilo
suppressalis.";
RL Insect Biochem. Mol. Biol. 32:999-1008(2002).
CC -|- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -|- SIMILARITY: Belongs to the nuclear hormone receptor family.

```

DR EMBL; AB067812; BAC11714.1; --
 DR HSP; P34021; IROO.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
 DR GO; GO:0005496; F:steroid binding; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003069; Ecdysd receptor.
 DR InterPro; IPR005336; Htrmn recept lig.
 DR InterPro; IPR001723; Stdhrmn receptor.
 DR InterPro; IPR008946; Str ncl-receptor.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR Pfam; PF00104; Hormone_recep; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR01283; ECDYSTEROIDR.
 DR PRINTS; PR00398; STRDHORMONER.
 DR PRINTS; PR00047; STROIDFINGER.
 DR ProDom; PD000035; Znf_C4steroid; 1.
 DR SMART; SM00430; HOLI; 1.
 DR SMART; SM00399; Znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
 DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
 KW Transcription regulation; Zinc; Zinc-finger.
 SQ SEQUENCE 547 AA; 61815 MW; 33528572066256E CRC64;

Query Match 50.5%; Score 1552.5; DB 2; Length 547;
 Best Local Similarity 85.0%; Pred. No. 4.6e-92;
 Matches 301; Conservative 18; Mismatches 12; Indels 23; Gaps 2;

QY 191 MRPCVPESTCKNKRKEKAQREKDKLPVSTTTVDHMPAQMCDPPPPPEAARI----- 245
 DB 207 MRPCVPESTCKNKRKEKAQREKDKLPVSTTTVDHMPAQMCDPPPPPEAARI----- 266

QY 246 HGVPRFLTEKMEQNRKLNVTPLSANOKSLIARLVWYQDGEQSEEDLKRVTQWOSA 305
 DB 267 HGVPRFLTEKMEQNRKLNVTPLSANOKSLIARLVWYQDGEQSEEDLKRVTQWOSA 326

QY 306 DEEDSDMPFRQITTEMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVMMLRVA 365
 DB 327 DEEDSDMPFRQITTEMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVMMLRVA 386

QY 366 RYDAVSQVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVI 425
 DB 387 RYDAVSQVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVI 446

QY 426 FSDRGLQPOLVEIQRYLNTLRVYIMNQHSAASPRCAVYAKILSVLTETLGMONS 485
 DB 447 FSDRGLQPOLVEIQRYLNTLRVYIMNQHSAASPRCAVYAKILSVLTETLGMONS 506

QY 486 NMCISLKNRKLPPFLBEIWDVVKLAPPTDVSGLDELHGDVAMAHADALDD 539
 DB 507 NMCISLKNRKLPPFLBEIWDV-----ADVSAQAQAIMD 542

RESULT 4

Q6RVD3
 ID Q6RVD3 PRELIMINARY; PRT; 541 AA.
 AC Q6RVD3;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Ecdysone receptor.
 OS Plodia interpunctella (Indianmeal moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
 OC Pyralidae; Phycitinae; Plodia.
 OX NCBI_TaxID=58824;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Siaussat D., Debernard S., Bozzolan F., Queguiner I., Porcheron P.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.

RESULT 5

Q9U0R9
 ID Q9U0R9 PRELIMINARY; PRT; 339 AA.
 AC Q9U0R9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Ecdysteroid receptor (Fragment).
 GN Name=ecr;
 OS Junonia coenia (Peacock butterfly) (Precis coenia).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Papilionidae; Nymphalidae; Nymphalinae; Junonia.
 OX NCBI_TaxID=39708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Wing;
 RA Reinhardt R.K., Weber P., Koch P.B.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY489269; AAR84611.1; --
 DR HSP; P20393; 1A6Y.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
 DR GO; GO:0005496; F:steroid binding; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003069; Ecdysd receptor.
 DR InterPro; IPR005336; Htrmn recept lig.
 DR InterPro; IPR001723; Stdhrmn receptor.
 DR InterPro; IPR008946; Str ncl-receptor.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR Pfam; PF00104; Hormone_recep; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR01283; ECDYSTEROIDR.
 DR PRINTS; PR00398; STRDHORMONER.
 DR PRINTS; PR00047; STROIDFINGER.
 DR ProDom; PD000035; Znf_C4steroid; 1.
 DR SMART; SM00430; HOLI; 1.
 DR SMART; SM00399; Znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
 DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
 KW Transcription regulation; Zinc; Zinc-finger.
 SQ SEQUENCE 541 AA; 61030 MW; 1455888E2EFA07AD CRC64;

Query Match 49.7%; Score 1525.5; DB 2; Length 541;
 Best Local Similarity 88.0%; Pred. No. 2.5e-90;
 Matches 294; Conservative 16; Mismatches 17; Indels 7; Gaps 2;

QY 191 MRPCVPESTCKNKRKEKAQREKDKLPVSTTTVDHMPAQMCDPPPPPEAARIHEVVP 250
 DB 208 MRPCVPESTCKNKRKEKAQREKDKLPVSTTTVDHMPAQMCDPPPPPEAARIHEVVP 267

QY 251 RFLTEKMEQNRKLNVTPLSANOKSLIARLVWYQDGEQSEEDLKRVTQWOSA 310
 DB 268 RFLTEKMEQNRKLNVTPLSANOKSLIARLVWYQDGEQSEEDLKRVTQWOSA 327

QY 311 DSDMPFRQITTEMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVMMLRVARRYDA 370
 DB 328 --DMPFRQITTEMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVMMLRVARRYDA 385

QY 371 VDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVIFSDRP 430
 DB 386 ATDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVIFSDRP 445

QY 431 GLEQPOLVEEQRYLNTLRVYIMNQHSAASPRCAVYAKILSVLTETLGMONS 490
 DB 446 GLEQPOLVEEQRYLNTLRVYIMNQHSAASPRCAVYAKILSVLTETLGMONS 505

QY 491 LKLNKRKLPPFLBEIWDVVKLAPPTDVSGLDELH 524
 DB 506 LKLNKRKLPPFLBEIWDV-----ADVSTAQQLPL 534

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CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC EMBL: AJ251809; CAB63485.1; -.
DR HSSP; P34021; IROO.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:0005496; F:steroid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003699; Ecdystd_receptor.
DR InterPro; IPR000536; Hrmn_recept_lig.
DR InterPro; IPR001723; Strdhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; Zf-C4; 1.
DR PRINTS; PR01283; ECDYSTEROIDR.
DR PRINTS; PR00398; STRDHOMONER.
DR SMART; SM00430; HOL1; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39363 MW; 3EC1C7AD294782EB CRC64;

Query Match 49.0%; Score 1504; DB 2; Length 339;
Best Local Similarity 89.6%; Pred. No. 3.3e-89;
Matches 283; Conservative 22; Mismatches 11; Indels 0; Gaps 0;

QY 191 MRPECVPESTCKNKRKEKAQREKDKLPVSTTTVDHMPAIMQCDDPPPPAAARIHEVVP 250
DB 24 MRPECVPESTCKNKRKEKAQREKDKLPVSTTTVDHMPIMQCDDPPPPAAARIHEVVP 83

QY 251 RFLTEKLMQNRLKNVTPLSANOKSLIARLVWYQGYEQPSDEDLKRVTTQTWQSADEDE 310
DB 84 RFLTEKLMQNRLKNVTPLSANOKSLIARLVWYQGYEQPSDEDLKRVTTQTWQSADEDE 143

QY 311 DSDMPFROITTEMTILTVLIQVFAKGLPGFSKISQDQITLLKACSSSEVMMLRVARVDA 370
DB 144 ESDLFPROITTEMTILTVLIQVFAKGLPGFSKISQDQITLLKACSSSEVMMLRVARVDA 203

QY 371 VSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVIFSDRP 430
DB 204 TTDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVIFSDRP 263

QY 431 GLEQQLVVEEQRYVLTIRVYIMNQHSAPRCAYIAKILSVLTTELTLGMQNSNMICIS 490
DB 264 GLEQQLVVEEQRYVLTIRVYIMNQHSAPRCAYIAKILSVLTTELTLGMQNSNMICIS 323

QY 491 LKLNKRLKLPPLFEEIW 506
DB 324 LKLNKRLKLPPLFEEIW 339

RESULT 6
ECR_HELVI STANDARD; PRT; 576 AA.
AC O18473;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone receptor) (20E receptor) (HVECR).
GN Name=ECR; Synonyms=NKRIH;
OS Heliothis virescens (Noctuid moth) (Owlet moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditryaia; Noctuoidea;
OC Noctuidae; Heliothinae; Heliothis.
OX NCBI_TaxID=7102;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRC;
RX MEDLINE=99457718; PubMed=10528411; DOI=10.1016/S0965-1748(99)00067-3;

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RA Martinez A., Scanlon D., Gross B., Perara S.C., Palli S.R.,
RA Greenland A.J., Windass J., Pongs O., Broad P., Jepson I.,
RT "Transcriptional activation of the cloned Heliothis virescens
RT (Lepidoptera) ecdysone receptor (HVECR) by muristeroneA.";
RL Insect Biochem. Mol. Biol. 29:915-930(1999).
CC -!- FUNCTION: Receptor for ecdysone. Binds to ecdysone response
CC elements (ECRES) (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI
CC subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (see http://www.ebi.ac.uk/ebis/
CC or send an email to license@ebi.ac.uk).
CC
CC EMBL; Y09009; CAA70212.1; -.
DR PDB; 1R1K; X-ray; D=288-550.
DR InterPro; IPR000536; Hrmn_recept_lig.
DR InterPro; IPR001723; Strdhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; Zf-C4; 1.
DR PRINTS; PR00398; STRDHOMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR PRODOM; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW 3D-structure; DNA-binding; Nuclear protein; Receptor;
KW Transcription regulation; Zinc-finger.
FT DOMAIN 1 162 Modulating (Potential).
FT DNA_BIND 163 228 Nuclear receptor-type.
FT ZN_FING 163 183 C4-type.
FT ZN_FING 199 223 C4-type.
FT DOMAIN 326 545 Hormone-binding (Potential).
SQ SEQUENCE 576 AA; 64638 MW; D13EF787BF263A8 CRC64;

Query Match 47.9%; Score 1470.5; DB 1; Length 576;
Best Local Similarity 88.5%; Pred. No. 1e-86;
Matches 286; Conservative 15; Mismatches 13; Indels 9; Gaps 2;

QY 191 MRPECVPESTCKNKRKEKAQREKDKLPVSTTTVDHMPAIMQCDDPPPPAAARI----- 245
DB 228 MRPECVPESTCKNKRKEKAQREKDKLPVSTTTVDHMPIMQCDDPPPPAAARILECVQ 287

QY 246 HEVVPRELTEKLMQNRLKNVTPLSANOKSLIARLVWYQGYEQPSDEDLKRVTTQTWQSA 305
DB 288 HEVVPRELTEKLMQNRLKNVTPLSANOKSLIARLVWYQGYEQPSDEDLKRVTTQ----- 343

QY 306 DEDEDSMDPFRQITTEMTILTVLIQVFAKGLPGFSKISQDQITLLKACSSSEVMMLRVA 365
DB 344 DEDEDSMDPFRQITTEMTILTVLIQVFAKGLPGFSKISQDQITLLKACSSSEVMMLRVA 403

QY 366 RRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVI 425
DB 404 RRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVI 463

QY 426 FSDRPGLEQQLVVEEQRYVLTIRVYIMNQHSAPRCAYIAKILSVLTTELTLGMQNS 485
DB 464 FSDRPGLEQQLVVEEQRYVLTIRVYIMNQHSAPRCAYIAKILSVLTTELTLGMQNS 523

QY 486 NMCIISLKLKRNKLPPLFEEIWDV 508
DB 524 NMCIISLKLKRNKLPPLFEEIWDV 546

RESULT 7
O77240

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```
ID O77240 PRELIMINARY; PRT; 513 AA.
AC O77240;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Ecdysone receptor isoform A.
GN Name=Ecr;
OS Chorisoneura fumiferana (Spruce budworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Tortricinae; Chorisoneura.
OX NCBI_TaxID=7141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99359183; PubMed=10432225; DOI=10.1016/S0303-7207(99)00058-1;
RA Retnakaran A., Palli S.R.; Ladd T.R., Dhadialla T.S., Krell P.J., Sohi S.S.,
RA "Studies on two ecdysone receptor isoforms of the spruce budworm,
RT Chorisoneura fumiferana.";
RL Mol. Cell. Endocrinol. 152:73-84(1999).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AF092030; AAC61596.2; -.
DR HSP; F34021; IROO.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:000496; F:steroid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003069; Ecdystd receptor.
DR InterPro; IPR000536; Strhmn recept lig.
DR InterPro; IPR001723; Strhmn recept lig.
DR InterPro; IPR008946; Str ncl receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR01283; ECDYSTEROIDR.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 513 AA; 57622 MW; F110540A30308602 CRC64;

Query Match 47.8%; Score 1467; DB 2; Length 513;
Best Local Similarity 86.2%; Pred. No. 1.4e-86;
Matches 274; Conservative 27; Mismatches 17; Indels 0; Gaps 0;

QY 191 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPPAARIHEVVP 250
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
178 MRPECVVPTQCAMKRKEKAQKDKLPVSTTTVDHMPPIMQCEPPPPPPAARIHEVVP 237
QY 251 RELTEKLMQNRLKNVTPLSANQSLIARLVWYQGYEOPSEDLKRVTTQWQSADEDE 310
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
238 RFLSKLLETNRQKNIPQLTANQQLIARLVWYQGYEOPSEDLKRVTTQWQADDENE 297
QY 311 DSDMPFRQITEMTILTVQLIVEFAKGLPGFSGKISQPDQITLLKACSEVMMLRVARRYDA 370
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
298 ESDTTPFRQITEMTILTVQLIVEFAKGLPGFAKISQPDQITLLKACSEVMMLRVARRYDA 357
QY 371 VSDSVLFANNOAYTRDNRKAGMAYVIEDLLHFCRCMYSMDNVHYALLTAIVFSDRP 430
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
358 ASDSVLFANNOAYTRDNRKAGMAYVIEDLLHFCRCMYSMDLNTHYALLTAIVFSDRP 417
QY 431 GLEQPOLVBEIORYYVLTNRVYIMNHQSPRCVAVIYAKILSVLTSLTELGMNSNMCIIS 490
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
418 GLEQPOLVBEIORYYVLTNRVYILNQLSGSARSSVIYKILSLTELGMNSNMCIIS 477
QY 491 LKLNKRLPPPLEEIIWDV 508
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
478 LKLNKRLPPPLEEIIWDV 495
```

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RESULT 8
O77255 PRELIMINARY; PRT; 541 AA.
ID O77255
AC O77255;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Ecdysteroid receptor Ecr-B.
OS Chorisoneura fumiferana (Spruce budworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Tortricinae; Chorisoneura.
OX NCBI_TaxID=7141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96191152; PubMed=8641050;
RA Kothapalli R., Palli S.R.; Ladd T.R., Sohi S.S., Cress D.,
RA Dhadialla T.S., Tzertzinis G., Retnakaran A.;
RT "Cloning and developmental expression of the ecdysone receptor gene
RT from the spruce budworm, Chorisoneura fumiferana.";
RL Dev. Genet. 17:319-330(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX Kothapalli R., Palli S.R.; Ladd T., Retnakaran A.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Palli R.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; U29531; AAC36491.2; -.
DR HSP; P34021; IROO.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:000496; F:steroid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003069; Ecdystd receptor.
DR InterPro; IPR000536; Hrmn recept lig.
DR InterPro; IPR001723; Strhmn recept lig.
DR InterPro; IPR008946; Str ncl receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR01283; ECDYSTEROIDR.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 541 AA; 61153 MW; C78D28D7D2B868CD CRC64;

Query Match 47.8%; Score 1467; DB 2; Length 541;
Best Local Similarity 86.2%; Pred. No. 1.5e-86;
Matches 274; Conservative 27; Mismatches 17; Indels 0; Gaps 0;

QY 191 MRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPAIMQCDPPPPPPAARIHEVVP 250
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
206 MRPECVVPTQCAMKRKEKAQKDKLPVSTTTVDHMPPIMQCEPPPPPPAARIHEVVP 265
QY 251 RELTEKLMQNRLKNVTPLSANQSLIARLVWYQGYEOPSEDLKRVTTQWQSADEDE 310
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
266 RFLSKLLETNRQKNIPQLTANQQLIARLVWYQGYEOPSEDLKRVTTQWQADDENE 325
QY 311 DSDMPFRQITEMTILTVQLIVEFAKGLPGFSGKISQPDQITLLKACSEVMMLRVARRYDA 370
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
326 ESDTTPFRQITEMTILTVQLIVEFAKGLPGFAKISQPDQITLLKACSEVMMLRVARRYDA 385
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QY 371 VSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYMSMDNVHVALTAIVFSDRP 430
Db 386 ASDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMALDNIHVALTAIVFSDRP 445
QY 431 GLEQPOLVEEQRYYLNTLRVYIMNHQSHASPRCAVIYAKILSVLTELRTLGWQSNMCIS 490
Db 446 GLEQPOLVEEQRYYLNTLRVYILNQLSGSARSSVIYKILSVLSELRTLGWQSNMCIS 505
QY 491 LKLKRNKRLPPFLEEIWDV 508
Db 506 LKLKRNKRLPPFLEEIWDV 523

RESULT 9
Q9U3U4
ID Q9U3U4 PRELIMINARY; PRT; 346 AA.
AC Q9U3U4;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Ecdysteroid receptor (Fragment).
GN Name=ecr;
OS Bicyclus anynana (squinting bush brown).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Satyrinae; Elymnini; Mycalesina;
OC Bicyclus.
OX NCBI_TaxID=110368;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Wing.
RA Reinhardt R.K., Weber P., Koch P.B.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AJ251810; CAB63236.1; -.
DR HSP; P34021; IROO.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:0005496; F:steroid binding; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003069; Ecdystd_receptor.
DR InterPro; IPR000536; Hrmn_recept_lig.
DR InterPro; IPR001723; Strhnm_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zfc-C4; 1.
DR PRINTS; PRO1283; ECDYSTEROIDR.
DR PRINTS; PRO0398; STRDHORMONER.
DR SMART; SM00430; HOL1; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
FT NON_TER 1
FT NON_TER 346
SQ SEQUENCE 346 AA; 40036 MW; 04323E79C2D055D2 CRC64;

Query Match 46.2%; Score 1418; DB 2; Length 346;
Best Local Similarity 84.2%; Pred. No. 1.2e-83;
Matches 272; Conservative 23; Mismatches 22; Indels 6; Gaps 2;

QY 191 MRPCVPESTCNKRKEKAQREKDKLPVSTTTVDHMPAIMQCDPPPPAAARI----- 245
Db 24 MRPCVPESTCNKRKEKAQREKDKLPVSTTTVDHMPAIMQCDPPPPAAARILECLQ 83
QY 246 HEVVPREFTEKLMQENKNTVPLSANOKSLIARLVWYQDGEQSEEDLKRVTQTWQSA 305
Db 84 HEVVPREFTEKLMQENKNTVPLSANOKSLIARLVWYQDGEQSEEDLKRVTQTWQAD 143
QY 306 DEE-DESDMPFRQITMTILTQVLFVFAKGLPGFKSISQPDQITLLKACSSYVMMLRV 364

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Db 144 TEEIGASDLPPRQITMTILTQVLFVFAKGLPGFAKISQPDQITLLKACSSYVMMLRV 203
QY 365 ARRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYMSMDNVHVALTAIV 424
Db 204 SRRYDMSDTSVMPFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYMSMDNVHVALTAIV 263
QY 425 IFSDRPGLEQPOLVEEQRYYLNTLRVYIMNHQSHASPRCAVIYAKILSVLTELRTLGWQ 484
Db 264 IFSDRPGLEQPOLVEEQRYYLNTLRVYILNQLSGSARSSVIYKILSVLSELRTLGWQ 323
QY 485 SNMCISLKLKRNKRLPPFLEEIWD 507
Db 324 SNMCISLKLKRNKRLPPFLEEIWD 346

RESULT 10
ECR_BOMMO
ID ECR_BOMMO STANDARD; PRT; 606 AA.
AC P49881;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone receptor) (20E receptor).
GN Name=ECR; Synonyms=NR1H1;
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Myosore; TISSUE=Ovary;
RX MEDLINE=95360029; PubMed=7633470; DOI=10.1016/0965-1748(95)00024-P;
RA Swevers L., Drevet J.R., Lunke M.D., Iatrou K.;
RT "The silkworm homolog of the Drosophila ecdysone receptor (B1 isoform): cloning and analysis of expression during follicular cell differentiation."
RL Insect Biochem. Mol. Biol. 25:857-866(1995).
RN [2]
RP SEQUENCE OF 61-606 FROM N.A.
RC STRAIN=Kinshu X Showa; TISSUE=Fat body;
RA Kamimura M., Tomita S., Fujiwara H.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for ecdysone. Binds to ecdysone response elements (ECRES). May play a role in the implementation of the chorionic program at the end of vitellogenesis.
CC -1- SUBUNIT: Heterodimer of ECR and CFI (Potential).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P49881-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P49881-2; Sequence=VSP_003663;
CC -1- DEVELOPMENTAL STAGE: It is present in constant amounts in follicular cells throughout vitellogenesis but disappears transiently at the onset of chorionogenesis and reappears during the later stages of chorionogenesis.
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI subfamily.
CC -1- CAUTION: It is uncertain whether Met-1 or Met-61 is the initiator.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/announcements or send an email to license@ebi.ac.uk).
CC EMBL; L35266; AAA87341.1; -.
CC EMBL; L35266; AAA87340.1; -.
DR

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DR EMBL; D43943; BAA07890.1; -.
DR HSP; P20393; IAGY.
DR InterPro; IPR000536; Hrmn recept lig.
DR InterPro; IPR001723; Strhmn receptor.
DR InterPro; IPR008946; Str ncl receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00047; STROIDFINGER.
DR PRINTS; PR00047; STROIDFINGER.
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
KW Alternative splicing; DNA-binding; Nuclear protein; Receptor;
FT DOMAIN 1 206 Modulating (Potential).
FT ZN_FING 207 272 Nuclear receptor-type.
FT ZN_FING 207 272 C4-type.
FT ZN_FING 243 267 C4-type.
FT ZN_FING 243 267 Hormone-binding (Potential).
FT DOMAIN 364 586 Poly-Gln.
FT DOMAIN 134 142 Poly-Pro.
FT DOMAIN 317 320 Missing (in isoform 2).
FT VARSPLIC 380 382 /FTID=VSP 003663.
FT CONFLICT 67 67 N -> D (in Ref. 2).
FT CONFLICT 81 81 S -> T (in Ref. 2).
FT CONFLICT 108 108 R -> G (in Ref. 2).
FT CONFLICT 469 470 OG -> KA (in Ref. 2).
FT CONFLICT 591 591 A -> P (in Ref. 2).
SQ SEQUENCE 606 AA; 68201 MW; 960E8B9A1E4F2202 CRC64;

Query Match 46.1%; Score 1416; DB 1; Length 606;
Best Local Similarity 82.7%; Pred. No. 3.6e-83;
Matches 278; Conservative 25; Mismatches 17; Indels 16; Gaps 5;

QY 191 MRPCVVPESCKNREKEAQRKDKK---LPVSTTTVDHMPAIMQCDPPPEAA 247
DB 191 MRPCVVPESCKNREKEAQRKDKK---LPVSTTTVDHMPAIMQCDPPPEAA 247
QY 248 VVPRFLTEKLEQNRKKNVPLSANQKSLIARLVWYQGYEQPSSEDLKRVTTQWSADE 307
DB 248 VVPRFLTEKLEQNRKKNVPLSANQKSLIARLVWYQGYEQPSSEDLKRVTTQWSADE 307
QY 308 EDESDMPFRQITMTILTVQIVFAKGLPGFSKISQPDQITLLKACSSVMMMLRVARR 367
DB 308 EDESDMPFRQITMTILTVQIVFAKGLPGFSKISQPDQITLLKACSSVMMMLRVARR 367
QY 368 YDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMDNVHYALLTAIVIFS 427
DB 368 YDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMDNVHYALLTAIVIFS 427
QY 428 DRPGLEQPOLVEEIQRYLYLNTLVYIMNHQASPRCAVIYAKILSVLTGLTGMNSNM 487
DB 428 DRPGLEQPOLVEEIQRYLYLNTLVYIMNHQASPRCAVIYAKILSVLTGLTGMNSNM 487
QY 488 CISLKLKNRKLPPFLEEIWDV-----KLAPPTD 515
DB 488 CISLKLKNRKLPPFLEEIWDV-----KLAPPTD 515
QY 567 CISLKLKNRKLPPFLEEIWDVAEVATTHTPTVLPPTN 602
DB 567 CISLKLKNRKLPPFLEEIWDVAEVATTHTPTVLPPTN 602

RESULT 11
Q9U3Y4
ID Q9U3Y4 PRELIMINARY; PRT; 680 AA.
AC Q9U3Y4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE Ecdysteroid receptor.
GN Name=Ecd;
OS Aedes albopictus (Forest day mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.
OX NCBI_TaxID=7160;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=20112665; PubMed=10644973;
RX DOI=10.1002/(SICI)1520-6327(200002)43:2<87::AID-ARCHS>3.0.CO;2-O;
RA Jayachandran G., Fallon A.M.;
RT "Evidence for expression of Ecr and USP components of the 20-
RT hydroxyecdysone receptor by a mosquito cell line.";
RL Arch. Insect Biochem. Physiol. 43:87-96(2000).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AF210733; AAF19032.1; -.
DR HSP; P34021; 1R00.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004894; F:ecdysteroid hormone receptor activity; IEA.
DR GO; GO:000496; F:steroid binding; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003069; Ecdystd_receptor.
DR InterPro; IPR000536; Hrmn_recep_lig.
DR InterPro; IPR001723; Strhmn_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR01283; ECDYSTEROIDE.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 680 AA; 74924 MW; 272C8E6AB1021C98 CRC64;

Query Match 37.2%; Score 1142; DB 2; Length 680;
Best Local Similarity 60.3%; Pred. No. 2.1e-65;
Matches 228; Conservative 61; Mismatches 67; Indels 22; Gaps 7;

QY 191 MRPCVVPESCKNREKEAQRKDKL---PVSSTTV---DDHMPAIMQCDPPPEAA 243
DB 191 MRPCVVPESCKNREKEAQRKDKL---PVSSTTV---DDHMPAIMQCDPPPEAA 243
QY 244 RIHEVPRFLTEKLEQNRKKNVPLSANQKSLIARLVWYQGYEQPSSEDLKRVTTQW 303
DB 244 RIHEVPRFLTEKLEQNRKKNVPLSANQKSLIARLVWYQGYEQPSSEDLKRVTTQW 303
QY 311 --HQAIPL--LLPEKLLQENLRNIPLLTANQMAVYKLIWYQGYEQPSSEDLKRI--MIG 365
DB 311 --HQAIPL--LLPEKLLQENLRNIPLLTANQMAVYKLIWYQGYEQPSSEDLKRI--MIG 365
QY 304 SADEDESDMPFRQITMTILTVQIVFAKGLPGFSKISQPDQITLLKACSSVMMMLR 363
DB 304 SADEDESDMPFRQITMTILTVQIVFAKGLPGFSKISQPDQITLLKACSSVMMMLR 363
QY 366 SPNEEDSDHVFHRIHTITLTVQIVFAKGLPAFTKIPQEDQITLLKACSSVMMMLR 425
DB 366 SPNEEDSDHVFHRIHTITLTVQIVFAKGLPAFTKIPQEDQITLLKACSSVMMMLR 425
QY 364 VARRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMDNVHYALLTAI 423
DB 364 VARRYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMDNVHYALLTAI 423
QY 426 MARRYDAATDSILFANNRSYTRDSYRMAGMADTIEDLLHFCRCMFSLTVDNVEYALLTAI 485
DB 426 MARRYDAATDSILFANNRSYTRDSYRMAGMADTIEDLLHFCRCMFSLTVDNVEYALLTAI 485
QY 424 VIFSDRPGLEQPOLVEEIQRYLYLNTLVYIMNHQASPRCAVIYAKILSVLTGLTGMQ 483
DB 424 VIFSDRPGLEQPOLVEEIQRYLYLNTLVYIMNHQASPRCAVIYAKILSVLTGLTGMQ 483
QY 486 VIFSDRPGLEQAEIYVETIYIDTRIYILNRHAGDPKCSVIFAKLISILTLRTLNQ 545
DB 486 VIFSDRPGLEQAEIYVETIYIDTRIYILNRHAGDPKCSVIFAKLISILTLRTLNQ 545
QY 484 NSNMCIKLNKRLPPFLEEIWDVCLAPPTDVLGDELHLDG---EDVAHADALDDF 540
DB 484 NSNMCIKLNKRLPPFLEEIWDVCLAPPTDVLGDELHLDG---EDVAHADALDDF 540
QY 546 NSEMFSLKLNKRLPPFLEEIWDVQDIPP---SMQAMHSHGTPTQSSSSSSSSSSSS 602
DB 546 NSEMFSLKLNKRLPPFLEEIWDVQDIPP---SMQAMHSHGTPTQSSSSSSSSSSSS 602

RESULT 12
ECR_AEDAE
ID ECR_AEDAE STANDARD; PRT; 675 AA.
AC P49880;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

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311 --HQAP-LJPEKLLQENLRNIPLLTANQAVIYKLIWQDGEQPSSEDLKRI--MIG 363

304 SADEEDEDMPFROITEMILTIVQLIVEFAGKLPGFSKI SQDPQITLLKACSSSEVMMLR 363

366 SPNEBEDQHDVFRHTEITLITVQLIVEFAGKLPAPTKEIPQSDQITLLKACSSSEVMMLR 425

364 VARRYDAVSDSVLANQCAVTRDNYRKAGWAYVEDLLHFCRCWYSMDNVHYALLTAI 423

426 WARRYDAAATDSILFANNRSYTRDSYRWAGWADTIEDLLHFCRCQMFSLTVDNVHYALLTAI 485

424 VIFSDRPGLEQPOLVEBIEQRYLNTLRVYIMNHSASPRCAVYAYKILSVILTERLTGMQ 483

486 VFSDRPGLEQAEIVELHYSQYIDTLRIYILNRHAGDPKCSVIFAKLLSLITELRTLGMQ 545

484 NSNMCSISLKNRKLPPFLEIWDVKLAPTDVSGLDELHLGDGVAMAHADALDDFDLD 543

546 NSECMFSLKLNKRLPFLEIWDVDIPE---SMQAQMHSHGTQSSSSSSSSSSS---- 598

544 MLCGDGSDPGPFTPHDSAPYG 564

599 --SSNGSGNSGNSNSNSNSQHG 618

RESULT 13

Q6VA69 PRELIMINARY; PRT: 776 AA.

ID Q6VA69 AC

AC Q6VA69; AC

05-JUL-2004 (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE BCRA.

OS Aedes aegypti (Yellowfever mosquito).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.

NCBI_TaxID=71159;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=2274472; PubMed=12385823; DOI=10.1016/S0303-7207(02)00225-3;

RX Wang S.F., Li C., Sun G., Zhu J., Raikhel A.S.;

RT "Differential expression and regulation by 20-hydroxyecdysone of

RT mosquito ecdysteroid receptor isoforms A and B.";

RL Mol. Cell. Endocrinol. 196:29-42(2002).

RN [2]

RP SEQUENCE FROM N.A.

RA Wang S.F., Sun G., Raikhel A.S.;

RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family.

DR EMBL; AY345989; AAQ23183.1; -.

DR HSSP; P20393; IAGY.

DR GO; GO:0003634; C:nucleus; IEA.

DR GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.

DR GO; GO:0005496; F:steroid binding; IEA.

DR GO; GO:0003705; P:transcription factor activity; IEA.

DR GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro; IPR003069; Ecdystd_receptor.

DR InterPro; IPR000536; Hrmn_recept_lig.

DR InterPro; IPR001723; Strdhmn_receptor.

DR InterPro; IPR008946; Str_ncl_receptor.

DR InterPro; IPR001628; Znf_C4steroid.

DR Pfam; PF00104; Hormone_recep; 1.

DR Pfam; PF00105; zf_C4; 1.

DR PRINTS; PR01283; ECDYSTEROIDR.

DR PRINTS; PR00398; STRDHOHORMONR.

DR PRINTS; PR00047; STROIDFINGER.

DR ProDom; PD000035; Znf_C4steroid; 1.

DR SMART; SM00430; HOLI; 1.

DR SMART; SM00399; ZNF_C4; 1.

DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.

KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;

SW Transcription regulation; Zinc; Zinc-finger.

SO SEQUENCE 776 AA; 83645 MW; C9B1EB93C08E0CAC CRC64;

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Query Match      37.1%; Score 1139; DB 2; Length 776;
Best Local Similarity 59.6%; Pred. No. 4e-65;
Matches 227; Conservative 63; Mismatches 67; Indels 24; Gaps 7;

QY 191 MRPCVPESTCKNKRKEAQRKDKL---PVSTTTV---DDHMPALMQCDPPPPAA 243
DB 356 MRPCVVPENQCAIRKKAQKQKQVOTNATVSTTSTYRSEILPILMKCDPPPP--- 411
QY 244 RIHEVVPFLTKLEQNLKRVNPLSANQKSLARLVVYQDGYQPSSEEDLKRVTTQW 303
DB 412 --HQAIP-LLPEKLLQENLRNIPLLTANQMAVYKLIWYQDGYQPSSEEDLKRI--MIG 466
QY 304 SADEDESDMPFRQITMTILTQVLI VEFAGKLPFGFSKISQPDQITLLKACSSVMMLR 363
DB 467 SPNEEDQHDVHFHTEITILTQVLI VEFAGKLPFAFTKIPOEDQITLLKACSSVMMLR 526
QY 364 VARRYDAVSDSVLFANNOAYTRDNYRKAGMAVIEDLLHFCRCMYSMNDNVHYALLTAI 423
DB 527 MARRYDAATDSILFANNRSYTRDSYRMAGMADTIEDLLHFCRCMYSMNDNVHYALLTAI 586
QY 424 VIFSDRPGLEQPOLVEEIQRYVYNTLRVYIMNQHSPRCVAVIYAKILSVLTETLQW 483
DB 587 VIFSDRPGLEQAEVHEIQSYIDTRIYLNRHAGDPKCSVIFAKLLSILTELTGQ 646
QY 484 NSMCSILKLNKRLPPFLEEIWDVYKLPAPTDVSLGDELHGDGVAMAHADALDDFLD 543
DB 647 NSEMCFSLLKLNKRLPFLEEIWDVQDIPP---SMQAQWHSHTQSSSSSSSSSS--- 699
QY 544 MLGCDGSPGPGTPTDHSAPYG 564
DB 700 --SSNGSSNGSSNSNSNSQHG 719

RESULT 14
ECR_LUCCU      STANDARD;      PRT;      757 AA.
AC O18531;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone receptor) (20E receptor).
DE Name=ECR; Synonyms=NR1H1;
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Lucilia.
OX NCBI_TaxID=7375;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97449774; PubMed=9304790; DOI=10.1016/S0965-1748(97)00019-2;
RA Hannan G.N., Hill R.J.
RT "Cloning and characterization of LcECR: a functional ecdysone receptor from the sheep blowfly Lucilia cuprina."
RL Insect Biochem. Mol. Biol. 27:479-488(1997).
CC -!- FUNCTION: Receptor for ecdysone. Binds to ecdysone response elements (ECRES) (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NRI subfamily.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
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CC EMBL; U75355; AAB81130.1; -.
CC HSSP; P20393; IAS8.
CC InterPro; IPR000536; Hrmn_recept_lig.
CC InterPro; IPR001723; Stdhrmn_receptor.

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DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STEDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR PRODOM; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation; Zinc-finger.
FT DOMAIN 1 300 Modulating (Potential).
FT DNA_BIND 301 366 Nuclear receptor-type.
FT ZN_FING 301 321 C4-type.
FT ZN_FING 337 361 C4-type.
FT DOMAIN 454 674 Hormone-binding (Potential).
SQ SEQUENCE 757 AA; 83075 MW; C1511452ED37D359 CRC64;

Query Match      34.2%; Score 1050; DB 1; Length 757;
Best Local Similarity 63.5%; Pred. No. 2.2e-59;
Matches 207; Conservative 41; Mismatches 66; Indels 12; Gaps 4;

QY 191 MRPCVPESTCKNKRKEAQRKDKLPVS---TTTVDHMPALMQCDPPPPPEAARIHEV 248
DB 366 MRPCVVPENQCAKMRKKAQKQKQTSVCATEIKKEILDLMTCPPPS-----HPT 419
QY 249 VPRELTKLEMQNLKRVNPLSANQKSLARLVVYQDGYQPSSEEDLKRVTTQWQSADEE 308
DB 420 CP-LLPEDILAKQARNIPPLSYNQAVIYKLIWYQDGYQPSSEEDLKRI---MSSPDEN 475
QY 309 DEDSDMPFRQITMTILTQVLI VEFAGKLPFGFSKISQPDQITLLKACSSVMMLRVARRY 368
DB 476 ESQHDASFRHITEITILTQVLI VEFAGKLPFAFTKIPOEDQITLLKACSSVMMLRMARRY 535
QY 369 DAVSDSVLFANNOAYTRDNYRKAGMAVIEDLLHFCRCMYSMNDNVHYALLTAIVIFSD 428
DB 536 DHNSDSIFFANNRSYTRDSYRMAGMADNIEDLLHFCRCMYSMKVNDVHYALLTAIVIFSD 595
QY 429 RPLGEQPOLVEEIQRYVYNTLRVYIMNQHSPRCVAVIYAKILSVLTETLRTLGMSNMNC 488
DB 596 RPLGEAEAEVIAQSYIDTRIYLNRHCGDPSLVFFAKLLSILTELTGNGNAEMC 655
QY 489 ISLKLKLNKRLPPFLEEIWDVYKLPAPT 514
DB 656 FSLKLKLNKRLPKFLEEIWDVHYAIPPS 681

RESULT 15
Q9GPH1
ID Q9GPH1 PRELIMINARY; PRT; 784 AA.
AC Q9GPH1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ecdysone receptor.
GN Name=ECR;
OS Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=7373;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fat body;
RA Berlinger M., Hansen I.A., Meyer S.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
CC EMBL; AF252360; AAG46050.1; -.
CC HSSP; P34021; IRON.
CC GO; GO:0005634; C:nucleus; IEA.
CC GO; GO:0004884; F:ecdysteroid hormone receptor activity; IEA.

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DR GO:0005496; F:steroid binding; IEA.
DR GO:0003700; P:transcription factor activity; IEA.
DR GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR003069; Ecdystd_receptor.
DR InterPro: IPR000536; Hrmn_recept_lig.
DR InterPro: IPR001723; Stdhrmn_receptor.
DR InterPro: IPR008946; Str_ncl_receptor.
DR InterPro: IPR001628; Znf_C4steroid.
DR Pfam: PF00104; Hormone_recep; 1.
DR Pfam: PF00105; zf-C4; 1.
DR PRINTS: PR01283; ECDYSTEROIDR.
DR PRINTS: PR00398; STRDHORMONER.
DR PRINTS: PR00047; STROIDFINGER.
DR ProDom: PD000035; Znf_C4steroid; 1.
DR SMART: SM00430; HOL1_1.
DR SMART: SM00399; ZNF_C4; 1.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 784 AA; 85961 MW; 96381D080EDB630 CRC64;

Query Match 34.0%; Score 1046; DB 2; Length 784;
Best Local Similarity 63.2%; Pred. No. 4.2e-59;
Matches 206; Conservative 42; Mismatches 66; Indels 12; Gaps 4;

QY 191 MRPECVPESTCKNKRREKQREKDKLPVS--TTTVDDHMPAIMQCDPPPPPEAARIHEV 248
DB 381 MRPECVVFENQCMKREKKQKQKDKIQTSVCATEIKKEILDLMTCPPS-----HPT 434

QY 249 VPRFTEKLMQNRLKNVTPLSANQKSLIARLVWYQDGYEQSPSEDLKRVTTQWSADEE 308
DB 435 CP-LLPEDILAKQARNIPSSYNQLAVIYKLIWYQDGYEQSPSEDLKRI---MSSPDEN 490

QY 309 DEDSDMPROJTEMILTIVQLIVEFAKGLPGFSKISQDPDQITLAKCSSEVMMLRVARRY 368
DB 491 ESQHDVSPRHITETILTIVQLIVEFAKGLPAFTKIPQEDQITLLKACSSSEVMMLRMARRY 550

QY 369 DAVSDSVLFANNOAYTRDNYRKAGNAVYIEDLLHFCRCMYSMDNVHYALLTAIVIFSD 428
DB 551 DHNSDSIFFANNRSYTRDSYKAGWADNIEDLLHFCRCMYSMKVDNVYALLTAIVIFSD 610

QY 429 RPLGEPQLVEEIQRYLNTLRVYIMNQHSASPRCAVIYAKILSVLTSLRTLGQNSNMC 488
DB 611 RPLGEEAEVIAQSYIDTLRIYILNRHCGDPMSLVFFAKLSILTSLRTLGQNAEMC 670

QY 489 ISLKLKPKLPPLFEEIWDVKLAPT 514
DB 671 FSLKLKPKLPKFLFEEIWDVHAIPPS 696

Search completed: April 15, 2005, 14:51:44
Job time : 88 secs

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OM protein - protein search, using sw model

Run on: April 15, 2005, 14:36:56 ; Search time 43 Seconds
(without alignments)
1020.783 Million cell updates/sec

Title: US-10-087-167-121
Perfect score: 3072
Sequence: 1 MQQYVDFSPAFIRYLFAP.....ADFFEQMTDALGIDEYGG 588

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1582	51.5	546	US-09-393-839-2	Sequence 2, Appli
2	1545	50.3	556	US-09-564-418-11	Sequence 11, Appl
3	1534.5	50.0	557	US-08-653-648A-12	Sequence 12, Appl
4	1461.5	47.6	575	US-08-653-648A-5	Sequence 5, Appli
5	1461.5	47.6	575	US-09-564-418-5	Sequence 5, Appli
6	1449	47.2	319	US-08-653-648A-7	Sequence 7, Appli
7	1449	47.2	319	US-09-564-418-13	Sequence 13, Appl
8	1418.5	46.2	314	US-08-653-648A-16	Sequence 16, Appl
9	1418.5	46.2	314	US-09-564-418-7	Sequence 7, Appli
10	1416	46.1	606	US-08-891-298-3	Sequence 3, Appli
11	1416	46.1	606	US-08-653-648A-11	Sequence 11, Appl
12	1416	46.1	606	US-09-564-418-10	Sequence 10, Appl
13	1139	37.1	674	US-08-653-648A-14	Sequence 14, Appl
14	1139	37.1	674	US-09-564-418-12	Sequence 12, Appl
15	1129.5	36.8	560	US-09-435-019-6	Sequence 6, Appli
16	1129.5	36.8	560	US-09-435-019-9	Sequence 9, Appli
17	1129.5	36.8	560	US-10-065-200A-6	Sequence 6, Appli
18	1129.5	36.8	560	US-10-065-200A-9	Sequence 9, Appli
19	1129.5	36.8	561	US-09-435-019-14	Sequence 14, Appl
20	1129.5	36.8	561	US-09-435-019-17	Sequence 17, Appl
21	1129.5	36.8	561	US-10-065-200A-14	Sequence 14, Appl
22	1129.5	36.8	561	US-10-065-200A-17	Sequence 17, Appl
23	1027.5	33.4	746	US-09-042-488B-5	Sequence 5, Appli
24	1025.5	33.4	550	US-08-659-188-18	Sequence 18, Appl
25	1025.5	33.4	550	US-08-653-227-18	Sequence 18, Appl
26	1025.5	33.4	550	US-08-655-241-18	Sequence 18, Appl
27	1025.5	33.4	550	US-09-398-326-18	Sequence 18, Appl

28	1025.5	33.4	550	4	US-09-853-450-18	Sequence 18, Appl
29	1025.5	33.4	746	4	US-09-042-488B-7	Sequence 7, Appli
30	1025.5	33.4	1041	4	US-09-042-488B-9	Sequence 9, Appli
31	1021.5	33.3	746	3	US-09-144-759-18	Sequence 18, Appl
32	1021.5	33.3	746	4	US-09-570-267-18	Sequence 18, Appl
33	1021.5	33.3	764	3	US-09-144-759-20	Sequence 20, Appl
34	1021.5	33.3	764	3	US-09-570-267-20	Sequence 20, Appl
35	1005	32.7	878	3	US-08-653-648A-15	Sequence 15, Appl
36	1005	32.7	878	4	US-09-564-418-8	Sequence 8, Appli
37	1003.5	32.7	226	3	US-09-133-321-2	Sequence 2, Appli
38	999	32.5	536	3	US-08-653-648A-13	Sequence 13, Appl
39	999	32.5	536	4	US-09-564-418-9	Sequence 9, Appli
40	879	28.6	231	4	US-09-324-258-20	Sequence 20, Appl
41	847.5	27.6	219	4	US-09-435-019-65	Sequence 65, Appl
42	847.5	27.6	219	4	US-09-435-019-67	Sequence 67, Appl
43	847.5	27.6	219	4	US-10-065-200A-65	Sequence 65, Appl
44	847.5	27.6	219	4	US-10-065-200A-67	Sequence 67, Appl
45	768	25.0	496	4	US-08-840-713-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1

US-09-393-839-2
; Sequence 2, Application US/09393839
; Patent No. 6504082
; GENERAL INFORMATION:
; APPLICANT: Albertsen, Marc C.
; APPLICANT: Brooke, Catherine D.
; APPLICANT: Garmaat, Carl W.
; APPLICANT: Roth, Bradley A.
; TITLE OF INVENTION: NOVEL ECDYSONE RECEPTORS AND METHODS FOR THEIR USE
; FILE REFERENCE: 5718-26
; CURRENT APPLICATION NUMBER: US/09/393,839
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Ostrinia nubilalis
US-09-393-839-2

Query Match	51.5%	Score 1582;	DB 4;	Length 546;
Best Local Similarity	92.8%	Pred. No. 1.8e-135;		
Matches	308;	Conservative	7;	Mismatches 7; Indels 10; Gaps 2;
Qy	191	MRPECVPESTCKNKRREKAEQKDKLPVSTTTTVDHMPAIMQCDPPPPPEAARI-----	245	
Db	206	MRPECVPESTCKNKRREKAEQKDKLPVSTTTTVDHMPAIMQCDPPPPPEAARI-----	265	
Qy	246	HEVVPRLTEKLMQNRKLNKVTPLSANOKSLIARLVWYQDGEQSEEDLKRVTQTWQSA	305	
Db	266	HEVVPRLTEKLMQNRKLNKVTPLSANOKSLIARLVWYQDGEQSEEDLKRVTQTWQSA	325	
Qy	306	DEEDSDMPFRQITMTILTVQLIVPEFAKGLPGFSKISQDPDQITLLKACSEVNMRLVA	365	
Db	326	DEEDSDMPFRQITMTILTVQLIVPEFAKGLPGFSKISQDPDQITLLKACSEVNMRLVA	385	
Qy	366	RYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVI	425	
Db	386	RYDAVSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDVHYALLTAIVI	445	
Qy	426	FSDRPGLEQPOLVVEIQRYIYNTLRVYIMNQHSPRCAYIYAKILLSVLTRELTLGMQNS	485	
Db	446	FSDRPGLEQPOLVVEIQRYIYNTLRVYIMNQHSPRCAYIYAKILLSVLTRELTLGMQNS	505	
Qy	486	NMCISLKNRKLPPFLLEEIWDVKLAPPTDVS	517	
Db	506	NMCISLKNRKLPPFLLEEIWDV-----ADVS	532	

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RESULT 2
US-09-564-418-11
; Sequence 11, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jenson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Manduca sexta
US-09-564-418-11

Query Match      50.3%; Score 1545; DB 4; Length 556;
Best Local Similarity 90.9%; Pred. No. 4.4e-132;
Matches 299; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Qy 191 MRPECVVPESTCKNKRREKEAQREKDKLPVSTTTTVDHMPAIMQCDDPPPPPEAAARIHEVVP 250
Db 212 MRPECVVPESTCKNKRREKEAQREKDKLPVSTTTTVDHMPAIMQCDDPPPPPEAAARIHEVVP 271

Qy 251 RFLTEKLMQNRLKNVTPLSANQKSLIARLVWYQDGYEQPSEEDLKRVTQTWQSADEED 310
Db 272 RFLTEKLMQNRLKNVTPLSANQKSLIARLVWYQDGYEQPSEEDLKRVTQTWQLEEEEE 331

Qy 311 DSDMPFRQITMTILTVQLIVEFAKGLPGFSKISQPDQITLLKACSEVMMMLRVARRYDA 370
Db 332 ETDMPFRQITMTILTVQLIVEFAKGLPGFSKISQSDQITLLKASSSEVMMMLRVARRYDA 391

Qy 371 VSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFRCMYSMSMDNVHYALLTAIVIFSDRP 430
Db 392 ATDSVLFANNQAYTRDNYRKAGMSYVIEDLLHFRCMYSMSMDNVHYALLTAIVIFSDRP 451

Qy 431 GLEQPOLVEEIQRYVLTIRVYIMNQHSPRCVAVIYAKILSVLTTELRTLGQNSNMCIS 490
Db 452 GLEQPLLVEEIQRYVLTIRVYILNQHSASPRCAVLFGKILGVLTELRTLGTONSNMCIS 511

Qy 491 LKLKNRKLPPFLEEIWDVKLAPPTDVSIG 519
Db 512 LKLKNRKLPPFLEEIWDVAEVSTTQPTPG 540

RESULT 3
US-08-653-648A-12
; Sequence 12, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jenson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65

Query Match      47.6%; Score 1461.5; DB 3; Length 575;
Best Local Similarity 87.9%; Pred. No. 1.9e-124;
Matches 284; Conservative 16; Mismatches 14; Indels 9; Gaps 2;

Qy 191 MRPECVVPESTCKNKRREKEAQREKDKLPVSTTTTVDHMPAIMQCDDPPPPPEAAARI----- 245
Db 228 MRPECVVPEQNCAMKREKKAQREKDKLPVSTTTTVDHMPAIMQCDDPPPPPEAAARILBCVQ 287

Qy 246 HEVVPFLTEKLMQNRLKNVTPLSANQKSLIARLVWYQDGYEQPSEEDLKRVTQTWQSA 305
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Db 288 HEVPRFLNEKMEQNRLKNVPLTANQKSLIARLVWYQEGYEQSEEDLKRVTQ-----S 343
QY 306 DEEDSDMPFRQITTEMILTTLVQLIVEFAKGLPGFSKISQPDQITLLKACSEVMMLRVA 365
Db 344 DEEDSDMPFRQITTEMILTTLVQLIVEFAKGLPGFAKISQSDQITLLKACSEVMMLRVA 403
QY 366 RYDAVSQSVLPANNOQVTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNVHVALTAIVI 425
Db 404 RYDAATDSVLPANNOQVTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNVHVALTAIVI 463
QY 426 FSDRGLQPOLVEIQRYLNTLRVYIMNQHSASPRCAVIYAKILSVLTTLTLMQNS 485
Db 464 FSDRGLQPOLVEDIQRYLNTLRVYILNQNSASPRGAVIFGEILGILTEIRTLGMQNS 523
QY 486 NMCISLKLKRNKLPPLFLEEIDV 508
Db 524 NMCISLKLKRNKLPPLFLEEIDV 546

RESULT 5

US-09-564-418-5
; Sequence 5, Application US/09564418
; Patent No. 6610828

GENERAL INFORMATION:
; APPLICANT: Syngenta

; APPLICANT: Jepson, Ian

; APPLICANT: Martinez, Alberto

; APPLICANT: Greenland, Andrew James

; TITLE OF INVENTION: A GENE SWITCH

; FILE REFERENCE: 1392/4/3

; CURRENT APPLICATION NUMBER: US/09/564,418

; CURRENT FILING DATE: 2000-05-03

; PRIOR APPLICATION NUMBER: US 09/564,418

; PRIOR FILING DATE: 2000-05-03

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5

; LENGTH: 575

; TYPE: PRT

; ORGANISM: Heliothis virescens

US-09-564-418-5

Query Match 47.6%; Score 1461.5; DB 4; Length 575;
Best Local Similarity 87.9%; Pred. No. 1.9e-124;
Matches 284; Conservative 16; Mismatches 14; Indels 9; Gaps 2;

QY 191 MRPCVVPSTCKNRKEAQRKDKLPVSTTTVDHMPALMQCDPPPPPEAARI----- 245
Db 228 MRPCVVPENOCAMRKEKKAQRKDKLPVSTTTVDHMPPIMQCDPPPPPEAARILECVQ 287
QY 246 HEVPRFLTEKLMQNRLKNVPLSANQKSLIARLVWYQDGYEQSEEDLKRVTQTWOSA 305
Db 288 HEVPRFLNEKMEQNRLKNVPLTANQKSLIARLVWYQEGYEQSEEDLKRVTQ-----S 343
QY 306 DEEDSDMPFRQITTEMILTTLVQLIVEFAKGLPGFSKISQPDQITLLKACSEVMMLRVA 365
Db 344 DEEDSDMPFRQITTEMILTTLVQLIVEFAKGLPGFAKISQSDQITLLKACSEVMMLRVA 403
QY 366 RYDAVSQSVLPANNOQVTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNVHVALTAIVI 425
Db 404 RYDAATDSVLPANNOQVTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNVHVALTAIVI 463
QY 426 FSDRGLQPOLVEIQRYLNTLRVYIMNQHSASPRCAVIYAKILSVLTTLTLMQNS 485
Db 464 FSDRGLQPOLVEDIQRYLNTLRVYILNQNSASPRGAVIFGEILGILTEIRTLGMQNS 523
QY 486 NMCISLKLKRNKLPPLFLEEIDV 508
Db 524 NMCISLKLKRNKLPPLFLEEIDV 546

RESULT 6

US-08-653-648A-7
; Sequence 7, Application US/08653648A
; Patent No. 6379945
GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Spodoptera exigua
US-08-653-648A-7

Query Match 47.2%; Score 1449; DB 3; Length 319;
Best Local Similarity 87.9%; Pred. No. 1.1e-123;
Matches 284; Conservative 15; Mismatches 14; Indels 10; Gaps 3;

QY 192 RPECVVPSTCKNRKEAQRKDKLPVSTTTVDHMPALMQCDPPPPPEAARI-----H 246
Db 1 RPECVVPENOCAMRKEKKAQRKDKLPVSTTTVDHMPPIMQCDPPPPPEAARILECVQH 60
QY 247 EVPRFLTEKLMQNRLKNVPLSANQKSLIARLVWYQDGYEQSEEDLKRVTQTWQSAD 306
Db 61 EVPRFLNEKLMQNRLKNVPLTANQKSLIARLVWYQEGYEQSEEDLKRVTQ-----SD 116
QY 307 DEEDSDMPFRQITTEMILTTLVQLIVEFAKGLPGFSKISQPDQITLLKACSEVMMLRVA 366
Db 117 DEEDSDMPFRQITTEMILTTLVQLIVEFAKGLPGFAKISQSDQITLLKACSEVMMLRVA 176
QY 367 RYDAVSQSVLPANNOQVTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNVHVALTAIVI 426
Db 177 RYDAATDSVLPANNOQVTRDNYRKAGMAYVIEDLLHFCRCMYSMMDNVHVALTAIVI 236
QY 427 SDRFGLQPOLVEIQRYLNTLRVYIMNQHSASPRCAVIYAKILSVLTTLTLMQNSN 486
Db 237 SDRFGLQPOLVEIQRYLNTLRVYILNQNSASPRGAVIFGEILGILTEIRTLGMQNSN 296
QY 487 MCISLKLKRNKLPPLFLEEIDV 508
Db 297 MCISLKLKRNKLPPLFLEEIDV 319

RESULT 7

US-09-564-418-13
; Sequence 13, Application US/09564418
; Patent No. 6610828

GENERAL INFORMATION:
; APPLICANT: Syngenta

; APPLICANT: Jepson, Ian

; APPLICANT: Martinez, Alberto

; APPLICANT: Greenland, Andrew James

; TITLE OF INVENTION: A GENE SWITCH

; FILE REFERENCE: 1392/4/3

; CURRENT APPLICATION NUMBER: US/09/564,418

; CURRENT FILING DATE: 2000-05-03

; PRIOR APPLICATION NUMBER: US 09/564,418

; PRIOR FILING DATE: 2000-05-03

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 13
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Heliothis virescens
US-09-564-418-13

Query Match      47.2%; Score 1449; DB 4; Length 319;
Best Local Similarity 87.9%; Pred. No. 1.1e-123; Mismatches 14; Indels 10; Gaps 3;
Matches 284; Conservative 15;

Qy 192 RPECVVPSTCKNKRREKAEQKDKLPVSTTTTVDHMPAIMQCDPPPEAARI-----H 246
Db 1 RPECVVPENQCAMKREKKAQREKDKLPVSTTTTVDHMPPIMQCDPPPEAARILECVQH 60

Qy 247 EVVPRFLTEKMEQNRLKNVTPLSANQKSLIARLVWYQDGYEQPSEEDLKRVTQWQAD 306
Db 61 EVVPRFLNEKMEQNRLKNVPLTANQKSLIARLVWYQGYEQPSEEDLKRVTQ----SD 116

Qy 307 BEDESDMPFRQITMTILTVQLIVEFAKGLPGFSKISQDPQITLLKACSEVMMLRVAR 366
Db 117 EDESDMPFRQITMTILTVQLIVEFAKGLPGFSKISQDPQITLLKACSEVMMLRVAR 176

Qy 367 RYDAVSDSVLFANQAYTRDNRKAGMAYVIEDLLHFCRCMYSMDNVHYALLTAIVIF 426
Db 177 RYDAATDSVLFANQAYTRDNRKAGMAYVIEDLLHFCRCMYSMDNVHYALLTAIVIF 236

Qy 427 SDRGLEQPOLVEEIQRYLNTLRVYIMNQSASPRCAVIYAKILSVLTTELTLGMQNSN 486
Db 237 SDRGLEQPOLVEEIQRYLNTLRVYILNQSASPRGAVIFGEILGILTEIRTLGMQNSN 296

Qy 487 MCISLKNRKLPPPLEEI-WDV 508
Db 297 MCISLKNRKLPPPLEEIDWDV 319

RESULT 8
US-08-653-648A-16
; Sequence 16, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PDS0047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR FILING DATE: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 16
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Spodoptera exigua
US-08-653-648A-16

Query Match      46.2%; Score 1418.5; DB 3; Length 314;
Best Local Similarity 86.5%; Pred. No. 6.4e-121;
Matches 275; Conservative 18; Mismatches 20; Indels 5; Gaps 2;

Qy 192 RPECVVPSTCKNKRREKAEQKDKLPVSTTTTVDHMPAIMQCDPPPEAARIHEVVR 251
Db 1 RPECVVPENQCAMKREKKAQREKDKLPVSTTTTVDHMPPIMQCDPPPEAARIHEVVR 60

Qy 252 FLTEKMEQNRLKNVTPLSANQKSLIARLVWYQDGYEQPSEEDLKRVTQWQADEDED 311
Db 61 FLNEKLMERTLRNVPLTANQKSLIARLVWYQGYEQPSEEDLKRVTQ----SDEEEE 116

Qy 312 SDMPFRQITMTILTVQLIVEFAKGLPGFSKISQDPQITLLKACSEVMMLRVARVDV 371
Db 117 SDMPFRQITMTILTVQLIVEFAKGLPAFAKISQSDQITLLKACSEVMMLRVARVDAA 176

Qy 372 SDSVLFANNOAYTRDNRKAGMAYVIEDLLHFCRCMYSMDNVHYALLTAIVIFSRRPG 431
Db 177 TDSVLFANNOAYTRDNRKAGMAYVIEDLLHFCRCMYSMDNVHYALLTAIVIFSRRPG 236

Qy 432 LEQPOLVEEIQRYLNTLRVYIMNQSASPRCAVIYAKILSVLTTELTLGMQNSNMCI 491
Db 237 LEUTLLVEEIQRYLNTLRVYILNQSRSRPPCVIYAKILGILTELTLGMQNSNMCI 296

Qy 492 KLNKRLPPPLEEI-WDV 508
Db 297 KLNKRVPPPFEDIDWDV 314

US-09-564-418-7
; Sequence 7, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jepson, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Spodoptera exigua
US-09-564-418-7

Query Match      46.2%; Score 1418.5; DB 4; Length 314;
Best Local Similarity 86.5%; Pred. No. 6.4e-121;
Matches 275; Conservative 18; Mismatches 20; Indels 5; Gaps 2;

Qy 192 RPECVVPSTCKNKRREKAEQKDKLPVSTTTTVDHMPAIMQCDPPPEAARIHEVVR 251
Db 1 RPECVVPENQCAMKREKKAQREKDKLPVSTTTTVDHMPPIMQCDPPPEAARIHEVVR 60

Qy 252 FLTEKMEQNRLKNVTPLSANQKSLIARLVWYQDGYEQPSEEDLKRVTQWQADEDED 311
Db 61 FLNEKLMERTLRNVPLTANQKSLIARLVWYQGYEQPSEEDLKRVTQ----SDEEEE 116

Qy 312 SDMPFRQITMTILTVQLIVEFAKGLPGFSKISQDPQITLLKACSEVMMLRVARVDV 371
Db 117 SDMPFRQITMTILTVQLIVEFAKGLPAFAKISQSDQITLLKACSEVMMLRVARVDAA 176

Qy 372 SDSVLFANNOAYTRDNRKAGMAYVIEDLLHFCRCMYSMDNVHYALLTAIVIFSRRPG 431
Db 177 TDSVLFANNOAYTRDNRKAGMAYVIEDLLHFCRCMYSMDNVHYALLTAIVIFSRRPG 236

Qy 432 LEQPOLVEEIQRYLNTLRVYIMNQSASPRCAVIYAKILSVLTTELTLGMQNSNMCI 491
Db 237 LEUTLLVEEIQRYLNTLRVYILNQSRSRPPCVIYAKILGILTELTLGMQNSNMCI 296

Qy 492 KLNKRLPPPLEEI-WDV 508
Db 297 KLNKRVPPPFEDIDWDV 314

RESULT 10
US-08-891-298-3
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; Sequence 3, Application US/08891298
; Patent No. 6300488
; GENERAL INFORMATION:
; APPLICANT: Gage, Frederick H.
; TITLE OF INVENTION: Modified Lepidopteran Receptors
; TITLE OF INVENTION: and Hybrid Multi-Functional Proteins for Use in Transcription
; TITLE OF INVENTION: and Transgene Expression Regulation
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows DEMONSTRATION Version 2.0D
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,298
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 606 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-891-298-3

Query Match 46.1%; Score 1416; DB 3; Length 606;
Best Local Similarity 82.7%; Pred. No. 2.9e-120;
Matches 278; Conservative 25; Mismatches 17; Indels 16; Gaps 5;

Qy 191 MRPECVPESTCKNRKEAQRKDK---LPVSTTTVDHMPAIMQCDDPPPPAARIHE 247
Db 272 MRPECVIQEPS-KNKDRQRQ---KKDKGILLPVSTTTVEDHMPPIQMCDPPPPAARIHE 327
Qy 248 VVPRFLTEKLMEQNRKKNVTPLSANQKSLIARLVYQGYEQPSDEDLKRVTTQWQSADE 307
Db 328 VVPRYLSEKLMEQNRQKNIPPLSANQKSLIARLVYQGYEQPSDEDLKRVTTQWQSADE 386
Qy 308 EDESDMPFRQITTEMTILTVQLIVEFAKGLPGFSGKISQPDQITLLKACSSVMMMLRVARR 367
Db 387 EDESDLPFRQITTEMTILTVQLIVEFAKGLPGFSGKISQSDQITLLKASSSEVMMMLRVARR 446
Qy 368 YDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDNVHYALLTAIVIFS 427
Db 447 YDAASDSVLFANNAKAYTRDNYRQGGMAYVIEDLLHFCRCMFAMGMDNVHVFALLTAIVIFS 506
Qy 428 DRPGLQPOLVEEIQRYVYLTIRVYIMNOHSASPRCAVIYAKILSVLTETLGTQNSNM 487
Db 507 DRPGLQPSLVEEIQRVYLTIRIYIINQNSASRCACAVIYGRILSVLTETLGTQNSNM 566
Qy 488 CISLKLKNRKLPPFLEEIVDW-----KLAPPTD 515
Db 567 CISLKLKNRKLPPFLEEIVDWAEVATHTPTVLPPTN 602

; Sequence 10, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jepsen, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
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RESULT 11
US-08-653-648A-11
; Sequence 11, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepsen, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Bombyx mori
; US-08-653-648A-11

Query Match 46.1%; Score 1416; DB 3; Length 606;
Best Local Similarity 82.7%; Pred. No. 2.9e-120;
Matches 278; Conservative 25; Mismatches 17; Indels 16; Gaps 5;

Qy 191 MRPECVPESTCKNRKEAQRKDK---LPVSTTTVDHMPAIMQCDDPPPPAARIHE 247
Db 272 MRPECVIQEPS-KNKDRQRQ---KKDKGILLPVSTTTVEDHMPPIQMCDPPPPAARIHE 327
Qy 248 VVPRFLTEKLMEQNRKKNVTPLSANQKSLIARLVYQGYEQPSDEDLKRVTTQWQSADE 307
Db 328 VVPRYLSEKLMEQNRQKNIPPLSANQKSLIARLVYQGYEQPSDEDLKRVTTQWQSADE 386
Qy 308 EDESDMPFRQITTEMTILTVQLIVEFAKGLPGFSGKISQPDQITLLKACSSVMMMLRVARR 367
Db 387 EDESDLPFRQITTEMTILTVQLIVEFAKGLPGFSGKISQSDQITLLKASSSEVMMMLRVARR 446
Qy 368 YDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMNDNVHYALLTAIVIFS 427
Db 447 YDAASDSVLFANNAKAYTRDNYRQGGMAYVIEDLLHFCRCMFAMGMDNVHVFALLTAIVIFS 506
Qy 428 DRPGLQPOLVEEIQRYVYLTIRVYIMNOHSASPRCAVIYAKILSVLTETLGTQNSNM 487
Db 507 DRPGLQPSLVEEIQRVYLTIRIYIINQNSASRCACAVIYGRILSVLTETLGTQNSNM 566
Qy 488 CISLKLKNRKLPPFLEEIVDW-----KLAPPTD 515
Db 567 CISLKLKNRKLPPFLEEIVDWAEVARRHPVLPPTN 602

RESULT 12
US-09-564-418-10
; Sequence 10, Application US/09564418
; Patent No. 6610828
; GENERAL INFORMATION:
; APPLICANT: Syngenta
; APPLICANT: Jepsen, Ian
; APPLICANT: Martinez, Alberto
; APPLICANT: Greenland, Andrew James
; TITLE OF INVENTION: A GENE SWITCH
; FILE REFERENCE: 1392/4/3
; CURRENT APPLICATION NUMBER: US/09/564,418
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/564,418
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; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 10
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Bombyx mori
US-09-564-418-10

Query Match          46.1%; Score 1416; DB 4; Length 606;
Best Local Similarity 82.7%; Pred. No. 2.9e-120;
Matches 278; Conservative 25; Mismatches 17; Indels 16; Gaps 5;

Qy 191 MRPECVPESTCKNKRKEAQRKDK---LPVSTTTVDHMPAIMQCDPPPPAAARIHE 247
Db 272 MRPECVQEPS-KNKRQRQ---KKDKGILLPVSTTTVDHMPIMQCDPPPPAAARIHE 327

Qy 248 VVPRFLTEKLMQNRLKNVTPLSANOKSLIARLVYQDGYEQPSEEDLKRVTQTWQSADE 307
Db 328 VVPRYLSKLMQNQRKNIPLSANOKSLIARLVYQEGYEQPDEDLKRVTQTWQSD-DE 386

Qy 308 EDESDMPFRQITEMTILTVQIVFAKGLPGFSGKISQPDQITLLKACSSVMMMLRVARR 367
Db 387 EDESDLPFRQITEMTILTVQIVFAKGLPGFSGKISQSDQITLLKASSVMMMLRVARR 446

Qy 368 YDAVSDSVLFANNQATYTRNYRKAGMAYVIEDLLHFCRCMYSMDNVHYALLTAIVIES 427
Db 447 YDAASDSVLFANNKAYTRDNRQGMAYVIEDLLHFCRCMFGMDNVHFAALLTAIVIFS 506

Qy 428 DRPGLQEPOLVEEIQRYVYLTNRVYIMNOHSASPRCAVIYAKILSVLTLETLTGMSNM 487
Db 507 DRPGLQEPOLVEEIQRYVYLTNRVYINQNSASRCAVIYGRILSVLTLETLTGQNSNM 566

Qy 488 CISLKLKNRKLPPFLEEIWDV-----KLAPPTD 515
Db 567 CISLKLKNRKLPPFLEEIWDVAEVARRHPTVLPPTN 602

RESULT 13
US-08-653-648A-14
; Sequence 14, Application US/08653648A
; Patent No. 6379945
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Greenland, Andrew
; APPLICANT: Martinez, Alberto
; TITLE OF INVENTION: A Gene Switch
; FILE REFERENCE: PPD50047/US
; CURRENT APPLICATION NUMBER: US/08/653,648A
; CURRENT FILING DATE: 1996-05-24
; PRIOR APPLICATION NUMBER: GB 9510759.5
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: GB 9605656.9
; PRIOR FILING DATE: 1996-03-18
; PRIOR APPLICATION NUMBER: GB 9513882.2
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: GB 9517316.7
; PRIOR FILING DATE: 1995-08-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 14
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Aedes aegypti
US-08-653-648A-14

Query Match          37.1%; Score 1139; DB 3; Length 674;
Best Local Similarity 59.6%; Pred. No. 6e-95;
Matches 227; Conservative 63; Mismatches 67; Indels 24; Gaps 7;

Qy 191 MRPECVPESTCKNKRKEAQRKDKL-----PVSTTTV-----DHHMPAIMQCDPPPPAA 243
Db 255 MRPECVVPENQCAIKRKEKAQKEDKQVNTATVSTTNSYRSEILPILMKCDPPP----- 310

Qy 244 RIHEVVPRLTEKLMQNRLKNVTPLSANOKSLIARLVYQDGYEQPSEEDLKRVTQTWQ 303
Db 311 --HQATP-LLPEKLLQENLRNIPLLTANQMAVIYKLIWYQDGYEQPSEEDLKRI--MIG 365

Qy 304 SADEDESDMPFRQITEMTILTVQIVFAKGLPGFSGKISQPDQITLLKACSSVMMMLR 363
Db 366 SPNEEDQHDVHFRHTEITILTVQIVFAKGLPAFTKIPQEDQITLLKACSSVMMMLR 425

Qy 364 VARRYDAVSDSVLFANNQATYTRNYRKAGMAYVIEDLLHFCRCMYSMDNVHYALLTAI 423
Db 426 MARRYDAATDSILFANNRSYTRDSYRMAGMADTIEDLLHFCRCMFSLTVDNVYALLTAI 485

Qy 424 VIFSDRPGLEQPOLVEEIQRYVYLTNRVYIMNOHSASPRCAVIYAKILSVLTLETLGMQ 483
Db 486 VIFSDRPGLEQAEVLVEHIQSYIIDTLRIYILNRHAGDPKCSVIFAKLLSILTELTILGNQ 545

486 VIFSDRPGLEQAEVLVEHIQSYIIDTLRIYILNRHAGDPKCSVIFAKLLSILTELTILGNQ 545

Query Match          37.1%; Score 1139; DB 4; Length 675;
Best Local Similarity 59.6%; Pred. No. 6e-95;
Matches 227; Conservative 63; Mismatches 67; Indels 24; Gaps 7;

Qy 191 MRPECVPESTCKNKRKEAQRKDKL-----PVSTTTV-----DHHMPAIMQCDPPPPAA 243
Db 255 MRPECVVPENQCAIKRKEKAQKEDKQVNTATVSTTNSYRSEILPILMKCDPPP----- 310

Qy 244 RIHEVVPRLTEKLMQNRLKNVTPLSANOKSLIARLVYQDGYEQPSEEDLKRVTQTWQ 303
Db 311 --HQATP-LLPEKLLQENLRNIPLLTANQMAVIYKLIWYQDGYEQPSEEDLKRI--MIG 365

Qy 304 SADEDESDMPFRQITEMTILTVQIVFAKGLPGFSGKISQPDQITLLKACSSVMMMLR 363
Db 366 SPNEEDQHDVHFRHTEITILTVQIVFAKGLPAFTKIPQEDQITLLKACSSVMMMLR 425

Qy 364 VARRYDAVSDSVLFANNQATYTRNYRKAGMAYVIEDLLHFCRCMYSMDNVHYALLTAI 423
Db 426 MARRYDAATDSILFANNRSYTRDSYRMAGMADTIEDLLHFCRCMFSLTVDNVYALLTAI 485

Qy 424 VIFSDRPGLEQPOLVEEIQRYVYLTNRVYIMNOHSASPRCAVIYAKILSVLTLETLGMQ 483
Db 486 VIFSDRPGLEQAEVLVEHIQSYIIDTLRIYILNRHAGDPKCSVIFAKLLSILTELTILGNQ 545
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2005, 14:36:56 ; Search time 137 Seconds
(without alignments)
1426.525 Million cell updates/sec

Title: US-10-087-167-121

Perfect score: 3072

Sequence: 1 MQQYVDFSPAFIRYLFAW.....ADFFEQMTDALGIDEYGG 588

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	3072	100.0	588	14	US-10-087-167-121
2	3002.5	97.7	593	14	Sequence 121, App
3	2968.5	96.6	591	14	Sequence 125, App
4	2965	96.5	588	14	Sequence 119, App
5	2895.5	94.3	599	14	Sequence 123, App
6	2731	88.9	553	14	Sequence 127, App
7	2552	83.1	620	14	US-10-087-167-105
8	2551.5	83.1	615	14	US-10-087-167-137
9	2494.5	81.2	599	14	US-10-087-167-135
10	2493	81.2	602	14	Sequence 148, App
11	2312	75.3	475	14	US-10-087-167-143
12	2082	67.8	499	14	Sequence 129, App
13	2012.5	65.5	504	14	US-10-087-167-68
					Sequence 76, Appl

14	1978.5	64.4	502	14	US-10-087-167-66
15	1975	64.3	499	14	US-10-087-167-70
16	1975	64.3	505	14	US-10-087-167-94
17	1909	62.1	507	14	US-10-087-167-78
18	1905.5	62.0	510	14	US-10-087-167-80
19	1741	56.7	501	14	US-10-087-167-64
20	1716.5	55.9	500	14	US-10-087-167-92
21	1691	55.0	521	14	US-10-087-167-90
22	1670	54.4	513	14	US-10-087-167-74
23	1666.5	54.2	516	14	US-10-087-167-72
24	1638.5	53.3	496	14	US-10-087-167-86
25	1638	53.3	487	14	US-10-087-167-84
26	1582	51.5	546	14	US-10-295-370-2
27	1582	51.5	546	14	US-10-292-356-2
28	1582	51.5	546	14	US-10-292-324-2
29	1557	50.7	556	14	US-10-083-842A-7
30	1557	50.7	556	14	US-10-087-167-2
31	1545	50.3	556	15	US-10-606-060A-11
32	1467	47.8	401	15	US-10-468-199-70
33	1467	47.8	412	9	US-09-965-703-11
34	1467	47.8	412	9	US-09-965-703-12
35	1467	47.8	412	15	US-10-239-134-11
36	1467	47.8	412	15	US-10-239-134-12
37	1467	47.8	440	9	US-09-965-703-71
38	1467	47.8	440	15	US-10-239-134-63
39	1467	47.8	513	9	US-09-965-703-59
40	1467	47.8	513	15	US-10-239-134-50
41	1461.5	47.6	575	15	US-10-606-060A-5
42	1457	47.4	320	9	US-09-965-703-15
43	1457	47.4	320	15	US-10-239-134-15
44	1457	47.4	320	15	US-10-468-199-7
45	1457	47.4	334	9	US-09-965-703-13

ALIGNMENTS

RESULT 1

US-10-087-167-121
; Sequence 121, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 121
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Synthetic Construct
US-10-087-167-121

Query Match 100.0%; Score 3072; DB 14; Length 588;
Best Local Similarity 100.0%; Pred. No. 5.5e-248;
Matches 588; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQQYVDFSPAFIRYLFAWYCFRCSPCCVLLQSGATMKLLSSITEQACDLCRLKKL 60

Db 1 MQQYVDFSPAFIRYLFAWYCFRCSPCCVLLQSGATMKLLSSITEQACDLCRLKKL 60

Qy 61 KCSKEKPKCAKCLKNNECRYSPKTKSPPLTRAHLTEVESLERLEQLFLIFPREDLDM 120

Db 61 KCSKEKPKCAKCLKNNECRYSPKTKSPPLTRAHLTEVESLERLEQLFLIFPREDLDM 120

121 ILKWDSDI KALLTG L FVDQNNKDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180
121 ILKWDSDI KALLTG L FVDQNNKDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180
181 GORQ LTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVSTTTTVDHMPAIIQCDDPPPP 240
181 GORQ LTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVSTTTTVDHMPAIIQCDDPPPP 240
241 EAARIHEVVPFLTEKMEQNRLKNVTPLSANQSKLIARLVWYQDGYEQPSEEDL 300
241 EAARIHEVVPFLTEKMEQNRLKNVTPLSANQSKLIARLVWYQDGYEQPSEEDL 300
301 TWQSADEDESDMPFRQITMTTILTVQLIIVEFAKGLPGFSKISQPDQITLLKACSEVM 360
301 TWQSADEDESDMPFRQITMTTILTVQLIIVEFAKGLPGFSKISQPDQITLLKACSEVM 360
361 MLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMDNVHVAL 420
361 MLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMDNVHVAL 420
421 TAIIVFSDRPGLEQPOLVEEIQRYLYLNTLRVYIMNQHSA SPRCAVIYAKILSVLT 480
421 TAIIVFSDRPGLEQPOLVEEIQRYLYLNTLRVYIMNQHSA SPRCAVIYAKILSVLT 480
481 GMQNSNMCI S LKNRKLPPLEBIWVKLAPPTDVS LGDELHLDGEDVAMAHADLDDF 540
481 GMQNSNMCI S LKNRKLPPLEBIWVKLAPPTDVS LGDELHLDGEDVAMAHADLDDF 540
541 DLDMLGDGSPGPGFTPHDSAPY GALDMADFEFQMFTDALGIDEYGG 588
541 DLDMLGDGSPGPGFTPHDSAPY GALDMADFEFQMFTDALGIDEYGG 588

RESULT 2

US-10-087-167-125
; Sequence 125, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Synthetic Construct
US-10-087-167-125

Query Match 97.7%; Score 3002.5; DB 14; Length 593;
Best Local Similarity 97.0%; Pred. No. 3.6e-242;
Matches 575; Conservative 7; Mismatches 6; Indels 5; Gaps 1;

1 MQQLYVDFSPAFIRYLFAMYCFRCSPCCLVLLQGSATMKLLSSIEQACDICRLK 60
1 MQQLYVDFSPAFIRYLFAMYCFRCSPCCLVLLQGSATMKLLSSIEQACDICRLK 60
61 KCSKEPKCAKCLKNWECRYSPTKRSP LTRAH L TEVESRLERLEQLFLIIPREDLDM 120
61 KCSKEPKCAKCLKNWECRYSPTKRSP LTRAH L TEVESRLERLEQLFLIIPREDLDM 120
121 ILKWDSDI KALLTG L FVDQNNKDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180
121 ILKWDSDI KALLTG L FVDQNNKDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180

181 GORQ LTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVSTTTTVDHMPAIIQCDDPPPP 240
181 GORQ LTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVSTTTTVDHMPAIIQCDDPPPP 240
241 EAARI-----HEVVPFLTEKMEQNRLKNVTPLSANQSKLIARLVWYQDGYEQPSEEDL 295
241 EAARILECLQHEVVPFLSEKMEQNRLKNIPPLTANQQFLIARLVWYQDGYEQPSEEDL 300
296 KRVOTQWQSADEDESDMPFRQITMTTILTVQLIIVEFAKGLPGFSKISQPDQITLLKAC 355
301 KRVOTQWQSADEDESDMPFRQITMTTILTVQLIIVEFAKGLPGFSKISQPDQITLLKAC 360
356 SSEVMMLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMDNV 415
361 SSEVMMLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMDNV 420
416 HYALLTAIIVFSDRPGLEQPOLVEEIQRYLYLNTLRVYIMNQHSA SPRCAVIYAKILSVLT 475
421 HYALLTAIIVFSDRPGLEQPOLVEEIQRYLYLNTLRVYIMNQHSA SPRCAVIYAKILSVLT 480
476 ELRTLGQNSNMCI S LKNRKLPPLEBIWVKLAPPTDVS LGDELHLDGEDVAMAHAD 535
481 ELRTLGQNSNMCI S LKNRKLPPLEBIWVKLAPPTDVS LGDELHLDGEDVAMAHAD 540
536 ALDDFDLMDLGDGSPGPGFTPHDSAPY GALDMADFEFQMFTDALGIDEYGG 588
541 ALDDFDLMDLGDGSPGPGFTPHDSAPY GALDMADFEFQMFTDALGIDEYGG 593

RESULT 3

US-10-087-167-119
; Sequence 119, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 119
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Synthetic Construct
US-10-087-167-119

Query Match 96.6%; Score 2968.5; DB 14; Length 591;
Best Local Similarity 95.9%; Pred. No. 2.5e-239;
Matches 568; Conservative 13; Mismatches 6; Indels 5; Gaps 2;

1 MQQLYVDFSPAFIRYLFAMYCFRCSPCCLVLLQGSATMKLLSSIEQACDICRLK 60
1 MQQLYVDFSPAFIRYLFAMYCFRCSPCCLVLLQGSATMKLLSSIEQACDICRLK 60
61 KCSKEPKCAKCLKNWECRYSPTKRSP LTRAH L TEVESRLERLEQLFLIIPREDLDM 120
61 KCSKEPKCAKCLKNWECRYSPTKRSP LTRAH L TEVESRLERLEQLFLIIPREDLDM 120
121 ILKWDSDI KALLTG L FVDQNNKDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180
121 ILKWDSDI KALLTG L FVDQNNKDAVTDRLASVETDMLTLRQHRISATSSSESSNK 180
181 GORQ LTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVSTTTTVDHMPAIIQCDDPPPP 240
181 GORQ LTVSTRMRPECVVPSTCKNKRKEAQRKDKLPVSTTTTVDHMPAIIQCDDPPPP 240

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Qy 241 EAARIHEVVPRLTEKLMQNRKLVNTPLSANQKSLIARLVVYQGVQEPSEEDLKRVTQ 300
Db 241 EAARIHEVVPRLTEKLMQNRKLVNTPLSANQKSLIARLVVYQGVQEPSEEDLKRVTQ 300
Qy 301 TWQSADEDESDMPFRQITMTILTVQLIIVEFAKGLPGFSKISQSDQITLLKACSSVM 360
Db 301 TWQS-DEDESDMPFRQITMTILTVQLIIVEFAKGLPGFSKISQSDQITLLKACSSVM 359
Qy 361 MLRVARRDYAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHVAL 420
Db 360 MLRVARRDYAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHVAL 419
Qy 421 TAIIVFSRDRPGLQEPQVVEEIQRYLYNTLRVYINNOHSASPRCAVIYAKILSVLTELRTL 480
Db 420 TAIIVFSRDRPGLQEPQVVEEIQRYLYNTLRVYINNOHSASPRCAVIYAKILSVLTELRTL 479
Qy 481 GMQNSNMCIISLKLKRNKLPPLFEEIWDVYVIESGKLAPPTDVSLGDELHLDGEDVAMAHADA 536
Db 480 GMQNSNMCIISLKLKRNKLPPLFEEIWDVYVIESGKLAPPTDVSLGDELHLDGEDVAMAHADA 539
Qy 537 LDDFDLMLGDSGSPGPGFTPHDSAPYCALDMADFEPEQMTDALGIDEYGG 588
Db 540 LDDFDLMLGDSGSPGPGFTPHDSAPYCALDMADFEPEQMTDALGIDEYGG 591

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RESULT 4

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US-10-087-167-123
; Sequence 123, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Synthetic Construct
US-10-087-167-123

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Query Match 96.5%; Score 2965; DB 14; Length 588;
Best Local Similarity 96.3%; Pred. No. 4,9e-239;
Matches 566; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MQQLYVDFPSPAFIRYLFAMWCFPCRCSPCCVLVLLQGSATMKLLSSIEQACDICRLKKL 60
Db 1 MQQLYVDFPSPAFIRYLFAMWCFPCRCSPCCVLVLLQGSATMKLLSSIEQACDICRLKKL 60
Qy 61 KCSKEKPKCAKCLKNNWECRYSPKTKRSPLTRAHLTEVESLERLEQLFLIIFREDLDM 120
Db 61 KCSKEKPKCAKCLKNNWECRYSPKTKRSPLTRAHLTEVESLERLEQLFLIIFREDLDM 120
Qy 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMPDLTLRQHRISATSSSESSNK 180
Db 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMPDLTLRQHRISATSSSESSNK 180
Qy 181 GORQLTVSTRMRPECVWPSTCKNKRREKAEQKDKLPVSTTTVDHMPAIMQCDPPPP 240
Db 181 GORQLTVSTRMRPECVWPSTCKNKRREKAEQKDKLPVSTTTVDHMPAIMQCDPPPP 240
Qy 241 EAARIHEVVPRLTEKLMQNRKLVNTPLSANQKSLIARLVVYQGVQEPSEEDLKRVTQ 300
Db 241 EAARIHEVVPRLTEKLMQNRKLVNTPLSANQKSLIARLVVYQGVQEPSEEDLKRVTQ 300

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Qy 301 TWQSADEDESDMPFRQITMTILTVQLIIVEFAKGLPGFSKISQSDQITLLKACSSVM 360
Db 301 TWQLESEEBETDMPFRQITMTILTVQLIIVEFAKGLPGFSKISQSDQITLLKACSSVM 360
Qy 361 MLRVARRDYAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHVAL 420
Db 361 MLRVARRDYAVSDSVLFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHVAL 420
Qy 421 TAIIVFSRDRPGLQEPQVVEEIQRYLYNTLRVYINNOHSASPRCAVIYAKILSVLTELRTL 480
Db 421 TAIIVFSRDRPGLQEPQVVEEIQRYLYNTLRVYINNOHSASPRCAVIYAKILSVLTELRTL 480
Qy 481 GMQNSNMCIISLKLKRNKLPPLFEEIWDVYVIESGKLAPPTDVSLGDELHLDGEDVAMAHADA 540
Db 481 GTQNSNMCIISLKLKRNKLPPLFEEIWDVYVIESGKLAPPTDVSLGDELHLDGEDVAMAHADA 540
Qy 541 DLDMLGDSGSPGPGFTPHDSAPYCALDMADFEPEQMTDALGIDEYGG 588
Db 541 DLDMLGDSGSPGPGFTPHDSAPYCALDMADFEPEQMTDALGIDEYGG 588

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RESULT 5

```

US-10-087-167-127
; Sequence 127, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/242,969
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Synthetic Construct
US-10-087-167-127

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Query Match 94.3%; Score 2895.5; DB 14; Length 599;
Best Local Similarity 92.7%; Pred. No. 3.3e-233;
Matches 555; Conservative 17; Mismatches 16; Indels 11; Gaps 2;

Qy 1 MQQLYVDFPSPAFIRYLFAMWCFPCRCSPCCVLVLLQGSATMKLLSSIEQACDICRLKKL 60
Db 1 MQQLYVDFPSPAFIRYLFAMWCFPCRCSPCCVLVLLQGSATMKLLSSIEQACDICRLKKL 60
Qy 61 KCSKEKPKCAKCLKNNWECRYSPKTKRSPLTRAHLTEVESLERLEQLFLIIFREDLDM 120
Db 61 KCSKEKPKCAKCLKNNWECRYSPKTKRSPLTRAHLTEVESLERLEQLFLIIFREDLDM 120
Qy 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMPDLTLRQHRISATSSSESSNK 180
Db 121 ILKWDLSQDIKALLTGLFVQDNVKNDAVTDRLASVETDMPDLTLRQHRISATSSSESSNK 180
Qy 181 GORQLTVSTRMRPECVWPSTCKNKRREKAEQKDKLPVSTTTVDHMPAIMQCDPPPP 240
Db 181 GORQLTVSTRMRPECVWPSTCKNKRREKAEQKDKLPVSTTTVDHMPAIMQCDPPPP 240
Qy 241 EAARIHEVVPRLTEKLMQNRKLVNTPLSANQKSLIARLVVYQGVQEPSEEDLKRVTQ 295
Db 241 EAARILECLQHEVVPRLTEKLMQNRKLVNTPLSANQKSLIARLVVYQGVQEPSEEDLKRVTQ 300
Qy 296 KRVTTQWQSADEDESDMPFRQITMTILTVQLIIVEFAKGLPGFSKISQSDQITLLKAC 355
Db 301 KRVTTQWLESEEBETDMPFRQITMTILTVQLIIVEFAKGLPGFSKISQSDQITLLKAC 360

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Qy 356 SSEVMMLRARRYDAVSDVLPFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNV 415
Db 361 SSEVMMLRARRYDAATDSVLPFANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMSMDNV 420
Qy 416 HYALLTAIVFSDRPGLEQPOLVEEIQRYVYLNTRVYIMNQHSPRCNAVITYAKILSVLT 475
Db 421 HYALLTAIVFSDRPGLEQPOLVEEIQRYVYLNTRVYIMNQHSPRCNAVIFGKILGVLT 480
Qy 476 ELRTIGMNSNMCIISLKNRKLPPFLEEIWV-----KLAPPTDVSLGDELHLDGEDV 529
Db 481 ELRTIGTQNSNMCIISLKNRKLPPFLEEIWDAEVSTTKLAPPTDVSLGDELHLDGEDV 540
Qy 530 AMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYCALDMADFEFEQMTDALGIDEYGG 588
Db 541 AMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYCALDMADFEFEQMTDALGIDEYGG 599

RESULT 6
US-10-087-167-105
; Sequence 105, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
; LENGTH: 553
; TYPE: PRT
; ORGANISM: synthetic construct
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(3972)
; OTHER INFORMATION: GAL4-Manduca EcR-VP16 fragment in pCGS202
US-10-087-167-105
```

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Query Match 88.9%; Score 2731; DB 14; Length 553;
Best Local Similarity 95.3%; Pred. No. 1.7e-219;
Matches 527; Conservative 10; Mismatches 10; Indels 6; Gaps 1;

Qy 42 MKLSSIEQACDICRLKKLKCSKEPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 101
Db 1 MKLSSIEQACDICRLKKLKCSKEPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESR 60
Qy 102 LERLEQLFLIFPREDLMDILKMSLQDIKALLTGLFVQDNVNKDAVTDRLASVETDML 161
Db 61 LERLEQLFLIFPREDLMDILKMSLQDIKALLTGLFVQDNVNKDAVTDRLASVETDML 120
Qy 162 TLQHRISATSSSESSNKGQRQLTVSTRMRPECVPESTCKNKRKEAQRKDKLPVS 221
Db 121 TLQHRISATSSSESSNKGQRQLTVSTRMRPECVPESTCKNKRKEAQRKDKLPVS *180
Qy 222 TTTVDHMPALIMQCDPPPPPEARHEVVPFLTEKLMQNRLKNVTPLSANOKSLIARLV 281
Db 181 TTTVDHMPALIMQCDPPPPPEARHEVVPFLTEKLMQNRLKNVTPLSANOKSLIARLV 240
Qy 282 WYQGYEQPSSEDLKRVYQTQWQSEDEDESDMPFRQITMTILTVQIIVEFAKGLPGFS 341
Db 241 WYQGYEQPSSEDLKRVYQTQWQSEDEDESDMPFRQITMTILTVQIIVEFAKGLPGFS 300
Qy 342 KISQDQITLLKACSEVMMLRVARRYDAVSDVLPFANNOAYTRDNYRKAGMAYVIEDLL 401
Db 301 KISQDQITLLKACSEVMMLRVARRYDAATDSVLPFANNOAYTRDNYRKAGMSYVIEDLL 360
```

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Qy 402 HFRCMYSMSMDNVHYALLTAIVFSDRPGLEQPOLVEEIQRYVYLNTRVYIMNQHSP 461
Db 361 HFRCMYSMSMDNVHYALLTAIVFSDRPGLEQPOLVEEIQRYVYLNTRVYIMNQHSP 420
Qy 462 RCAVIYAKILSVLTTELRTLGQNSNMCIISLKNRKLPPFLEEIWV-----KLAPPTD 515
Db 421 RCAVIFGKILGVLTTELRTLGQNSNMCIISLKNRKLPPFLEEIWDAEVSTTKLAPPTD 480
Qy 516 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYCALDMADFEFEQ 575
Db 481 VSLGDELHLDGEDVAMAHADALDDFDLMDLGDGSPGPGFTPHDSAPYCALDMADFEFEQ 540
Qy 576 MFTDALGIDEYGG 588
Db 541 MFTDALGIDEYGG 553

RESULT 7
US-10-087-167-137
; Sequence 137, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 137
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Synthetic Construct
; OTHER INFORMATION:
US-10-087-167-137
```

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Query Match 83.1%; Score 2552; DB 14; Length 620;
Best Local Similarity 84.4%; Pred. No. 1.9e-204;
Matches 505; Conservative 19; Mismatches 45; Indels 30; Gaps 4;

Qy 1 MQQLYVDFSPAFIRYLFAMYCFRCSPCCLVLLQGSATMKLLSSIEQACDICRLKKL 60
Db 1 MQQLYVDFSPAFIRYLFAMYCFRCSPCCLVLLQGSATMKLLSSIEQACDICRLKKL 60
Qy 61 KCSKEPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESRLEQLFLIFPREDLMD 120
Db 61 KCSKEPKCAKCLKNWECRYSPKTKRSPLTRAHLTEVESRLEQLFLIFPREDLMD 120
Qy 121 ILKMSLQDIKALLTGLFVQDNVNKDAVTDRLASVETDMLTLQHRISATSSSESSN 180
Db 121 ILKMSLQDIKALLTGLFVQDNVNKDAVTDRLASVETDMLTLQHRISATSSSESSN 180
Qy 181 GQRQLTVSTRMRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPALIMQCDPPPP 240
Db 181 GQRQLTVSTRMRPECVPESTCKNKRKEAQRKDKLPVSTTTVDHMPALIMQCDPPPP 240
Qy 241 EAARIHEVVPFLTEKLMQNRLKNVTPLSANOKSLIARLVYQDGYEQPSSEDLKRVYQ 300
Db 241 EAARIHEVVPFLTEKLMQNRLKNVTPLSANOKSLIARLVYQDGYEQPSSEDLKRVYQ 300
Qy 301 TWQSEADEDESDMPFRQITMTILTVQIIVEFAKGLPGFSKISQDQITLLKACSEVM 360
Db 301 TWQSEADEDESDMPFRQITMTILTVQIIVEFAKGLPGFSKISQDQITLLKACSEVM 360
Qy 361 MLRVARRYDAVSDVLPFANNOAYTRDNYRKAGMAYVIEDLLHFCRCMYSMSMDNVHYALL 420
Db 361 MLRVARRYDAATDSVLPFANNOAYTRDNYRKAGMSYVIEDLLHFCRCMYSMSMDNVHYALL 420
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Qy 421 TAIVIFSDRPGLEQPOLVEEIQRYRYLNTLRVYIMNHQHSASPRCAVIYAKILSVLTSLRTL 480
Db 421 TAIVIFSDRPGLEQPOLVEEIQRYRYLNTLRVYIMNHQHSASPRCAVIFGKILGVLTLRTL 480
Qy 481 GMQNSNCISLKNRKLPPFLEEIWDVKLAPPTDVSIGDEL-----HLDG 526
Db 481 GTQNSNCISLKNRKLPPFLEEIWDVAEYSTTKLELATADPGKTATTTTTTSEITT 540
Qy 527 EDVAMAHADAL-----DDFDLMDLGDG--DSPPGPGFTPHDSA-----PYGALDM 568
Db 541 ETGALEDSDSLAAHLLQGTEDAEAVLGLSLDPPSAGAKAVLDDSDGSFVWPAASFDM 598

RESULT 8
US-10-087-167-135
; Sequence 135, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
; LENGTH: 615
; TYPE: PRN
; ORGANISM: Synthetic Construct
US-10-087-167-135

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Query Match	83.11%	Score 2551.5	DB 14	Length 615
Best Local Similarity	89.8%	Pred. No. 2.1e-204		
Matches 501	Conservative 11	Mismatches 35	Indels 11	Gaps 3
Qy	1	MOQLYVDFPSPAFTRYLPFWCYCFPCRCSPCCLVLLQGSATMKLLSSIEQACDICRLKKL	60	
Db	1	MOQLYVDFPSPAFTRYLPFWCYCFPCRCSPCCLVLLQGSATMKLLSSIEQACDICRLKKL	60	
Qy	61	KCSKEKPKCAKCLKNNECRRSPKTKRSPLTRAHLTEVESRLERLEQLFLFIFFREDLDM	120	
Db	61	KCSKEKPKCAKCLKNNECRRSPKTKRSPLTRAHLTEVESRLERLEQLFLFIFFREDLDM	120	
Qy	121	ILKWDLSQDIKALLTGLFPVQDNVNKDAVTDRLASVETDMPLTLRQHRISATSSSESSNK	180	
Db	121	ILKWDLSQDIKALLTGLFPVQDNVNKDAVTDRLASVETDMPLTLRQHRISATSSSESSNK	180	
Qy	181	GORQLTVSTRMRPECVPESTCKNKRKEQAQEKDKLPVSTTTVDDHMPAIMQCDPPPP	240	
Db	181	GORQLTVSTRMRPECVPESTCKNKRKEQAQEKDKLPVSTTTVDDHMPAIMQCDPPPP	240	
Qy	241	EAARIHEVVPFLTEKLEMEQNLKNVTPLSANQKSLIARLVVYQDGVEQPSSEEDLKRVQ	300	
Db	241	EAARIHEVVPFLTEKLEMEQNLKNVTPLSANQKSLIARLVVYQDGVEQPSSEEDLKRVQ	300	
Qy	301	TWQSADEDEDSMPFRQITWTITLTQIIVFEFAKGLPGFSKIISOPDQITLLKACSSVM	360	
Db	301	TWQLEEESEETDMPFRQITWTITLTQIIVFEFAKGLPGFSKIISQSDQITLLKASSVM	360	
Qy	361	MLRVARRYDAVSDSVLFANNOAYTRDNYRKAGMYVIEDLLHFCRCMTSMSMDNVHYALL	420	
Db	361	MLRVARRYDAATDSVLFANNOAYTRDNYRKAGMSYVIEDLLHFCRCMTSMSMDNVHYALL	420	
Qy	421	TAIIVIFSDRPGLEQPOLVEETORYYLNTLRVYIMNHQASPRCAVIYAKILSVLTELRTL	480	
Db	421	TAIIVIFSDRPGLEQPOLVEETORYYLKTLRVYILNHSASPRCALVFGKILGVLTELRTL	480	


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; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 68
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Synthetic construct
US-10-087-167-68

Query Match      67.8%; Score 2082; DB 14; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.9e-165;
Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 191 MRPECVPESTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPPEAARIHEVVP 250
Db 102 MRPECVPESTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPPEAARILECIQ 161

Qy 246 HEVVPRLFTEKLMQNRLKNVTPLSANOKSLIARLVYQDGYEQPSEEDLKRVTTQWQSA 305
Db 162 HEVVPRLFTEKLMQNRLKNVTPLSANOKSLIARLVYQDGYEQPSEEDLKRVTTQWQSA 221

Qy 306 DEDESDMPFRQITMTILTQVLIQVEFAKGLPGFSKISQPDQITLLKACSEVMMLRVA 365
Db 222 DEDESDMPFRQITMTILTQVLIQVEFAKGLPGFSKISQPDQITLLKACSEVMMLRVA 281

Qy 366 RRYDAVSDSVLFANNOAYTRDNRKAGMAYVIEDLLHFCRCMYSMNDNVHYALLTAIVI 425
Db 282 RRYDAVSDSVLFANNOAYTRDNRKAGMAYVIEDLLHFCRCMYSMNDNVHYALLTAIVI 341

Qy 426 FSDRPGLEQPOLVBEIQRYIYNTLRVYIMNQHSPRCVAVIYAKILSVLTSLRTIGMONS 485
Db 342 FSDRPGLEQPOLVBEIQRYIYNTLRVYIMNQHSPRCVAVIYAKILSVLTSLRTIGMONS 401

Qy 486 NMCISLKLKRNKLPFLFEEIWDVKLAPPTDVSGLDELHLDGEDVAMAHADALDDFDLML 545
Db 402 NMCISLKLKRNKLPFLFEEIWDVKLAPPTDVSGLDELHLDGEDVAMAHADALDDFDLML 461

Qy 546 GDGSPGPGFTPHDSAPYGALDMADFEFEQMTDALGIDEYGG 588
Db 462 GDGSPGPGFTPHDSAPYGALDMADFEFEQMTDALGIDEYGG 504

RESULT 14
US-10-087-167-66
; Sequence 66, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 66
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Synthetic construct
US-10-087-167-66

Query Match      64.4%; Score 1978.5; DB 14; Length 502;
Best Local Similarity 94.0%; Pred. No. 1.3e-156;
Matches 378; Conservative 13; Mismatches 6; Indels 5; Gaps 2;

Qy 191 MRPECVPESTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPPEAARIHEVVP 250
Db 102 MRPECVPESTCKNKRREKEAQRKDKLPVSTTTVDHMPAIMQCDDPPPPPEAARIHEVVP 161

Qy 251 RFLTEKLMQNRLKNVTPLSANOKSLIARLVYQDGYEQPSEEDLKRVTTQWQSADEDE 310
Db 162 RFLTEKLMQNRLKNVTPLSANOKSLIARLVYQDGYEQPSEEDLKRVTTQWQSADEDE 220

Qy 311 DSDMPFRQITMTILTQVLIQVEFAKGLPGFSKISQPDQITLLKACSEVMMLRVARRYDA 370
Db 221 DSDMPFRQITMTILTQVLIQVEFAKGLPGFSKISQPDQITLLKACSEVMMLRVARRYDA 280

Qy 371 VSDSVLFANNOAYTRDNRKAGMAYVIEDLLHFCRCMYSMNDNVHYALLTAIVIFSDRP 430
Db 281 ATDSVLFANNOAYTRDNRKAGMAYVIEDLLHFCRCMYSMNDNVHYALLTAIVIFSDRP 340

; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 76
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Synthetic construct
US-10-087-167-76

Query Match      65.5%; Score 2012.5; DB 14; Length 504;
Best Local Similarity 95.5%; Pred. No. 1.9e-159;
Matches 385; Conservative 7; Mismatches 6; Indels 5; Gaps 1;

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Qy 431 GLEQPLVEEIQRYYLNTLRVYIMNQHSASPRCAVIYAKILSVLTSLTGLMQNSNCIS 490
Db 341 GLEQPLAVEEIQRYYLNTLRVYILNQNSASPRCPWFPAKILGILTELTLGLMQNSNCIS 400
Qy 491 LKLNKRLPPFLEEIWV-----KLAPPTDVSIGDELHLDGEDVAMAHADALDDFDLMLG 546
Db 401 LKLNKRLPPFLEEIWVESRGLAPPTDVSIGDELHLDGEDVAMAHADALDDFDLMLG 460
Qy 547 DGDSPGGFTPHDSAPYCALDMADFEFEQMETDALGIDEXG 588
Db 461 DGDSPGGFTPHDSAPYCALDMADFEFEQMETDALGIDEXG 502
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RESULT 15

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US-10-087-167-70
; Sequence 70, Application US/10087167
; Publication No. US20030154509A1
; GENERAL INFORMATION:
; APPLICANT: Pascal, Erica
; APPLICANT: Valentine, Scott
; APPLICANT: Brown, Jeffrey
; APPLICANT: Cockrell, Adam
; APPLICANT: Johnson, Brian
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION IN PLANTS
; FILE REFERENCE: 50018A
; CURRENT APPLICATION NUMBER: US/10/087,167
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/242,969
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Synthetic construct
US-10-087-167-70
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Query Match 64.3%; Score 1975; DB 14; Length 499;
Best Local Similarity 94.5%; Pred. No. 2.6e-156;
Matches 376; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

Qy 191 MRPECVPESTCKNKRREKAEQKDLPVSTTTTVDHMPAIMQCDPPPEAAARIHEVVP 250
Db 102 MRPECVPESTCKNKRREKAEQKDLPVSTTTTVDHMPAIMQCDPPPEAAARIHEVVP 161
Qy 251 RFLTEKLMQNRLKNVTPLSANQKSLIARLWYQDGYEQPSEEDLKRVTQTWQSADDEE 310
Db 162 RFLTEKLMQNRLKNVTPLSANQKSLIARLWYQEGYEQPSEEDLKRVTQTWQLEEEEEE 221
Qy 311 DSDMPFQITMTILTQLIIVEFAKGLPGFSKISQPDQITLLKACSEVMMLRVARRYDA 370
Db 222 ETDMFPFQITMTILTQLIIVEFAKGLPGFSKISQSDQITLLKASSEVMMLRVARRYDA 281
Qy 371 VSDSVLFANNQAYTRDNYRKAGMAYVIEDLLHFCRCMYSMDNVHYALLTAIVIFSDDP 430
Db 282 ATDSVLFANNQAYTRDNYRKAGMSYVIGDLLHFCRCMYSMDNVHYALLTAIVIFSDDP 341
Qy 431 GLEQPLVEEIQRYYLNTLRVYIMNQHSASPRCAVIYAKILSVLTSLTGLMQNSNCIS 490
Db 342 GLEQPLAVEEIQRYYLNTLRVYILNQNSASPRCAVLFGKILGVLTELTLGLTQNSNCIS 401
Qy 491 LKLNKRLPPFLEEIWVKLAPPTDVSIGDELHLDGEDVAMAHADALDDFDLMLGDGDS 550
Db 402 LKLNKRLPPFLEEIWVKLAPPTDVSIGDELHLDGEDVAMAHADALDDFDLMLGDGDS 461
Qy 551 PGCGFTPHDSAPYCALDMADFEFEQMETDALGIDEXG 588
Db 462 PGCGFTPHDSAPYCALDMADFEFEQMETDALGIDEXG 499
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Search completed: April 15, 2005, 14:54:00
Job time : 139 secs